

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

CORRECTED VERSION

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
9 August 2001 (09.08.2001)

PCT

(10) International Publication Number  
**WO 01/57271 A2**

- (51) International Patent Classification<sup>7</sup>: C12Q 1/68. (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (21) International Application Number: PCT/US01/00662
- (22) International Filing Date: 30 January 2001 (30.01.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
- |            |                                |    |
|------------|--------------------------------|----|
| 60/180,312 | 4 February 2000 (04.02.2000)   | US |
| 60/207,456 | 26 May 2000 (26.05.2000)       | US |
| 09/608,408 | 30 June 2000 (30.06.2000)      | US |
| 09/632,366 | 3 August 2000 (03.08.2000)     | US |
| 60/234,687 | 21 September 2000 (21.09.2000) | US |
| 60/236,359 | 27 September 2000 (27.09.2000) | US |
| 0024263.6  | 4 October 2000 (04.10.2000)    | GB |
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(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

- without international search report and to be republished upon receipt of that report
- with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

(48) Date of publication of this corrected version:  
6 December 2001

(15) Information about Correction:

see PCT Gazette No. 49/2001 of 6 December 2001, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/57271 A2

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND BT 474 CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human BT 474 cells is described. Also described are single exon nucleic acid probes expressed in the BT 474 cells and their use in methods for detecting gene expression.

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Published:

— without international search report and to be republished upon receipt of that report

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(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human BT 474 cells is described. Also described are single exon nucleic acid probes expressed in the BT 474 cells and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND BT 474  
CELLS

5 CROSS REFERENCE TO RELATED APPLICATIONS

The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S. provisional patent application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY  
20 REFERENCE THEREOF

The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file named pto\_BT474.txt, created 24 January 2001, having 11,325,593 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

30 Field of the Invention

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome-

derived single exon nucleic acid probes expressed in human BT 474 cells and single exon nucleic acid microarrays that include such probes.

5 Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had 10 been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane 20 association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

25 More recently, however, the development of high throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes 30 understanding of the basic biology of the encoded protein product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of 35 mRNA – are of greatest initial interest. This "expressed

sequence tag" ("EST") approach has already yielded vast amounts of sequence data (see for example Adams et al., *Science* 252:1651 (1991); Williamson, *Drug Discov. Today* 4:115 (1999)). For nucleic acids sequenced by this 5 approach, often the only biological information that is known *a priori* with any certainty is the likelihood of biologic expression itself. By virtue of the species and tissue from which the mRNA had originally been obtained, most such sequences are also annotated with the identity of 10 the species and at least one tissue in which expression appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot 15 be presumed; often the only *a priori* biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing 20 approaches – and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species – there is an increasing need for methods that rapidly and effectively permit the functions of nucleic 25 sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and 30 apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, *Science* 35 280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),

there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears  
5 the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found  
10 by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST  
15 sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of  
20 the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and  
25 most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function  
30 difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al.,  
35 *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et

al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al., *Ismb* 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known,  
5 however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence.

Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

10 Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may  
15 need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the  
20 expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in  
25 Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books  
30 Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or  
35 from the construction of "problem specific" libraries

targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes 5 for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of 10 yeast nuclear genes, approximately 95% however, are single exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally 15 been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the breast are a significant cause of human morbidity and mortality. Increasingly, genetic 20 factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the breast, for the most part these disorders are believed to have 25 polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the human breast, particularly those diseases with polygenic etiology.

30 Summary of the Invention

The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional 35 information derived from genomic sequence. The present

invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel 5 genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids 10 identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single 15 exon nucleic acid probes for measuring gene expression in a sample derived from human breast, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 5,205 or a complementary sequence, or a portion of such a sequence.

20 By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of 25 said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality 30 of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single 35 exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 10,317 or a complimentary sequence, or a 5 portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, 10 preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 15 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is 20 preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

25 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane 30 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, 35 polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is  
5 provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of  
10 amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

15 In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon  
20 probes that include specifically-hybridizable fragments of SEQ ID Nos., 5,206 - 10,317, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 5,205.

25 Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human breast which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 -  
30 5,205 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human breast.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a  
35 nucleotide sequence as set out in any of SEQ ID NOS.: 5,206

- 10,317 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human breast  
5 which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOS.: 10,318 - 15,438 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human breast.

10 Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15,  
15 suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

20 In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

25 Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

30 In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3  
35 and Cy5 although other suitable dyes will be known to those

skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and  
5 bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is  
10 provided an amplifiable nucleic acid composition,  
comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

15 wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human Breast, comprising:

20 contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human Breast; and then

25 measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

30 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are  
35 derived from mRNA from the Breast of said eukaryote, said

probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the 5 invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

10 identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using 15 hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single 20 gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 10,317 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is 25 provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 5,206 - 10,317, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any 30 of SEQ ID NOS.: 1 - 5,205.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 10,318 - 15,438.

35 Accordingly in a eleventh aspect of the invention

there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 10,318 - 15,438, or fragment thereof.

In another aspect, the invention provides means 5 for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated 10 sequence.

#### Detailed Description of the Invention

##### 15 Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately 20 detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach 25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1) (suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the 30 term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner 35 et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000);

in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid 5 microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution 10 phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the 15 sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

20 As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop 25 codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

30 As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

35 As used herein, the term "peptide" refers to a

sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS... The codons 5 encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a 10 nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present 15 within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions"; it is 20 meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least  $10^7$ , 25 preferably at least  $10^8$ , more preferably at least  $10^9$  liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display 30 of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

35 As used herein, a "Mondrian" means a visual

display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

5

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and 10 examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in 15 meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

20 FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

25 FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

30 FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

35 FIG. 7 is a pictorial representation of the

expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 ( $1 \times 10^{-30}$ ) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than 1e-30 ( $1 \times 10^{-30}$ ) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

25 Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than

human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C. briggsii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

5        Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, 10 encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing 15 somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which 20 relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

25       Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic 30 assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

35       The subset of sequences output from process 300

is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

5        Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by  
10 incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for  
15 incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process  
20 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output  
25 from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational  
30 substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.  
35 Often, data will be stored after each, or at least a

plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to 5 process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be 10 identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction 15 analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of 20 sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend 25 upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the 30 sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in 35 subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40 kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence,

either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic,  
5 temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts  
10 that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST  
15 and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

20 If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the  
25 database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to  
30 report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional  
35 preprocessing 24, suitable and specific for the desired

analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as 5 processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis.

10 Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

15 Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using 20 programs well known in the art, such as CROSS\_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified 25 algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can 30 be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the 35 undesired sequence as, for example, by converting the

specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence,  
5 leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered  
10 occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

15 Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived  
20 from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the  
25 input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25,  
30 where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after  
35 transcription into mRNA, regulating message splicing after

transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X 5 chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, 10 for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described 15 become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene 20 prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and 25 GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For 30 the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 35 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase 5 reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

10 Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to 15 process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report 20 consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% 25 of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

30 Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process 35 can be repeated on the same input sequence, or subset

thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence,  
5 but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done  
10 in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional  
15 assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental  
20 verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the  
25 species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

30 Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify  
35 and select those ORFs that appear most likely successfully

to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that 5 subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, 10 reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

15 The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

20 As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The 25 combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In 30 particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

35 Putative ORFs as predicted by a consensus of gene

calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is 5 conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) 10 sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 15 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more 20 effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 25 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs 30 predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at 35 amplifying pieces of such ORFs is low, and that such

putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been

obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology 5 : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4<sup>th</sup> edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 10 2<sup>nd</sup> edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material 15 flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the 20 absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial 25 advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support 30 substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

35 Typically, the support substrate will be glass,

although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 5 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even 10 spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached 15 covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

20 Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources 25 (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays 30 typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 35 32 *E. coli* genes suffice to provide a robust measure of

background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural 5 nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the 10 immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, 15 the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed 20 using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using 25 nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid 30 probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For 35 example, each standard microscope slide can include at

least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

5        Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as 10 is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays 15 described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) 20 those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, 25 it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, 30 R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, 35 shown herein to represent only a fraction of expressed

genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message 5 successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression 10 measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences 15 that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, 20 optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor 25 cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from 30 genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST 35 approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

5 As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a  
10 spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention  
15 lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T,  
20 where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical  
25 derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the  
30 probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from  
35 genomic DNA. Typically, therefore, at least about 50, 60,

70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage.

5 Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including 10 probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

15 As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes 20 disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific 25 primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the 30 genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even 35 smaller amount of nonspecific sequence that would

contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the

probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-  
5 derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure  
10 tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

15 Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons  
20 for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic  
25 and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn  
30 from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

35 The genome-derived single exon microarrays of the

present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

5       Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization  
10 results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

In contrast, the longer probe length of the  
15 genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or  
20 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

25     A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound  
30 noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large  
35 percentage differences in the theoretically optimum

stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the 5 range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the 10 quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present 15 substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* – that is, only about 4 20 - 5% – have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons 25 on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm 30 expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% 35 of protein-encoding genes have introns. In preferred

embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about 5 one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present 10 invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, 15 through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA 20 sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single 25 cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased 30 commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a 35 fluorophore (fluorochrome; fluor; fluorescent dye); the

reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes 5 prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned 10 using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain 15 of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for 20 subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention 25 provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well 30 of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher 35 density arrays, such as are provided by microtiter plates

having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-  
5 noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each  
10 probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second,  
15 different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be  
20 packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a  
25 genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the  
30 genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation  
35 information, such as gene expression data. Such recordable

media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in 5 international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should 10 be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and 15 characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic 20 sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected 25 of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, 30 SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query - 35 including information on identical sequences and

information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence – can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200,  
5 process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such  
10 annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or  
15 by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

20 The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the  
25 information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively  
30 described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an  
35 annotated sequence, representation of individual

nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention 5 herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian 10 visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of 15 rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically – for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 – or through user intervention, 20 as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession 25 number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is 30 anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual 35 display 80 is used as a graphical user interface to

computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

5           Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle  
10 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach  
15 identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of  
20 horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the  
25 functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or  
30 approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from  
35 GRAIL or GRAIL II, rectangles 83b can represent the results

from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method 5 and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to 10 report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where 15 display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by 20 pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 25 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as 30 many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. 35 However, the increased visual complexity occasioned by such

display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

5 Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted 10 functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the 15 results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function 20 by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is 25 protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe 30 immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

35 Rectangle 87 is used to present the results of

bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as

can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of 5 expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which 10 often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right 15 borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of 20 rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, 25 individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the 30 spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such 35 relative expression (expression ratios) and absolute

expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

### 30 Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present

invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of 5 single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present 10 invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon 15 microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 5,205 of these ORFs in BT 474 cells.

The BT474 cell line is a human mammary ductal carcinoma cell line that is tumorigenic in nude mice. It was isolated from a solid, invasive ductal carcinoma of the breast, Lasfargues et al., J. Natl Cancer Inst. 61(4):967-78 (1978), and is epithelial and neoplastic. The cell line 25 grows as adherent patches of epithelial cells with compact, multilayered colonies, rarely become confluent.

The cell line is aneuploid human female (X0 usually), with most chromosome counts in the hypertetraploid range. Several chromosomes (N11, N13, and N22) are absent, and 30 others are clearly under-represented (N9, N14, and N15) with respect to the other normal chromosomes. Chromosome N7 tends towards over-representation in several karyotypes. Some of the missing normal chromosomes are represented by their involvement in the nine stable marker chromosomes.

As would immediately be appreciated by one of skill in

the art, each single exon probe having demonstrable expression in BT 474 cells is currently available for use in measuring the level of its ORF's expression in breast cells.

5           Diseases of the breast are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been  
10 identified as causative for some diseases of the breast, for the most part these disorders are believed to have polygenic etiologies.

For example, according to the American Cancer Society (ACS), carcinoma of the breast is the second most common cancer in women and, after lung cancer, is the second deadliest. The ACS estimates that in the U.S. there occurred 182,800 new cases of malignant breast cancer in 2000, and about 40,800 deaths from the disease. Although incidence of breast cancer is said to have declined, the  
20 disease clearly continues to represent a serious risk to the health and life of American women. Indeed, about one in nine U.S. women will develop breast cancer in her lifetime, and at present mortality rates, about a third of such women will eventually die from the disease.

25           A variety of factors are known to increase the risk of breast carcinoma. Sex is one: breast cancer in men is rare. Age is another: as women age, their risk for developing breast cancer increases, a 70 year old woman having three times the risk of developing cancer and five  
30 times the risk of dying from the disease as compared to a 40 year old woman. Most breast cancers occur after age 50, although in women with a genetic susceptibility, breast cancer tends to occur at an earlier age than in sporadic cases. Reproductive and menstrual history are also known  
35 to affect risk, with risk increasing with early menarche

and late menopause, and is reduced by early first full term pregnancy. Additional risk factors, oft-times termed "lifestyle factors", include weight gain, obesity, fat intake, alcohol consumption, and level of physical  
5 activity.

That genetic factors underlie the etiology of breast cancer is suggested by the approximately two-fold increased risk for development of breast cancer by women with a first-degree relative who has also developed breast  
10 cancer. After gender and age, a positive family history is the strongest known predictive risk factor for breast cancer. Genetic linkage analysis in families with high rates of inherited cancer have facilitated the identification of several genes in which mutations can be  
15 shown to contribute substantially to the development and progression of breast cancer, including BRCA1, BRCA2, p53, and PTEN/MMAC1. Further study has made clear, however, that these genes are not alone sufficient to explain all genetic contributions to breast cancer.

20 For example, BRCA1 appears to be responsible for disease in up to 90% of families with both breast and ovarian cancer, but in only 45% of families with multiple cases of breast cancer without occurrence of ovarian cancer. And mutations in BRCA2, localized to the long arm  
25 of chromosome 13, are thought to account for only approximately 35% of multiple case breast cancer families. Furthermore, despite the strong correlation between germline mutations in BRCA1 or BRCA2 and development of breast cancer, only weak connections have been made between  
30 these genes and sporadic breast cancer.

Epistatic effects of BRCA1 and BRCA2 mutations on other genetic loci, only some of which have been identified, have been postulated to account for some of the deleterious effects of mutations in these two genes.

35 Thus, mutations in p53 seem to be much more

frequent in BRCA1 breast cancers (20/26) and somewhat more frequent in BRCA2-associated breast cancers (10/22) than in grade-matched sporadic cancers (7/20). BRCA mutation-associated cancers contain p53 mutations not typically found in sporadic breast cancer, and 12 individual hereditary breast cancers have been shown to contain more than a single p53 mutation. Mutations of BRCA1 and BRCA2 may thus confer a "mutator" phenotype permitting the accumulation of genetic abnormalities, with p53 inactivation selected during tumor progression.

Additionally, genome-wide screening for chromosomal gains or losses in breast cancers harboring BRCA1 or BRCA2 mutations demonstrated more regions that were amplified or deleted compared to controls, suggesting a generalized increase in large-scale genomic instability. Chromosomes 5q, 4q, and 4p had very frequent loss of heterozygosity in BRCA1 tumors, while BRCA2 tumors were characterized by losses at 13q (near the BRCA2 locus itself) and 6q, and chromosomal gains at 17q (outside of the HER2/neu locus) and 20q.

Mutations of other genes have also been implicated in susceptibility to development or aggressiveness of breast cancer. For example, germline mutations in the ATM gene, localized to chromosome 11q22-23, result in an increased risk of breast cancer among female heterozygote carriers with an estimated relative risk of 3.9 to 6.4; it is unclear, however, if mutations in the ATM gene itself contribute to breast cancer.

Normal allelic variation in a variety of genes, as opposed to frank mutation, may also influence susceptibility to developing breast carcinoma and the propensity for the disease to progress. Such polymorphisms may thus explain why particular women or ethnic groups who do not otherwise bear mutations in genes

known to be linked to breast cancer are at greater risk, especially in the context of exposure to environmental agents and other nonhereditary risk factors.

Polymorphically expressed genes may code for enzymes that 5 metabolize estrogens or detoxify drugs and environmental carcinogens.

For example, molecular epidemiologic studies of cancer of the breast have examined associations with p450 cytochrome genotypes including CYP1A1, CYP2D6, and CYP17.

10 The CYP1A1 gene, located on chromosome 15q, encodes the enzyme aryl hydrocarbon hydroxylase (AHH), present in breast tissue, and which catabolizes polycyclic aromatic hydrocarbons and arylamines. AHH is strongly inducible, i.e., greater enzymatic activity is seen with greater 15 exposure to substrates. AHH catalyzes the monooxygenation of polycyclic aromatic hydrocarbons to phenolic products and epoxides that may be carcinogenic. AHH is also involved in the conversion of estrogen to hydroxylated conjugated estrogens such as 2-hydroxyestradiol.

20 Three polymorphisms in the CYP1A1 gene have been identified: an MspI RFLP of the 3' end of the gene (MspI); an adenine to guanine mutation in exon 7, causing an isoleucine to valine substitution (Ile-Val); and a polymorphism of the CYP1A1 gene identified among Negroids. 25 The frequencies of the MspI and Ile-Val polymorphisms vary considerably by race, being higher among Japanese and Hawaiian populations as compared with Caucasians and Negroids.

The CYP2D6 gene is located on chromosome 22q and 30 encodes the enzyme debrisoquine hydroxylase, which metabolizes a variety of drugs and other xenobiotics. Like other polymorphically expressed p450 enzymes, it may activate procarcinogens or, conversely, detoxify carcinogens. A number of alleles have been characterized 35 at the CYP2D6 locus. The "poor metabolizer" phenotype

(CYP2D6 mutant/mutant genotype), which is rare in Asians, occurs in about 5% to 10% of Caucasians and in 2% of Negroids.

As another example, the N-acetyl transferase-1 (NAT1) and N-acetyl transferase-2 (NAT2) genes are located on chromosome 8q. Allelic variation in the NAT genes may contribute to variation in populations as to the susceptibility of individuals to development of breast carcinoma, particularly in the context of exposure to compounds present in tobacco. NAT2 detoxifies or, conversely, activates aromatic amines found in tobacco smoke such as 4-aminobiphenyl. Both phenotypic assays and genotypic assays for NAT2 can be used to classify individuals as rapid or slow acetylators. Genetic variants of the NAT2 gene have been cloned and 6 alleles at this locus have been identified: the F1 allele confers the fast acetylator phenotype. The distribution of NAT1 and NAT2 alleles differs widely between racial and ethnic groups.

As yet another example, the glutathione S-transferase-M1 (GSTM1) gene is located on chromosome 1 and the gene for glutathione S-transferase-T1 (GSTT1) is located on chromosome 11q. A glutathione S-transferase-P1 (GSTP1) gene has also been identified. Glutathione S-transferases detoxify a variety of carcinogens and cytotoxic drugs (for example, benzo(a)pyrene, monohalomethanes such as methyl chloride, ethylene oxide, pesticides, and solvents used in industry) by catalyzing the conjugation of a glutathione moiety to the substrate. Allelic variation in the glutathione-S-transferase genes may contribute to variation in populations as to the susceptibility of individuals to development of breast carcinoma, particularly in the context of exposure to environmental toxins. Individuals homozygous for deletions in the GSTM1, GSTT1, or GSTP1 genes may have a higher risk of cancer of the breast and

other sites because of their impaired ability to metabolize and eliminate carcinogens.

GSTM1 is polymorphically expressed and 3 alleles at the GSTM1 locus have been identified: GSTM1-0 (homozygous deletion genotype), GSTM1a, and GSTM1b. The null allele (GSTM1-0) is present in about 38% to 67% of Caucasians and 22% to 35% of Negroids. GSTM is not expressed in breast tissue at high levels. Two functionally different genotypes at the GSTT1 locus have been described: GSTT1-0 (homozygous deletion genotype) and GSTT1-1 (genotypes with 1 or 2 undeleted alleles). A polymorphism of the GSTP1 gene, A313G (changing codon 105 from Ile to Val), has been identified. The GSTT1-0 allele has been associated with accelerated age of first breast cancer diagnosis as compared with the GSTT1-1 allele.

Many other genes have been suggested to be involved in the development and/or progression of breast cancer, either as a result of gain of function or loss of function mutations, or as a result of normal allelic variation within different populations. A nonexhaustive list of such genes, each followed by the gene's chromosomal location, if known, follows: AMPH 7p14-p13; AMPHL (BIN1 , SH3P9) 2q14; API4 (survivin, SVV) 17q25(?); ARHA (ARH12, RhoA) 3p21.3; ARHC (RhoC) 1p21-p13; ATM (ATA, ATC) 11q22.3; BAG1 9p12; BARD1 2q34-q35; BCAR1 16q23.1; BCAR2; BCAR3 (NSP2); BCAS1 (NABC1, AIBC1) 20q13.2-q13.3; BRCA1 17q21; BRCA2 13q12.3; CCND1 (D11S287E, Cyclin D, PRAD1) 11q13; CD44 (MDU3, HA, MDU2) 11pter-p13; CD9 (p24, MIC3, BA2) 12p13; CDKN1B (KIP1, P27) 12p13; CDKN2A (P16, INK4A, MTS1) 9p21; COMT 22q11.2; COT (MAP3K8, TPL-2, EST) 10p11.2; CSK (c-src) 15q23-q25; CTSD (CPSD) 11p15.5; CYP17 10q24.3; CYP19 15q21.1; CYP1A1 (CYP1) 15q22-q24; CYP1B1 (GLC3A) 2p22-p21; EFNB2 (EPLG5, LERK5, ephrin-B2) 13q33; EIF3S6 (INT6) 8q22-q23; EIF4E (EIF-4E) 4q21-q25; EMS1 11q13; ERBB2 (HER2, NEU) 17q11.2-q12; ERBB3 (HER3) 12q13; ESR1 (ESRA) 35

6q25.1; ESR2 (ESRB, ERBeta) 14q; FGF8 (AIGF)  
10q24; GSTM1 (GST1, MU) 1p13.3; GSTP1 (FAEES3, GST3, PI)  
11q13; GSTT1 22q11.23; HRAS 11p15.5; HSPB1 (HSP27) 7q;  
HSPCA (HSP90A, HSPC1); HSPCB (HSP90B, HSPC2) 6p12; IGF1  
5 12q22-q24.1; IGF1R (JTK13) 15q25-q26; IGF2 11p15.5; IL6  
(IFNB2) 7p21; ING1 13q34; KISS1 (KISS-1) 1q32; KLK3 (PSA,  
APS) 19q13; LASP1 (MLN50) 17q11-q21.3; LIBC 6q22; MAP2K4  
(MKK4, SEK1, JNKK1) 17p11.2; MKI67 (Ki-67) 10q25-qter;  
MMP11 (STMY3, STR3) 22q11.2; MMP2 (CLG4A, CLG4, GELA)  
10 16q13; MUC1 (PUM, PEM) 1q21; MYC (CMYC, C-MYC) 8q24.12-  
q24.13; NOTCH4 (INT3, NOTCH3) 6p21.3; PCNA 20p12; PI5  
(maspin) 18q21.3; PLAU (uPA, URK) 10q24; PSEN2 (D21S21,  
HPS2, BCEI) 21q22.3; RARB (NR1B2, HAP) 3p24; RB1 (Rb)  
13q14.2; S100A4 (MTS1, P9KA, metastasin) 1q21; SLC22A1L  
15 (BWSCR1A, ORCTL2, IMPT1) 11p15.5; SNCG (BCSG1) 10q23.2-  
q23.3; SRD5A2 2p23; STIP1 (HSP70) 11?; STK11 (LKB1, PJS)  
19p13.3; TFAP2A (AP2, AP2TF) 6p24; TFAP2B (AP2B) 6p12;  
TFAP2C 20q13.2; TFF1 (D21S21, BCEI) 21q22.3; TGFBR2 3p22;  
TIMP2 17q25; TP53 (p53, P53) 17q13.1; TPD52 (D52) 8q21;  
20 TPD52L1 (D53, hD53) 6q22-q23; TSG101 11p15.2-p15.1.

The etiology of non-cancerous disorders of the breast may also involve genetic factors. Such disorders include disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease, and non-carcinoma tumors.

Disorders of development of the breast include supernumerary nipples or breasts; accessory axillary breast tissue; congenital inversion of the nipples; and macromastia.

30 Inflammatory diseases of the breast include acute mastitis; periductal mastitis, also called recurrent subareolar abscess and squamous metaplasia of the lactiferous ducts; mammary duct ectasia; fat necrosis; and granulomatous mastitis, including granulomatous lobular  
35 mastitis. Systemic granulomatous diseases that can affect

the breast include Wegener granulomatosis and sarcoidosis.

Proliferative breast diseases include epithelial hyperplasia; sclerosing adenosis; and small duct papillomas. Non-carcinoma tumors include stomal tumors including fibroadenoma and phyllodes tumor, and sarcomas that include angiosarcoma, rhabdomyosarcoma, liposarcoma, leiomyosarcoma, chondrosarcoma and osteosarcoma. Other breast tumors include epithelial cell tumors including large duct papillomas.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human breast, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be expressed at detectable levels in human breast cancer cells, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, diagnosis, grading, and/or staging of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known to be characteristic of a given breast disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the patient's breast to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed

in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of breast disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human breast. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the BT 474 cells has been demonstrated are useful for both measurement in the breast and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was

measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

5         Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

10         The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

15         Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

20         Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell 25 Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999)); 30 35 Voehringer et al., "Gene Microarray Identification of Redox

and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., 10 "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway 35 of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents – whether in lead compound discovery or in subsequent screening of lead compound derivatives – the inability of the agent to alter 5 a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile 10 and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

15 Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-  
20 derived single-exon probes known to be expressed in BT 474 cells.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity 25 sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA 30 complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes 35 can include phosphorothioates, methylphosphonates,

morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, inter alia, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO '97/19193 and WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe

composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 5,206 - 10,317, respectively, for probe SEQ ID NOS. 1 - 5,205. The minimum amount of ORF required to be included in the probe of the present invention in order to

provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 5,206 - 10,317 individually by routine experimentation using standard high stringency  
5 conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl 10 poly(dA), 0.2 µg/µl human c<sub>ot</sub>1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high 15 stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in 20 temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of 25 other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

30 Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are 35 maximally about 5 kb will be used, more typically no more

than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly 5 translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further 10 be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have 15 sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or 20 both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution 25 hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as  $^3\text{H}$ ,  $^{32}\text{P}$ ,  $^{33}\text{P}$ ,  $^{35}\text{S}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR<sup>®</sup>

30 Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or 35 enhanced chemiluminescent detection; labels suitable for

ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for 5 hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is 15 obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, 20 different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen 25 for the common attribute of expression in the human BT 474 cells.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell 30 type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF 35 by (i) screening of cDNA libraries; (ii) rapid

amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to 5 provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome- 10 derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human BT 474 cells. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group 15 consisting of SEQ ID NOS.: 1 - 5,205.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of 20 probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the 25 same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with 30 a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to 35 their utility as probes of gene expression, particularly as

probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 5,205 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 5,206 - 10,317, that encodes a 5 protein domain. Thus, each of SEQ ID NOS. 1 - 5,205 can be used, or that portion thereof in SEQ ID NOS. 5,206 - 10,317 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

10            Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; 15 Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment 20 and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis 25 (Oxford Chemistry Primers, No 7), Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention 30 to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 5,206 - 10,317. Such amino acid sequences are set out in SEQ ID NOS: 10,318 - 15,438. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, 35 can be conjugated to a carrier protein and used to generate

antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

5

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

- 10 Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

Bioinformatics Results

15 All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

20 After masking repetitive elements using the program CROSS\_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden 25 Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

30 The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of 35 genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed.

- 5 That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two 10 criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb 15 window.

#### PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, 20 as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino- 25 modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per 30 gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 35 5' primer, and a second, different, additional sequence was

commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences 5 also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the 10 universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, 15 CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band 20 appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF 25 length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 30 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 35 500 bp, it was found that long exons had a higher PCR

failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp,  
5 constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and  
10 reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear,  
15 but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with  
20 hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression  
25 ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which  
30 were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average  
35 hybridization signal of which was used as a measure of

background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

5 One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than  $1 e^{-100}$ ) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA  
10 (BLAST E values from  $1 e^{-5}$  to  $1 e^{-99}$ ). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were  
15 then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

20

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			Function Predicted from Comparative Sequence Analysis
Total	V6 chip	V7 chip	
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase

36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

#### EXAMPLE 2

#### Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 20 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA<sup>+</sup> mRNA performed using 1 µg oligo(dT)<sub>12-18</sub> primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After

snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100 $\mu$ M dATP, 100  $\mu$ M dGTP, 100  $\mu$ M dTTP, 50  $\mu$ M dCTP, 50  $\mu$ M Cy3-dCTP or Cy5-dCTP 50  $\mu$ M, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5.

10 Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30  $\mu$ l hybridization solution containing 50% formamide, 5X SSC, 0.2  $\mu$ g/ $\mu$ l poly(dA), 0.2  $\mu$ g/ $\mu$ l human c<sub>o</sub>t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 20 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, 35 both signal and expression ratios (the latter hereinafter,

"expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when  
5 signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is  
10 presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all  
15 tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue  
20 or cell type. Of the gene elements showing significant signal — where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) — 39% (991) were expressed in all 10 tissues. The next most common class  
25 (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

30 FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative  
35 expression of a clone in that tissue is indicated at the

respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results 5 returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant 10 homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective 15 tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more 20 "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested 25 tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence 30 databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

35 Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The 5 data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (designated "unknown") upon query of existing EST, NR and SwissProt databases, and 10 shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than 1e-30 ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

15 As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

20 However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes 25 will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and 30 further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

#### Verification of Gene Expression

To ascertain the validity of the approach 35 described above to identify genes from raw genomic

sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis  
5 of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene  
10 expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300\_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734\_1 was shown by microarray experiment to be present  
15 in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

20 Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the  
25 observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes  
30 from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

35 For this latter analysis, sequences that showed

high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, 5 approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

10 Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain.				
Microarray Sequence Name	Normal Signal	Expressi on Ratio	Homology to EST present	Gene Function as described by GenBank in GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca <sup>2+</sup> binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a

				synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein

				Phosphatase PP2A, neuronal/ downregulates activated protein kinases
--	--	--	--	---

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be 5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca<sup>2+</sup> binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097  
10 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 15 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed 20 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless 25 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to 30 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2

were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 $\alpha$  (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH	
---	--

	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ± 0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±
Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

### EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the

information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the 5 paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate 10 synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully 15 identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be 20 from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show 25 identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. 30 Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very 35 good. A novel gene is also found from 86.6 kb to 88.6 kb,

upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following 5 colors indicate a known gene (top to bottom): red = kallistatin protease inhibitor (P29622); purple = plasma serine protease inhibitor (P05154); turquoise =  $\alpha 1$  anti-chymotrypsin (P01011); mauve = 40S 10 ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring 15 Human Gene Expression

The protocols set forth in Examples 1 and 2, supra, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique 20 exons in the human genome that could be shown to be expressed at significant levels in BT 474 cells.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon 25 microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the 30 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 5,205 single exon probes, each fragment corresponding to an extension product from one of 35 the two amplification primers.)

The structures of the 5,205 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 5,205. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 5,206 - 10,317, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than 10 one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give 20 a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the 25 population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining 30 control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) 35 are eliminated. Spots with such high signals are considered

to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

5 The mean + 3x the standard deviation (mean +  
5 (3\*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any  
10 signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5.  
Example 5 presents the subset of probes that is significantly expressed in the human BT 474 cells and thus  
15 presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human BT 474 cells.

The sequence of each of the exon probes identified by SEQ ID NOS.: 5,206 - 10,317 was individually  
20 used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were  
25 scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted  
30 in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective  
35 probes (by "AMPLICON SEQ ID NO.:" and additionally by the

SEQ ID NO.: of the exon contained within the probe: "EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be 5 expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the 10 name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide 15 sequences. These are set out as PEPTIDE SEQ ID NOS.: . The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs 20 are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the 25 exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all 30 of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from each of the three queried databases.

Table 4 further lists, for each probe, a portion 35 of the descriptor for the top hit ("Top Hit Descriptor") as

provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about 1e-05 and 1e-100), the descriptor reveals the likely function of the  
5 protein encoded by the probe's ORF.

Using BLAST E value cutoffs of 1e-05 (i.e.,  $1 \times 10^{-5}$ ) and 1e-100 (i.e.,  $1 \times 10^{-100}$ ) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of 1e-30 was used as  
10 the boundary when only two classes were to be defined for analysis (unknown,  $>1e-30$ ; known  $<1e-30$ ) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about 1e-100 — which is  
15 probative evidence that the query sequence has previously been shown to be expressed — the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even  
20 the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent  
25 a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOS.: 1 - 5,205) and probe exon (SEQ ID NOS.: 5,206 - 10,317, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

30 (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST  
35 query of the EST database, with accession number and BLAST

E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

5 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

10 EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human BT 474 cells

15 Table 4 (214 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human BT 474 cells, human epithelial cells isolated from a solid, invasive ductal carcinoma of the breast and available commercially from American Type Culture Collection under 20 catalogue number HTB-20.

Page 1 of 214  
 Table 4  
 Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
449	56117	10762	4.28				
850	60440	11211	7.04				
1047	61688		2.6				
1306	64310	11611	12.4				
1627	6765	11949	2.17				
1847	6776	11867	4.24				
1738	6886	12069	1.89				
1761	6887	12083	1.25				
1787	6893	12100	6.38				
1838	70117	12238	0.86				
1880	7097	12328	1.31				
2147	7261	12508	1.73				
2256	7366	12622	2.11				
3167	8318	13480	2.71				
3431	8573	13733	1.47				
3500	8641	13807	11.21				
3547	86888		0.74				
3634	8773	13929	0.83				
3919	9045		0.92				
4169	9285	14433	1.84				
4235	8360	14492	6.08				
4265	9380	14512	0.87				
4266	9280	14613	0.87				
4314	9438		1.18				
4803	8916	16067	1.18				
5028	10128	15257	5.94				
5037	10139	15271	1.43				
2627	7726	12879	2.67	8.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (pM/M) envelope glycoprotein (E) polyprotein mRNA, partial cds
2627	7726	12980	2.67	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (pM/M) envelope glycoprotein (E) polyprotein mRNA, partial cds
2889	8043	13207	2.89	9.4E+00	AB043785.1	NT	Mus musculus A13 gene (or orthologous), complete cds
439	6608	10752	2.08	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
2947	8101	13265	2.66	7.2E+00	L12051.1	NT	Lycopersicum esculentum Mill. G17 ace (SAR2) mRNA, complete cds

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accesion No.	Top Hit Database Source	Top Hit Descriptor
2847	8101	13263	2.68	7.2E+00	L12051.1	NT	Lycoperdon esculentum Mill. GTPase (SAR2) mRNA, complete cds
3510	8851		0.9	8.8E+00	7661557	NT	Homo sapiens DESC1 protein (DESC1), mRNA
4762	8851	15014	1.25	5.3E+00	L43128.1	NT	Bacillus immunodeficiency-like virus surface envelope gene, 5' end of cds
4036	9167		10.68	4.8E+00	AF186255.1	NT	Eunice australis histone H3 (H3) gene, partial cds
287	5476	10617	2.31	4.7E+00	BF240552.1	EST_HUMAN	601876654F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:40897105
288	5476	10617	1.89	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:40897105
3257	8407	13668	1.84	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C80
3012	8168	13323	0.63	4.4E+00	BF530883.1	EST_HUMAN	602072585F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:42152845
3012	8168	13324	0.63	4.4E+00	BF530883.1	EST_HUMAN	602072585F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:42162846
3488	8827	13784	5.32	3.9E+00	BA4518.1	NT	Nabidium chitinase gene 50 for class I chitinase C
4298	9420		0.69	3.9E+00	AF056486.1	NT	Mus musculus sentinel vesicle secretion protein 88 (MSVSP88) gene, promoter region
2595	7698		1.75	3.8E+00	AE001562.1	NT	Helicobacter pylori strain J96 section 123 of 132 of the complete genome
3904	9123	14272	12.89	3.7E+00	AL161639.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
681	6763	10860	9.76	3.6E+00	AV761055 MDS Homo sapiens cDNA clone MDSBUE105	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE105
3230	8380	13540	1.12	3.6E+00	AF221538.1	NT	Cryptosporidium falls heat shock protein 70 (HSP70) gene, partial cds
1526	6853	11839	3.27	3.4E+00	AF284577.1	NT	Breviseta rapis RP85 mRNA, complete cds
600	6687	10802	1.43	3.2E+00	BA8422.1	NT	Danio rerio zp-50 POU gene
3899	5887	10802	0.81	3.2E+00	BA8422.1	NT	Danio rerio zp-50 POU gene
4698	8812	14980	1.65	3.2E+00	4502404	NT	Homo sapiens ceratoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
2789	7859	13121	1.47	3.0E+00	892384	NT	Homo sapiens hypothetical protein PR00689 (PR00689), mRNA
2008	7128	12362	1.47	2.9E+00	AE002225.2	NT	Chlamydomonas reinhardtii section 53 of 64 of the complete genome
1469	6588	11784	7.24	2.8E+00	AF188398.1	NT	Bufo calamita matutina K (mk) gene, partial cds; cholinesterase gene for cholinesterase product
1643	6771		1.64	2.8E+00	AL161652.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
229	6423	10560	13.16	2.7E+00	68758308	NT	Mus musculus peroxisome repeat gene 3 (Pbx3), mRNA
229	6423	10561	13.16	2.7E+00	68758308	NT	Mus musculus peroxisome repeat gene 3 (Pbx3), mRNA
4846	9784	14908	5.56	2.6E+00	AF058749.1	NT	Mus musculus sphingomyelin kinase (SphK1b) mRNA, complete cds
1476	6803	11788	1.77	2.5E+00	AL271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1476	6803	11789	1.77	2.6E+00	AL271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
2894	8138	13303	0.85	2.4E+00	MF24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4881	8892	16139	5.5	2.4E+00	450352	NT	Homo sapiens double 22'-like domains, alpha (DODCA) mRNA
1257	63186	11563	11.33	2.3E+00	Z45724.1	NT	Gadomesticus artificialis chain antibody gene (L3)
4083	9222		1.44	2.3E+00	AL401081.1	NT	Bos taurus partial cytb gene for cytochrome b
3992	9128	14271	1.39	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	Off-Seq ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4280	84112	14847	3.83	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4280	84112	14548	3.83	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
568	7894	10881	6.54	2.1E+00	AF132681.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3676	8716		0.76	2.1E+00	AW446358.1	EST_HUMAN	U1H-B13_ek-e-0B-0-U_51 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2734650 3'
1189	6332	11501	1.31	2.0E+00	AF160527.1	NT	Homo sapiens p22Ddelta (DOKDEL) mRNA, complete cds
1189	6332	11602	1.31	2.0E+00	AF160527.1	NT	Homo sapiens p22Ddelta (DOKDEL) mRNA, complete cds
1340	6468	11649	0.86	2.0E+00	AF204927.1	NT	Oryctodinus curicus Nat-K-ATPase beta 1 subunit mRNA, complete cds
1586	67117		2.41	2.0E+00	P25582	SWISSPROT	PUTATIVE RNA METHYLTRANSFERASE SPB1
2133	7247	12482	10.19	2.0E+00	Z78278.1	NT	R.norvegicus mRNA for collagen alpha1 type I
2133	7247	12493	10.19	2.0E+00	Z78278.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4076	9209	14342	1.8	2.0E+00	AW664486.1	EST_HUMAN	h13d65x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
4076	9209	14343	1.9	2.0E+00	AW664486.1	EST_HUMAN	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
3088	82119	13371	1.67	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3097	8250	13389	1.82	1.8E+00	U04358.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (rbaA) and ATP synthase epsilon subunit (rbaE) genes, complete cds
3097	8250	13400	1.92	1.8E+00	U04358.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (rbaA) and ATP synthase epsilon subunit (rbaE) genes, complete cds
1108	6247	11410	2.95	1.7E+00	Q80114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2250	7360	12617	1.65	1.7E+00	AL168280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2363	7460	12718	0.88	1.7E+00	AL1141007.1	EST_HUMAN	ox43h3x1 Stcres_NHMPU_51 Homo sapiens cDNA clone IMAGE:1678137 3'
4438	9557	14689	0.76	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2028	7145	12385	4.48	1.6E+00	AF168339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2037	7155	12394	2.2	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2041	7168	12388	1.13	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
2260	7370		1.15	1.6E+00	X98373.1	NT	B.napus gene encoding endo-polysaccharidase
2830	8084	13251	1.66	1.6E+00	W58426.1	EST_HUMAN	2z23f01.71 Scares, fetal heart NCI CGAP cDNA clone IMAGE:341669 5' similar to
4006	9138		5.78	1.6E+00	BF570077.1	EST_HUMAN	gb:J23805 NACETYLACTOSAMINE SYNTHASE (HUMAN);
4329	9451	14584	1.52	1.6E+00	AF165827.1	NT	Homo sapiens SNF2-like protein (SMARCA8) mRNA, complete cds
4329	9451	14585	1.62	1.6E+00	AF165827.1	NT	Homo sapiens SNF2-like protein (SMARCA8) mRNA, complete cds

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit No.	Top Hit Database Source	Top Hit Descriptor	
5087 10169	15303	2.59	1.6E+00	Y11344.1	NT	Mus musculus ST6GALNACII gene, exon 2		
5087 10169	15304	2.69	1.6E+00	Y11344.1	NT	Mus musculus ST6GALNACII gene, exon 2		
31 5242	10353	3.73	1.6E+00	U83448.1	NT	Rattus norvegicus Jun dimerization protein 2 (Jdp-2) mRNA, complete cds		
230 5424	10502	2.47	1.6E+00	AEG022201.2	NT	Chlamydomonas reinhardtii ARS9, section 32 of 94 of the complete genome		
618 6778		2.04	1.6E+00	6752861	NT	Mus musculus a disintegrin and metalloprotease domain (ADAM) 15 (metaradin) (Adam15), mRNA		
2387 7483	12748	1.38	1.5E+00	AJ31402.1	NT	Poletia virus A RNA complete genome, isolate U		
2486 7590	12839	1.38	1.5E+00	6878350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA		
3116 7493	12746	2.41	1.5E+00	AJ31402.1	NT	Poletia virus A RNA complete genome, isolate U		
3386 88011	13869	0.8	1.6E+00	AEG01846.1	NT	Dermococcus radiosus R1 section 82 of 228 of the complete chromosome 1		
28 6239	10354	1.12	1.4E+00	7681985	NT	Hamo sapiens DKFZP_586M0122 protein (DKFZP_586M0122), mRNA		
28 6239	10355	1.12	1.4E+00	-	7681985	NT	Hamo sapiens DKFZP_586M0122 protein (DKFZP_586M0122), mRNA	
2316 7423		6.48	1.4E+00	U87022.1	NT	Ovis aries prion protein genes, complete cds		
2630 7728	12884	1.41	1.4E+00	X74483.1	NT	Human papillomavirus type 7 genomic DNA		
2735 7828	13083	227.51	1.4E+00	AFO84584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds		
2735 7828	13084	227.51	1.4E+00	AFO84584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds		
3316 8462		0.8	1.4E+00	54591733	NT	Hamo sapiens Maf4 homolog (Maf4) mRNA		
4659 8677		1.57	1.4E+00	Bf681547.1	EST HUMAN	602168687F1 NIH MGSC 83 Hamo sapiens cDNA clone IMAGE:4287658 6'		
5031 10133	16203	0.92	1.4E+00	Y18213.1	NT	Hamo sapiens putative psf1/HBA pseudogene for hair keratin, exons 2 to 7		
5659 5733		1.6	1.3E+00	Z73840.1	NT	Manucciobius genes encoding 4-Dihydronethyldisporamide dehydrogenase		
903 60153	11223	2.68	1.3E+00	AJ271192.1	NT	Cantharidellus sp. partial 25S rRNA gene, isolate Tibet		
1130 6267		23.68	1.3E+00	Y18213.1	NT	Hamo sapiens putative psf1/HBA pseudogene for hair keratin, exons 2 to 7		
1301 6431	11603	12.87	1.3E+00	4807988	NT	Hamo sapiens zinc finger protein 157 (ZF-22) (ZNF157) mRNA		
1301 6431	11603	12.87	1.3E+00	4807988	NT	Hamo sapiens zinc finger protein 157 (ZF-22) (ZNF157) mRNA		
1363 6492		1.49	1.3E+00	U811750.2	NT	Cole lacryma-faci dihydrolipocalin hate synthase (dpsA) gene, complete cds		
1623 6751		2.09	1.3E+00	AEG022358.2	NT	Chlamydomonas reinhardtii, section 68 of 95 of the complete genome		
2521 7628		1.26	1.3E+00	BEP86735.2	EST HUMAN	601661238R1 NIH MGSC 72 Hamo sapiens cDNA clone IMAGE:3916945 3'		
2905 8058	13227	0.74	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spn1), mRNA		
3583 8724	13882	0.82	1.2E+00	AFO16494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 65kd erythrocyte membrane protein (P95), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete >		
649 5610	10945	8.47	1.2E+00	AA676246.1	EST HUMAN	2122d08.s1 Socates fetal liver spleen_1 NF1Ls_S1 Hamo sapiens cDNA clone IMAGE:431635 3'		

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Probe Seq ID No:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
824	5977	11141	1.11	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
824	5977	11142	1.11	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
824	6977	11143	1.11	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
870	6020		1.11	1.2E+00	69724234	NT	Human sepien's hypothetical protein PRC03077 (PRC03077), mRNA
1168	6298	11484	6.19	1.2E+00	AF080246.2	NT	Elulus oliferae sepien's sepiase mRNA, complete cds
1208	6340	11610	1.88	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1208	6340	11511	1.88	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2386	7463	12719	0.88	1.2E+00	AF158495.1	NT	Human sepien's post-synaptic density 65 (DLG4) gene, complete cds
3038	8239	13388	0.88	1.2E+00	AB020681.1	NT	Human sepien's mRNA for KIAA0874 protein, partial cds
3144	8295	13483	5.63	1.2E+00	AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
3144	8295	13454	6.63	1.2E+00	AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
3270	8419		3.42	1.2E+00	PF4961	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBRE PRECURSOR
3356	8482	13649	0.68	1.2E+00	AF188740.1	NT	Human caplano LHX3 gene, Intron 2
3691	8829	13983	7.07	1.2E+00	U75902.1	NT	Mus musculus subunit-like serine protease 1 [PC (PC) gene, exons 1 to 6, partial cds]
3861	9098	14248	1.8	1.2E+00	BP378570.1	EST HUMAN	MRC0-F70175-0569300-203-908_1_F70175 Human sepiens cDNA
4274	9482	13849	1.07	1.2E+00	AF188740.1	NT	Human sepiens LHX3 gene, Intron 2
4450	9569		1.82	1.2E+00	M870650.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4497	8816	14767	1.04	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4534	8852	14797	1.81	1.2E+00	AF156495.1	NT	Human sepien's post-synaptic density 65 (DLG4) gene, complete cds
4692	9880		5.91	1.2E+00	Y09200.1	NT	T. plamellatum chlrophyll a/b/cobilin protein, gene, partial
4693	5631	10770	1.04	1.1E+00	DB8880.1	NT	Human mRNA for KIAA0277 gene, partial cds
1773	6859	12107	1.22	1.1E+00	AV885353.1	EST HUMAN	Q70351_HUMAN Q12888_P53-BINDING PROTEIN 53BP1 ;
3311	8458	13820	6.79	1.1E+00	AL163213.2	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3811	8458	13621	6.78	1.1E+00	AL163213.2	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3468	8810	13776	0.7	1.1E+00	88226341	NT	Human sepiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3567	8708	13869	0.82	1.1E+00	AI808350.1	EST HUMAN	W54h11_X1_Scores_NF_1_GBC_S1_Human sepiens DNA clone IMAGE2359401 3 similar to
3689	8838	13980	1.49	1.1E+00	AE0038886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3698	8838	13950	1.48	1.1E+00	AE0038886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3705	8932		0.73	1.1E+00	XP653174.1	NT	H. parvula endofollicular lymphocyte (lymphM(C)), hphM(C), hphR and monB genes
3916	9051	14210	1.01	1.1E+00	88226341	NT	Human sepien's hypothetical protein FLJ10748 (FLJ10748), mRNA
3995	9129	14273	0.79	1.1E+00	8765205	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Psmb7), mRNA
4189	8915		6.62	1.1E+00	5836331	NT	Runciconis complete mitochondrial genome
4655	9772		1.78	1.1E+00	U349892.1	NT	Carcharhinus plumbeus Ig lambda light chain gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4978	10088	15221		3.51	1.1E+00 U18468.1	NT	African swine fever virus complete genome
85	6304			2.28	1.0E+00 U23808.1	NT	Xenopus laevis nodospin genes, complete cds
109	6313	10452		1.96	1.0E+00 D88426.1	NT	Cavia cobaya mRNA for centrifugal factor genes, complete cds
417	6585			2.14	1.0E+00 AB021684.1	NT	Canis lupus mRNA for 26S rRNA, 5S rRNA, 5.8S rRNA and 28S rRNA
674	5738	10885		2.43	1.0E+00 AF1251660.1	NT	Macaca fasciata polymorphic genes for 26S rRNA, 5S rRNA, 5.8S rRNA and 28S rRNA
678	6834	10874		8.37	1.0E+00 AL1683218.2	NT	Grindelia lignina mRNA for homeodomain transcription factor (iso gene)
677	6835			1.31	1.0E+00 AF-125894.1	NT	Homo sapiens chromosome 21 segment HS21C018
1395	7916			2.27	1.0E+00 X650416.1	NT	Ardea alba mielkili-like protein MUC1 mRNA, complete cds
2459	7583	12815		1.02	1.0E+00 P48355	SWISSPROT	Vaccinia Ag8-CAM mRNA
2459	7583	12816		1.02	1.0E+00 P48356	SWISSPROT	DNA GYrase subunit B
2841	798	13154		3.78	1.0E+00 P24008	SWISSPROT	DNA GYrase subunit B
2841	798	13155		3.78	1.0E+00 P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2839	8090			0.78	1.0E+00 O14226	SWISSPROT	HYPOTHETICAL 67 kD PROTEIN C8F12.0<8C IN CHROMOSOME 1
3182	8333	13498		1.13	1.0E+00 AA282453.1	EST_HUMAN	Scorpius scorpioides total serum Nb2HFB_8w Homo sapiens cDNA clone IMAGE:10328330 3' similar to WP_042083 CE04204 contains element MER22 MER22 repetitive element;
3585	8304			0.73	1.0E+00 U23808.1	NT	Xenopus laevis nodospin genes, complete cds
3659	8797	13953		1.44	1.0E+00 AF122816.1	NT	Agaricus bisporus mRNA for tyrosinase
4044	9175	14316		0.8	1.0E+00 AF223391.1	NT	Homo sapiens cadmium channel epsilon1E subunit (CACNA1E) gene, exons 7-9, and partial cds, alternatively spliced
4249	8574			0.68	1.0E+00 85922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4773	6888	15032		3.01	1.0E+00 AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6184	10234			0.63	1.0E+00 AF200817.1	NT	Pick whale morbillivirus phosphoprotein (P) gene, partial cds
3580	8730			8.61	9.9E-01 AF-174885.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
621	6659	10819		1.68	9.8E-01 P22357	SWISSPROT	AMINO ACID ACETYL TRANSFERASE (N-ACETYLY GLUTAMATE SYNTHASE)(AGS)/(AGS)
2762	7858			1.19	9.8E-01 AF-174844.1	NT	Xenopus laevis rho GTPase mRNA, complete cds
4418	8538	14674		0.66	9.6E-01 AF197825.1	NT	Bromus tectorum putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4418	6636	14876		0.68	9.6E-01 AF197825.1	NT	Bromus tectorum putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4437	6558	14639		1.52	9.6E-01 AW709874.1	EST_HUMAN	PM2UM0053-240500-005-f12 UM0053 Homo sapiens cDNA
3781	8898	14048		1.82	9.6E-01 BE092340.1	EST_HUMAN	6016766389F1 NIH MGCC 21 Homo sapiens cDNA clone IMAGE:3858473 6
3761	8898	14049		1.82	9.6E-01 BE092340.1	EST_HUMAN	6016766389F1 NIH MGCC 21 Homo sapiens cDNA clone IMAGE:3858473 5
3184	8336			3.87	9.4E-01 AF165990.1	NT	Bartonia clandestina RNA polymerase beta subunit (pbB) gene, partial cds
3203	8354			1.68	9.4E-01 AF080595.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds

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Probe Seq ID No:	Exon seq ID No:	ORF seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1745 6871	12854	1.14	9.3E-01	AF242382.1	NT	Human sapiens phytolactam-CoA hydroxylase (PHYL1) gene, exon 8	
2659 7699	12854	2.9	9.3E-01	BE071172.1	EST_HUMAN	RC3-BT0503-271183-01-801 BT0503 Human sapiens cDNA	
4009 6142	14282	0.78	9.3E-01	MW2019.1	NT	Bovine papillomavirus type 2, complete genome	
4009 9142	14283	0.78	9.3E-01	MA2019.1	NT	Bovine papillomavirus type 2, complete genome	
3224 8374	13537	3.14	9.2E-01	BE622702.1	EST_HUMAN	60144133871 NIH-MCGC_72 Human sapiens cDNA clone IMAGE:39161843'	
2116 7231		1.21	9.1E-01	89223056	NT	Human sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA	
3189 8340	13501	1.03	9.1E-01	1726418.1	EST_HUMAN	AB200088R Infant brain, LNL array of Dr. M. Soares 1NIB Human sapiens cDNA clone LLAB20038 5'	
3189 8340	13502	1.03	9.1E-01	1726418.1	EST_HUMAN	AB200088R Infant brain, LNL array of Dr. M. Soares 1NIB Human sapiens cDNA clone LLAB20038 5'	
3191 8342	13503	0.78	9.0E-01	7881625	NT	Human sapiens DK7ZP564MN2423 protein (DK7ZP564MN2423), mRNA	
4358 9480	14618	1.77	9.0E-01	AE068610.1	NT	Human sapiens neuron II-alpha gene, partial cds	
6001 10103	16223	0.81	9.0E-01	AF011772.1	NT	Oncodengue virus capsid R651 (RAD51) mRNA, complete cds	
4516 6833	14773	1.69	8.8E-01	Q28350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE	
484 5632	10771	1.49	8.7E-01	AF106953.2	NT	Human sapiens SOS1 (SOS1) gene, partial cds	
2380 7486	12740	1.03	8.7E-01	6801683	NT	Human sapiens AT-binding transcription factor 1 (ATBF1), mRNA	
2889 7894	13162	13.39	8.7E-01	AA1686888.1	EST_HUMAN	AA1686888.1 NCI_OGA-P74.1 Human sapiens cDNA clone IMAGE:1076877	
4884 10100		3.43	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-hexameric 1,2-dioxogenase beta-ISP protein OhbB (ohbS), end pdp>	
474 6841		2.14	8.6E-01	X17012.1	NT	Rat (Gf) gene for insulin-like growth factor II	
8359 6010	11182	6.02	8.6E-01	W68089.1	EST_HUMAN	Zd44fe03.1 Soares, fetal heart, NbbH119W Human sapiens cDNA clone IMAGE:343516 5'	
3602 8741	13895	0.68	8.6E-01	AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65	
3776 8915	14067	1.3	8.6E-01	U49724.1	NT	Drosophila melanogaster marin (Dmarin) mRNA, complete cds	
740 6838	11048	2.34	8.3E-01	M83437.1	NT	Thermus thermophilus cytochrome c-652 (cytc) and CycB (cytb) genes, complete cds	
2068 8221	13372	9.2	8.3E-01	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18	
3987 6121	14268	2.82	8.3E-01	Y19177.1	NT	Synechocystis sp. PCC6803 polyketide biosynthetic gene cluster	
2044 7160	12399	1.35	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds	
3440 8582	13742	2.55	8.1E-01	AF05066.1	NT	Human sapiens MHC class 1 region	
3440 8582	13743	2.55	8.1E-01	AF05066.1	NT	Human sapiens MHC class 1 region	
4801 10012		0.83	8.1E-01	AF202684.1	NT	Drosophila melanogaster NaK-ATPase beta subunit isoform 4 (JYHs2) mRNA, complete cds	
172 5367		2.34	8.0E-01	AJ271610.1	NT	Staphylococcus aureus partial pta gene for phosphate acetyltransferase allele 16	
288 5475	10616	12.52	8.0E-01	AJ132772.1	NT	Bos taurus fbf end ttf genes	
1613 6741	11936	0.98	8.0E-01	8394087	NT	Rattus norvegicus protease (prosome, macropain) 28 subunit alpha (Psmet), mRNA	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2029	7147			1	8.0E-01	BF530892.1	EST_HUMAN	6020727473F_NCI_CGA_P_Bm67 Homo sapiens cDNA clone IMAGE:4215091 5'
3049	8203	13359	1.08	8.0E-01	AF-27897.1	NT	Selktin D11lersis offactor / receptor (S8027) gene, partial cds	
3294	8441	13603	1.1	8.0E-01	AB0065193.1	NT	Mus musculus gene for myofascial glycoprotein, complete cds	
3680	8819			1.68	8.0E-01	AL162768.2	NT	Nelsena meningitidis serogroup A strain Z2401 complete genome segment 7/7
4507	86248	14763	6.59	8.0E-01	JE83739.2	NT	Gagillus mRNA for nicotinio acetylcholine receptor (nAChR) beta 3 subunit	
4968	10074	15212	1.12	8.0E-01	765752.2	NT	Mus musculus myosin Xb (Myo5b), mRNA	
4433	56211	10784	0.97	7.9E-01	D11476.1	NT	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds	
713	58707		0.73	7.8E-01	AEG02130.1	NT	Ureaplasma urealyticum section 31 of 69 of the complete genome	
1618	67448		10.36	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds	
1688	67977		0.69	7.9E-01	JG2739.1	NT	Haemophilus influenzae Rd section 54 of 162 of the complete genome	
2243	7354	12811	4.45	7.9E-01	AB004816.1	NT	Oryzopsis curvula mRNA for mitogen-activated protein kinase 29, complete cds	
2244	7356	12812	1.07	7.9E-01	AE130459.1	NT	Danio rerio Tip4-associated protein Tap1A (tap1A) mRNA, complete cds	
3591	88442	13808	2.73	7.9E-01	AF-228864.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds	
4277	9400		1.82	7.9E-01	JG283612.1	EST_HUMAN	601192333F_NIH_MGF_7 Homo sapiens cDNA clone IMAGE:3535785 5'	
4683	87011	14839	0.91	7.9E-01	6753745	NT	Mus musculus embryo (Emb) mRNA	
4683	87011	14840	0.91	7.9E-01	6753745	NT	Mus musculus embryo (Emb) mRNA	
5140	10240		0.65	7.9E-01	AF-339718.1	NT	Chrysomya bezziana pectenophila-48 precursor, gene, complete cds	
6168	10258	16397	1.28	7.9E-01	AF-228843.1	NT	Mus musculus WNT-2 gene, partial cds; putative enoyl-CoA-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene	
877	6027		1.78	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1K104	
2254	7364	12620	1.49	7.8E-01	AW959567.1	EST_HUMAN	E5T371637 MAGE sequences, MAGF Homo sapiens oDNA	
4670	9788	14931	1.11	7.8E-01	UB7305.1	NT	Rattus norvegicus transmembrane receptor Uncash1 mRNA, complete cds	
6019	10121		0.75	7.8E-01	AW763353.1	EST_HUMAN	RC3-C70254-130100-023-002 C70254 Homo sapiens cDNA	
139	6338	10480	4.6	7.7E-01	AF184346.1	NT	Lyceoperdon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds	
3337	8483			1.32	7.7E-01	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAlpha) and major Histocompatibility protein class II beta chain (IIBeta) genes, complete cds; butyrophilin-like (NG3), butyrophilin-1p	
3588	8726	13884	3.69	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds	
4375	9468	14840	3.06	7.7E-01	AF188488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds	

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Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4376 8498		14841	3.06	7.7E-01	AF188468.1	NT	Catombic catomix lapponica sub-species lapponica beta-actin mRNA, partial cds
511 5877			1.29	7.8E-01	AL168301.2	NT	Homo sapiens chromosome 21 segment HS21C101
562 5745	10873		1.98	7.8E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 6
3341 8487	13653		0.98	7.8E-01	C14203	Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-037E11 6'	
1131 6268	11430		1.4	7.4E-01	AI568148.1	EST_HUMAN	th14D09_x1 NCI_CGAP_Bm28 Homo sapiens cDNA clone IMAGE:2187577 3' similar to contains Alu repetitive element contains element MIR repetitive element;
2324 7432	12684		0.98	7.4E-01	AB011108.1	EST_HUMAN	Homo sapiens mRNA for KIAA0534 protein, partial cds
3707 8846	13899		1.07	7.4E-01	AF1126538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
3978 9014	14171		0.58	7.4E-01	AF13310.1	NT	Vibrio cholerae phage CTXφh Catechol-β-D-tartrate (tartrate) and Calcium-β-D-tartrate (tartrate) genes, complete cds
4228 9410	14546		7.53	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2969 8123	13298		0.83	7.3E-01	PR09710	SWISSPROT	HYPOTHETICAL PROTEIN HKLF1 (TRL1)
4687 9706	14843		0.76	7.3E-01	AE001168.1	NT	Borrelia burgdorferi (section 62 of 70) of the complete genome
4869 9785	14830		4.1	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
832 6584			1.44	7.2E-01	L28281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2α) mRNA, complete cds
1981 7078	12302		7.25	7.2E-01	X78140.1	NT	Nebacum Nai-7A13 mRNA
3039 8183	13348		1.3	7.2E-01	AF188100.1	NT	Poxvirus, complete genome
3434 8579	13736		2.23	7.2E-01	AF086608.1	NT	Giardia intestinalis varian-specific surface protein (vp417-6) gene, vp417-6/A-1 allele, complete cds
4735 8849	14694		3.19	7.2E-01	D80314.1	NT	L-mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5098 10193	15338		1.13	7.2E-01	AF188778.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α2
5098 10193	16337		1.13	7.2E-01	AF188778.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α2
680 6847	10890		8.62	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3035 8169	13345		12.51	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 1E-16
4180 8306	14442		3.92	7.1E-01	7305320	NT	Mus musculus obgelin (Obg), mRNA
4180 8303	14443		3.32	7.1E-01	7305320	NT	Mus musculus obgelin (Obg), mRNA
1232 6363	11636		1.84	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1232 6363	11638		1.84	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds

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Probe SEQ ID NO:	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5038	10140		1.55	7.0E-01	AL163301.2	NT	Human sapiens chromosome 21 segment HS21C101
5168	10286	15407	3.95	7.0E-01	TR8328.1	EST_HUMAN	Y441h03.1 Strategene liver (R#37224) Human sapiens cDNA clone IMAGE:83285 3' similar to g3K03020 PHENYLALANINE-4-HYDROXYLASE (HUMAN);
871	6118	11287	13.08	6.8E-01	U68674.1	NT	Candida albicans squelans epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
971	6118	11288	13.08	6.9E-01	U69674.1	NT	Candida albicans squelans epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1314	8444	11621	1.98	6.9E-01	AA593530.1	EST_HUMAN	AA593530.1 NCI_CGAP_Gen1 Human sapiens cDNA clone IMAGE:10851176 3'
3204	8355	13516	1.41	6.9E-01	AE022271.2	NT	Chlamydia muridarum, section 3 of 86 of the complete genome
858	6108	11276	1.78	6.8E-01	AF011774.1	NT	Glandia intestinalis cathepsin kinase gene, complete cds
2835	7733		2.28	6.8E-01	DS0817.1	NT	Synecdochis sp. PCC8003 complete genome, 27/27, 3418852-3373470
2789	6758	11950	1.22	6.8E-01	AA864476.1	EST_HUMAN	AA75455.1 Soces_Parathyroid tumor NBPA Human cDNA clone IMAGE:1402256 3' similar to gb:X58411_mef ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4644	8862	14805	1.28	6.8E-01	J00762.1	NT	Rat/hooded prolactin gene - exon III and flanks
288	5484	10628	24.41	6.7E-01	AF213884.1	NT	Human sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds
337	6520	10858	16.88	6.7E-01	AA451884.1	NT	Human sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds
2131	7245	12489	1.07	6.7E-01	AA451884.1	EST_HUMAN	AA212g12.51 Soces_biot_fetus_N21IF8_Bw Human ciliapins cDNA clone IMAGE:788310 3' similar to 2x11
							contains element TARI1 repetitive element;
2148	7834	12509	1.89	6.7E-01	AF186073.1	NT	Drosophila melanogaster Ms285C gene, complete cds; NM004165 isoform (Nm004165) gene, complete cds, alternatively spliced; and transcription factor (RefSeq) gene, complete cds, alternatively spliced
2884	8118	13281	3.1	6.7E-01	68778580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4431	8850	14693	0.64	6.7E-01	X74421.1	NT	S.tuberorum mRNA for diucose-6-phosphate dehydrogenase
4947	10058	15194	1.03	6.7E-01	AW079110.1	EST_HUMAN	X95g12.4 NCI_CGAP_Co17 Human sapiens cDNA clone IMAGE:2574568 3'
2681	7757	13008	1.24	6.6E-01	AF186339.1	NT	Human sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3470	8812	13778	1.02	6.6E-01	4508680	NT	Human sapiens sema domain, seven thrombospondin repeats (type I and type I-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3835	8774	13930	3.70	6.6E-01	Y07589.1	NT	C.abbiescens random DNA marker, 282bp
4085	9214		0.72	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoR $\gamma$ T gene, and sodium phosphate transporter (NP73) gene, complete cds
5170	10288	15409	1.21	6.6E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68

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Probe seq ID	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar (T <sub>top</sub> ) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
622	5782	10912	1.19	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
622	5782	10913	1.19	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3414	8567	13716	4.01	6.5E-01	AB041226.1	NT	Mus musculus gene for Tab2, complete cds
4266	9381	14614	4.73	6.5E-01	AJ212295.1	NT	Homo sapiens SFP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
6045	10147	15276	2.62	6.5E-01	U28921.1	NT	Phascolites vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
249	5440	10580	6.59	6.4E-01	U48948.1	NT	Drosophila melanogaster Skid dynamic light chain mRNA, complete cds
3438	8569	13740	3.29	6.4E-01	U48954.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3840	8979	14131	1.22	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1807 protein, partial cds
433	8602	10749	3.11	6.3E-01	F052228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFFRP-II)
533	5689	10831	1.69	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 183 of the complete genome
2344	7259	12564	1.04	6.3E-01	U81138.1	NT	Streptomyces flavescens multi antibiotic resistance locus
2642	7846	12896	35.36	6.3E-01	U76831.1	NT	Gallus gallus bone morphogenic protein 1 (BMP1) mRNA, partial cds
2542	7845	12898	35.38	6.3E-01	U76831.1	NT	Gallus gallus bone morphogenic protein 1 (BMP1) mRNA, partial cds
2887	8142		0.7	6.3E-01	Y11725.1	NT	Lycoperdon esculentum p88c genes, complete CDS
2371	7477		2.11	6.1E-01	6878076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
5182	10289		1.04	6.1E-01	BF314183.1	EST HUMAN	801801013F1 NIH MIGC_18 Homo sapiens cDNA clone IMAGE:4130978 6'
494	5881	10797	1.02	6.0E-01	D87876.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
560	5725		2.77	6.0E-01	6828989	NT	Homo sapiens endoplasmic reticulum protein complex 3, mu 2 subunit (C1A20), mRNA
1371	9498	11682	1.83	6.0E-01	AF095253.1	NT	Human respiratory syncytial virus strain CH32-E1b attachment protein (G) gene, complete cds
3782	8929	14077	0.82	6.0E-01	AJ233398.1	NT	Viral hemophagis septicaemia virus N, P, M, G, NV, L genes, French strain 07-71
4007	9140	14281	1.3	6.0E-01	X16842.1	NT	Xenopus laevis (or) desmosin
4169	9295		1.94	6.0E-01	AF058395.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
1001	8147	11314	2.24	6.0E-01	U32701.1	NT	Haemophilus influenzae Rd section 18 of 183 of the complete genome
1409	6538	11714	1.11	5.9E-01	6680232	NT	Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgcl), mRNA
3263	8403	13684	8.03	5.9E-01	AL168287.2	NT	Homo sapiens chromosome 21 segment 11S21Q087
3253	8405	13565	5.03	5.9E-01	AL168297.2	NT	Homo sapiens chromosome 21 segment 11S21Q087
4168	8323		5.04	5.9E-01	AF162766.1	NT	Rattus norvegicus centrom 2 mRNA, partial cds
1913	7032	12262	1.03	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
3867	8082	14244	1.03	5.8E-01	BF685738.1	EST HUMAN	601852474F1 NIH MIGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4468	9807	14745	4.55	5.8E-01	AB068077.1	NT	Vigne redista mRNA for proton pyrophosphatase, complete cds
4765	9878		0.92	5.8E-01	AF110846.1	NT	Megastoma scalaris sex-lethal homolog (Megsl) gene, partial cds, alternatively spliced products
1507	6834	11820	0.83	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
1607	6834	11821	0.86	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3015	8169		0.87	5.7E-01	6755253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3208	8359	13520	1.87	5.7E-01	QBWT12	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3487	8628		2.48	5.7E-01	AB033503.1	NT	Populus euphydryoides Peace-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6183	10290	15418	1	5.7E-01	L41867.1	NT	Drosophila extra sex comb gene, exon 1-4, complete cds
3245	8491	13657	1.31	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3245	8491	13658	1.31	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4218	8343	14473	1	5.6E-01	D85135.1	NT	Chicken TBP gene, exons 8, complete cds
1214	8348	11616	2.95	5.6E-01	83638912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pcb), mRNA
2682	7758	13009	2.01	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2682	7758	13010	2.01	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2684	8038	132023	0.84	5.5E-01	5502085	NT	Homo sapiens superkiller viralcds activity 2(S, ceratitis capitata) like (SKIV2L), mRNA
3038	8162		1.93	5.6E-01	H46219.1	EST_HUMAN	ye18ar10.s1 Scores adult brain N26-HB56Y Homo sapiens cDNA clone IMAGE:1782683'
3219	8370	13533	3.87	5.6E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3687	8806	13982	2.13	5.6E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
140	6337	10481	12.97	5.4E-01	7657288	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
140	6337	10482	12.97	5.4E-01	7657286	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
583	5748	10974	1.14	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsA (gsA) genes, complete cds, and unknown genes
583	6748	10976	1.14	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsA (gsA) genes, complete cds, and unknown genes
1275	8444	11578	2.32	5.4E-01	AW886087.1	EST_HUMAN	CVA4-NNN0040-070400-160-cd4 NN0040 Homo sapiens cDNA Chlamydomonas reinhardtii AR39, section 74 or 84 of the complete genome
2097	7212		2.04	5.4E-01	AE002247.2	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-carotene gene)
2235	7347	12602	1.13	5.4E-01	AJ276882.1	NT	Homo sapiens MLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes >
514	5686	10814	2.01	5.3E-01	AF01943.1	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPZ21) mRNA
2744	7838	13092	12.78	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPZ21) mRNA
2744	7838	13093	12.76	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPZ21) mRNA
3227	6377	13658	3.1	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSLC1) gene, complete cds

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
4184	8310		1.28	5.3E-01	U398587.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome	
817	6970	11131	0.27	6.2E-01	L20770.1	NT	Drosophila melanogaster helix-deep-helix mRNA, complete cds	
1188	6301	11487	6.81	5.2E-01	Q8WVY30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NFAT5)	
1183	6327	11494	3.83	6.2E-01	AF224492.1	NT	(RELD DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)	
1884	7013		4.02	6.2E-01	AL163295.2	NT	Homo sapiens phosphatidyl scramblase 1 gene, complete cds	
2130	7244	12483	1.48	6.2E-01	AB018268.2	NT	Homo sapiens chromosome 21 segment HS21C085	
3086	8249	13398	1.39	5.2E-01	U65942.1	NT	Chlamydomonas abortus strain S2613 POMP81A and POMP81B precursor, genes, complete cds	
3222	8373		0.68	6.2E-01	D73443.1	NT	Azotobacter vinelandii lsd gene 1 for lactoclate dehydrogenase, complete cds	
3386	8630		1.73	5.2E-01	AL116780.1	NT	Batrachis cicharea strain T74 cDNA library under conditions of nitrogen deprivation	
3425	8567	13728	2.15	6.2E-01	AA984165.1	EST_HUMAN	AAm77905.1 of Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1618504 3'	
3612	8751		1.28	5.2E-01	AF0202389.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p11mfd) mRNA, nuclear gene encoding chloroplast protein, complete cds	
4054	8761		0.64	5.2E-01	AF0202389.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p11mfd) mRNA, nuclear gene encoding chloroplast protein, complete cds	
5114	10215		1.1	6.2E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081	
614	6774	10805	2.44	6.1E-01	M58508.1	NT	Human adrenomedullin peptide gene, exons 3 to 12	
647	5803	10942	4.03	6.1E-01	AJ238944.1	NT	Polyangium vitellinum (strain FI_Vt) 16S rRNA gene	
647	5803	10943	4.08	6.1E-01	AJ238944.1	NT	Polyangium vitellinum (strain FI_Vt) 16S rRNA gene	
16635	6793		1.04	5.1E-01	AF97885.1	NT	R. norvegicus mRNA for mammalian fusca protein	
4052	9183	14325	4.78	5.1E-01	AI858495.1	EST_HUMAN	WS2612x1 NCL_CGAP_Urt Homo sapiens cDNA clone IMAGE:2427283 3'	
4168	8284	14420	2.65	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)	
3634	6783	13948	1.18	6.0E-01	AE001785.1	NT	Theriotoga maritima section 97 of 138 of the complete genome	
3728	8859	14020	0.77	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoprecipitin light chain IgM mRNA, antibody 353p, 138, partial cds	
3809	8948	14086		1.12	6.0E-01	U38483.1	NT	Rattus norvegicus legged protein mRNA, complete cds
3831	8987	14142	3.05	5.0E-01	AB0533010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds	
790	6944	11104	2.2	4.8E-01	BF571462.1	EST_HUMAN	Xenopus laevis mRNA for c-Jun protein, 1878 BP	
1872	6801	11986	1.23	4.8E-01	AJ243956.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-A) mRNA, complete cds	
1911	7030	12250	1.11	4.8E-01	U40683.1	NT	G522a09.51 Scores_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:1625144 3'	
3525	8686		1.14	4.8E-01	AJ812842.1	EST_HUMAN	G01289358F_NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3829188 6'	
3832	8018		1.38	4.7E-01	BE07975.1	EST_HUMAN	G01289358F_NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'	
3724	8862	14016	1.52	4.6E-01	BF698300.1	EST_HUMAN	G02081103F_NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'	
3724	8862	14018	1.62	4.6E-01	BF698300.1	EST_HUMAN	G02081103F_NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'	
6117	10218		1.08	4.6E-01	W11267.1	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2834	7889	13149	4.74	4.5E-01	AA677088.1	EST_HUMAN	Z555002_61 Soares_fetal_liver_spleen_INFSL_S1 Homo sapiens cDNA clone IMAGE:4541783'
3288	8445	13807	4	4.5E-01	Q037783	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPO-1) (PERLECAN) (PLC)
3369	8504	13871	1.01	4.5E-01	AF126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pde) gene, exons 2 through 12
4001	9134		1.29	4.5E-01	Q282247	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN
4050	9181	14323	1.02	4.5E-01	AI708908.1	EST_HUMAN	as18602_x1 Bertrand et al. HPLRB6 Homo sapiens cDNA clone IMAGE:23534803'
4147	10317		4.15	4.5E-01	AW873495.1	EST_HUMAN	hs00092_x1 SoaresNFL_T_GBC_31 Homo sapiens cDNA clone IMAGE:30418103'
4920	10030	15172	1.18	4.5E-01	BB683445.2	EST_HUMAN	60165722R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:385650233'
2030	7148		2.19	4.4E-01	68801563	NT	Mus musculus Integrin membrane-associated protein 1 (Imap1), mRNA
2366	7472	12727	2.49	4.4E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3283	8443	13805	1.3	4.4E-01	AF056780.1	NT	Batrachus nonnegligible SyngAP-b mRNA, complete cds
3286	8443	13806	1.3	4.4E-01	AF056790.1	NT	Rattus norvegicus SyngAP-b mRNA, complete cds
3300	8447	13809	2.03	4.4E-01	BF056726.1	EST_HUMAN	7B10d2_x1 NCI CGAP_B118 Homo sapiens cDNA clone IMAGE:23383785
4213	8338		1.64	4.4E-01	BE378707.1	EST_HUMAN	601237159F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:38608383
410	5578	10728	2.01	4.3E-01	AF165218.1	NT	Caenorhabditis elegans MN/LW opsin gene, upstream flanking region
410	5578	10727	2.01	4.3E-01	AF165218.1	NT	Caenorhabditis elegans MN/LW opsin gene, upstream flanking region
1617	8746	11840	1	4.3E-01	AW886556.1	EST_HUMAN	QV4-SN0024-200400-183-001 SN0024 Homo sapiens cDNA CM2-D1003-01-02300-077-001 DT0003 Homo sapiens cDNA MRO-BN0070-270300-008-004 BN0070 Homo sapiens cDNA
2838	7881		1.85	4.3E-01	AW886569.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
3032	8188	13241	0.81	4.3E-01	AW89277.1	EST_HUMAN	Xenopus laevis granular virus, complete genome
4123	8251	14388	1.16	4.3E-01	JG0308.1	NT	Human somatosatin 1 gene and flanks
4385	5578	10726	1.2	4.3E-01	AF165218.1	NT	Caenorhabditis elegans MN/LW opsin gene, upstream flanking region
4385	5578	10727	1.2	4.3E-01	AF165218.1	NT	Caenorhabditis elegans MN/LW opsin gene, upstream flanking region
4838	10048		1.1	4.3E-01	AL181502.2	NT	Araihidopsis thaliana DNA chromosome 4, contig fragment No. 14
6094	10164		0.89	4.3E-01	9835260	NT	Xenopus laevis granular virus, complete genome
1357	7916	11678	1.08	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FISH HOMOLOG PRECURSOR
3683	8732	13886	4.15	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 83 of 229 of the complete genome
3616	8734	13910	0.97	4.2E-01	AI280338.1	EST_HUMAN	CP94b01_x1 Soares_NhlHMPu_S1 Homo sapiens cDNA clone IMAGE:15788345
3650	10316		0.67	4.2E-01	N81203.1	EST_HUMAN	788IE1_fetal brain cDNA clone IMAGE:788IE1-K similar to R07876_240498
3857	8993	14160	0.62	4.2E-01	AW832527.1	EST_HUMAN	QV0-L70015-182010-1274701 L70015 Homo sapiens cDNA
3965	8030	14243	1.14	4.2E-01	Q04888	SWISSPROT	SOX-8 PROTEIN
4686	9782	14926	5.49	4.2E-01	AA6344083.1	EST_HUMAN	ribM01_61 NCI CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4748	6831	16010	3.83	4.2E-01	R13487.1	EST_HUMAN	y77601_1 Soares_infant brain TNIB Homo sapiens cDNA clone IMAGE:282785

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T <sub>bp</sub> ) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1085	6233	11398	1.46	4.1E-01	AI005481.1	EST_HUMAN	RC-BT081-210188-142 BT081 Homo sapiens cDNA clone AD8AHf08 6'
1104	8242	11405	1.2	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone AD8AHf08 6'
1104	8242	11406	1.2	4.1E-01	AV705248.1	EST_HUMAN	AV705248 ADB Homo sapiens cDNA clone AD8AHf08 6'
2872	7768	13020	1.09	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2803	8059	13228	1.98	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2806	8059	13229	1.98	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
4248	8373	14506	3.92	4.1E-01	AI249207.1	NT	Rhodococcus sp. AD6 IsoQ, IsoH, IsoI, IsoA, IsoB, IsoC, IsoD, IsoE and IsoF genes
4282	8405		0.72	4.1E-01	AA868257.1	EST_HUMAN	cmt3d02.61 Scores: NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:1642219 3'
4837	9755	14802	1.1	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
4852	9789	14816	1.23	4.1E-01	AA480097.1	EST_HUMAN	268607.11 Scores: total Jesus Nb2tIF8_8W Homo sapiens cDNA clone IMAGE:788428 6'
1041	6181	11346	0.83	4.0E-01	8404888	NT	Laeusus rubellus mitochondrial, complete genome
1344	6473	11653	1	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dafnrta (dmt) mRNA, complete cds
1495	6822		2.81	4.0E-01	6879298	NT	Mus musculus placental derived growth factor receptor, beta polypeptide (Pgrfb), mRNA
2788	8334	10479	2.2	4.0E-01	6878480	NT	Mus musculus ubiquitin-protein ligase 63 component n-Ecognition (Ubr1), mRNA
2837	8081	13257	1.3	4.0E-01	AL1632280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2837	8081	13258	1.3	4.0E-01	AL1632280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3872	8811	13869	2	4.0E-01	AF086803.1	NT	Streptococcus pneumoniae YIC (YID) (YID) penicillin-binding protein 2x (pbp2x), and undecapeptide-phosphate-UDP-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3808	8933	14091	3.15	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRD2), exon 1
3906	8943	14092	3.15	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRD2), exon 1
4786	8889		8.37	4.0E-01	Q31849	SWISSPROT	NADPH:FLAVONONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
1387	6315	111897	1.92	3.9E-01	AF2086918.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2805	7704	12860	2.05	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1183 protein, partial cds
2887	7763	13013	2.86	3.9E-01	XB20322.1	NT	H. sapiens B-myb gene
2687	7763	13014	2.86	3.9E-01	XB20322.1	NT	H. sapiens B-myb gene
3070	8223	13374	4.04	3.9E-01	AJ226886.1	NT	Sinorhizobium meliloti eg1, syrB2, cysG genes and orf3
4058	8188	14328	1.34	3.9E-01	BFG92611.1	EST_HUMAN	781601-XI_NCI_CGAP_Brief Homo sapiens cDNA clone IMAGE:3339169 3'
4877	10085	15220	1.05	3.8E-01	BE728687.1	EST_HUMAN	60166848F-1_NTR_MGC_20 Homo sapiens cDNA clone IMAGE:3833899 6'
155	6352		13.75	3.8E-01	7018488	NT	Homo sapiens protein kinase PKNbeta (phnbeta), mRNA
605	6671		0.81	3.8E-01	AB029291.1	NT	Mus musculus pcm-1 mRNA for per centidiol material-1, complete cds
2536	7839	12887	3.74	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2597	7845	12951	2.31	3.8E-01	6678002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
2873	8127		0.81	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP/1213)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3020	8174	13332	1.83	3.8E-01	AF043383.1	NT	Pleurotoxetes americanus aminopeptidase N (ampN) gene, partial cds
3465	8607	13771	7.75	3.8E-01	AL161618.2	NT	Arabidopsis thaliana DNA chromatome 4, contig fragment No. 30
3540	8867		0.82	3.8E-01	AL807219.1	EST_HUMAN	NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2267885 3'
3737	8875	14028	0.83	3.8E-01	BE164080.1	EST_HUMAN	PM04HT0339-2004-00010-C01 HT0339 Homo sapiens cDNA
4040	9171	14312	0.75	3.8E-01	AL271361.2	NT	Tekfifg1 (uniprot: YW12 (partial), frank01, cfr and farr12 (partial) genes
5030	10132	16262	1.07	3.8E-01	AF0386833.1	NT	Homo sapiens May17 protein (NPV17) gene, partial cds; and uncocin gene, complete cds
2454	7558	12809	4.15	3.7E-01	AB037681.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3442	8684	13746	8.82	3.7E-01	AF088338.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3849	8985	14141	0.7	3.7E-01	AA319482.1	EST_HUMAN	EST:T2715 Adrenal gland tumor Homo sapiens cDNA 5' end
4207	9332	14485	6.9	3.7E-01	AL218707.1	EST_HUMAN	Q38C07_X11 Scores NSF_F8_BW_OT_PA_P_S11 Homo sapiens cDNA MFR3-O1007-080300-104-b02_O10007 Homo sapiens cDNA
4297	8419	14652	1.3	3.7E-01	AV878837.1	EST_HUMAN	MFR3-O1007-080300-104-b02_O10007 Homo sapiens cDNA section 50 of 208 of the complete genome
4388	8489	14833	3.08	3.6E-01	AE022408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 208 of the complete genome
238	6448	10581	0.64	3.6E-01	AB038698.1	NT	Bimaculidae nephus mRNA for MAP4K epsilon2 protein
988	6142		8.33	3.6E-01	US82941.1	NT	Human mmp8 gene, partial cds
1318	6447	11628	2.54	3.6E-01	180285.1	EST_HUMAN	Y038e0611 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1318	6447	11627	2.64	3.6E-01	780255.1	EST_HUMAN	Y038e0611 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 6'
1919	7039	12258	9.85	3.6E-01	AW580184.1	EST_HUMAN	hg35R02_X11_NCI_CGAP_QC8 Homo sapiens cDNA clone IMAGE:2847418 3'
1919	7038	12259	3.85	3.6E-01	AW580184.1	EST_HUMAN	hg35R02_X11_NCI_CGAP_QC8 Homo sapiens cDNA clone IMAGE:2847418 3'
1996	7073	12293	3.28	3.6E-01	AF216207.1	NT	Mus musculus fibroblast protein S19 (Fps19) gene, complete cds
2387	7473		1.87	3.6E-01	AF8725.1	NT	P-imiquimide (P3804) gene for arachin
2884	10014		8.6	3.6E-01	AF1984485.1	NT	Drosophila melanogaster super transporter 3 (stu3) mRNA, complete cds
3481	8593	13756	2.12	3.6E-01	XJ6758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
3451	8593	13757	2.12	3.6E-01	XJ6758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
4388	8808	14648	1.13	3.6E-01	BE707883.1	EST_HUMAN	RC1+HT0545-150600-014-b12-HT0545 Homo sapiens cDNA
4888	8802	14948	0.87	3.6E-01	AF071838.1	NT	Mus musculus protein tyrosine kinase Tec (Tec) gene, alternative exons 4 and 4a, exons 5 through 7 and Tec1 isoform, complete cds
4888	8802	14949	0.97	3.6E-01	AF071838.1	NT	Mus musculus protein tyrosine kinase Tec (Tec) gene, alternative exons 4 and 4a, exons 5 through 7 and Tec1 isoform, complete cds
4720	8834	14978	0.65	3.6E-01	Y11529.1	NT	Z.mays mRNA for casein kinase II alpha subunit
4761	9874	15028	1.32	3.6E-01	AJ229237.1	EST_HUMAN	Bacterium from anode bulk cell 1GS rRNA gene (strain X845)
4897	10103	16234	2.4	3.6E-01	AW339383.1	EST_HUMAN	IbaC094_X11_NCI_CGAP_Luz24 Homo sapiens cDNA clone IMAGE:2872568 3'
111	6316	10454	0.83	3.5E-01	AL161538.2	NT	Arabidopsis thaliana DNA chromatome 4, contig fragment No. 36
206	5401	10543	2.38	3.5E-01	6878833	NT	Mus musculus mannose receptor, C type 2 (MrC2), mRNA
723	5878	11027	1.02	3.5E-01	7706138	NT	Homo sapiens GAP-III-like protein (LOC51306), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
723	6978	11028	1.02	3.5E-01	77081381	NT	Homo sapiens GAP-like protein (LOQ51308), mRNA
789	5655	11083	2.89	3.6E-01	BF_29798.1	EST_HUMAN	601811060R1 NIH_3T3 MGC_48 Homo sapiens cDNA clone IMAGE:4033951 3'
1631	6760	11956	1.07	3.5E-01	BF_310888.1	EST_HUMAN	601684653F2 NIH_3T3 MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1851	6778	11971	2.33	3.6E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2239	7369	12825	1.03	3.6E-01	PC08798	SWISSPROT	HOMEBOX PROTEIN HOXA4 (HOXA-4) (M-H-3)
2671	7844	12928	2.4	3.5E-01	AA223252.1	EST_HUMAN	2008609.01 Stratagene NT2 neuronal precursor 637230 Homo sapiens cDNA clone IMAGE:6503972 3'
2888	7762		1.11	3.6E-01	U058897.1	NT	Fibroblast sucrose-ischaemate S85 endoglycanase E (celIE) and endoglycanase D (celD) gene, complete cds
3784	8921		1.46	3.5E-01	AA4642138.1	EST_HUMAN	nt80d03.31 NCI_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4238	9361	14493	1.81	3.5E-01	AF071283.1	NT	Danio rerio homeobox protein (fracto5) gene, complete cds
4911	10021	15166	5.47	3.5E-01	MI18349.1	NT	Rat leukocyte common antigen (L-CyA) gene, exons 1 through 6
705	6882		1.61	3.4E-01	AI242858.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
977	6123	11283	5.3	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, colS genes, oriZ22 and partial traA gene
1331	8460	11639	2.1	3.4E-01	Y006564.1	NT	Azotobacter vinelandii traA gene for NTA protein (positive regulatory element)
2378	7486	12739	2	3.4E-01	DS08098.1	NT	Synechocystis sp. PCe3803 complete genome, 11/27, 1311235-1430418
2871	8125	13288	0.68	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2871	8125	13289	0.68	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3127	8279	13435	0.68	3.4E-01	DS0909.1	NT	Synechocystis sp. PCe3803 complete genome, 11/27, 1311235-1430418
3140	8281	13448	6.85	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3325	8472	13634	0.7	3.4E-01	AF034682.1	NT	Homo sapiens pulmonary surfactant protein D promoter region and exon 1
3618	8658	13828	5.42	3.4E-01	AF106885.1	NT	Methylococcus sp. strain SS1 putative GtpE (gtpE), DnaK (dnak), and putative DnaJ (dnaj) genes, complete cds
3769	8906		2.04	3.4E-01	BF4469010.1	EST_HUMAN	7n846d11_x1 NCI_CGAP_DnaJ18 Canis lupus IMAGE:3572232 3' similar to TR:QBUU15
4010	9143		0.82	3.4E-01	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4026	9157		1.3	3.4E-01	AA584196.1	EST_HUMAN	no11b1_0.31 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4813	9731	14868	1.87	3.4E-01	BE068912.1	EST_HUMAN	MR4-BT0403-2302010-202-01 BT0403 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
4830	10040		4.7	3.4E-01	AI240875.1	EST_HUMAN	d195c05-x1 NCI_CGAP_Kl33 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
13	5224	10386	7.33	3.3E-01	X07850.1	NT	Rhizobium leguminosarum sym plasmid pRL5.11 nroX gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit No.	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
102	6224	10336	3.16	3.3E-01	X07880.1	NT	Rhizobium leguminosarum sym plasmid pRLSJ1 nadK gene	
447	6616	10761	1.27	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45	
632	6783	10827	1.14	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA	
1203	6338	11507	5.33	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17	
1311	6441	11618	2.69	3.3E-01	BF5688380.1	EST HUMAN	60218401671 NIH MGC_42 Homo sapiens cDNA clone IMAGE:4300261 3'	
1368	6495	11677	1.22	3.3E-01	U43626.1	NT	Human chromosome 16q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster	
1618	6747	11841	1.68	3.3E-01	6753685	NT	Mus musculus dihydrofolate reductase 5 (Dfr5), mRNA	
1750	6876	2.18	3.3E-01	AA332734.1	EST HUMAN	EST36722 Embryo, 8 week (Homo sapiens cDNA 6 and EST36722)		
2382	7488		2.65	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (uridyl phosphoryl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA	
2816	8569	13241	2.39	3.3E-01	AL251805.1	NT	Bacteriophage phi-X174 Q3-12 complete genome	
2988	8141		0.83	3.3E-01	002743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)	
3027	8181	13337	0.77	3.3E-01	AJ007832.2	NT	Streptomyces argillaceus milbemycin biosynthetic genes	
3478	8918	13784	1.15	3.3E-01	AB0128922.1	NT	Homo sapiens MTA1-1 gene, complete cds	
3787	8924	14074	1.88	3.3E-01	084845	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN	
3798	8933	14086	1.12	3.3E-01	P22802	SWISSPROT	GENOME POLYPROTEIN (CONTAINS: N-Terminal PROTEIN (P), HELPER COMPONENT PROTEINASE (HC-PRO), PROTEIN P3)	
3858	9074	14228	1.56	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10	
3976	9110	14258	1.82	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds	
4348	9468		3.18	3.3E-01	D31682.1	NT	Retusa nonneurax DNA (or regulatcdn, partial cds)	
4660	9776		1.49	3.3E-01	AI639114.1	EST HUMAN	b78b12-x1 NCI CGAP U3 Homo sapiens cDNA clone IMAGE:2205407 3' similar to qbx57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);	
4805	9817	16053	1.12	3.3E-01	D84003.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2889768	
486	5624		1.78	3.2E-01	AF016261.1	NT	Rattus norvegicus Eh-damsh binding protein Epsilon mRNA, complete cds	
716	5973		0.62	3.2E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61	
1164	6298	11465	11.49	3.2E-01	AF047013.1	NT	Fusarium roseum virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds	
1286	8416	11691	1.63	3.2E-01	260202.1	NT	P. vulgaris arc5-1 gene	
1397	6825	11704	5.03	3.2E-01	Q48824	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)	
1784	6810	12118	1.45	3.2E-01	Z38041.1	NT	S.cerevisiae chromosome II reading frame ORF YBR172c	
1794	6820	12130	3.16	3.2E-01	AW887184.1	EST HUMAN	EST369264 MAGE sequences, MAGD Homo sapiens cDNA	
1794	6820	12131	3.15	3.2E-01	AW887184.1	EST HUMAN	EST369264 MAGE sequences, MAGD Homo sapiens cDNA	
2142	7258	12502	1.18	3.2E-01	BF2038817.1	EST HUMAN	601883804F1 NIH MGC_17 Homo sapiens cDNA clone IMAGE:4116712 5'	

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Probe Seq ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2512	7615		1.29	3.E-01	7710078 NT	Mus musculus Pbx/Notch1 homolog (Pbxn1), mRNA	
3095	8248	13397	0.65	3.E-01	BF380745.1	EST_HUMAN	IL2-UT073-18050-161-H11 UT0073 Homo sapiens cDNA
3924	8080		0.65	3.E-01	AL161548.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
4318	9438	14571	1.15	3.E-01	4759785 NT	Homo sapiens synaptobin (SYNB), mRNA	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudo genes) and beta globin polypeptides, complete cds
4372	9493	14837	1.41	3.E-01	IM18818.1	NT	SWISSPROT HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4476	8598	14735	1.25	3.E-01	Q10288	EST_HUMAN	602081972E1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4708	98222		7.84	3.E-01	BF5883817.1	EST_HUMAN	602081972E1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4817	89229	16070	1.1	3.E-01	4657558 NT	Homo sapiens E7A binding protein p300 (EP300) mRNA	
5188	10285	16421	1.32	3.E-01	AL161514.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28 yes008.1 Scores fetal liver spleen INF-S Homo sapiens cDNA clone IMAGE:125051 5' similar to yes008.1
2652	7730	12087	1.38	3.E-01	R18051.1	EST_HUMAN	gb M64241 QM PROTEIN (HUMAN)
2658	7879	13004	2.52	3.E-01	7681871 NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA	
2658	7879	13005	2.52	3.E-01	7681871 NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA	
2821	7877		1.08	3.1E-01	AW628039.1	EST_HUMAN	HA6708X1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875391 3'
3163	8204		3.29	3.E-01	AB029069.1	NT	Mus musculus gene for Ser/Thr kinase KIAAMRE, exon 6
3884	9020	14117	1.15	3.1E-01	A1251588.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4942	10052	16180	0.64	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 or 228 of the complete genome
71	7859	10418	1.35	3.0E-01	6755693 NT	Mus musculus protein kinase (Prkca), mRNA	
251	5442	10582	7.64	3.0E-01	A1271735.1	NT	Homo sapiens Xg basethiosubosomal region, segment 1/2 xs63f08X1 Scores_NFL_CGA_P_Kid11 Homo sapiens cDNA clone IMAGE:2774349 3'
1226	6358	11528	2.11	3.0E-01	AW300400.1	EST_HUMAN	
1623	6850	11838	3	3.0E-01	AJ005755.1	NT	Bulaneoptera physalina gene encoding atrial natriuretic peptide
2877	6131		1.03	3.0E-01	AB008877.1	NT	Bos taurus mRNA for UDP-glucuronosyltransferase, complete cds
3188	8339		0.68	3.0E-01	X83361.5.1	NT	Spermatic pecten gene
3188	8347		1.28	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alpPG gene for polyglutamate lyase, complete cds
3844	8580	14135	1.71	3.0E-01	AW817785.1	EST_HUMAN	PMI-ST0282-28119-001-591 ST0282 Homo sapiens cDNA
3947	9082	14234	0.82	3.0E-01	A1271738.1	NT	Homo sapiens Xq pseudobasosomal region, segment 1/2
4487	9608	14744	1.8	3.0E-01	AJ005755.1	NT	Bulaneoptera physalina gene encoding atrial natriuretic peptide
2229	7341	12894	1.01	2.8E-01	AF222718.1	NT	Chrysochromalus symmetricus mitochondrial, complete genome
3163	8316	13478	1.05	2.8E-01	AF078111.1	NT	Xanthopus loco transcription factor E/F mRNA, complete cds
3234	8384	13545	3.56	2.8E-01	AW754239.1	EST_HUMAN	PMI-CT0326-171289-001-f12 CT0326 Homo sapiens cDNA
3234	8384	13546	3.68	2.8E-01	AW754239.1	EST_HUMAN	PMI-CT0326-171289-001-f12 CT0326 Homo sapiens cDNA
3873	9009	14165	0.83	2.8E-01	AJ610838.1	EST_HUMAN	tp21a11_X1 NC_CGA_P_Gaa-Homo sapiens cDNA clone IMAGE:21884123 similiar to tp21a11_X1 NC_FINGER PROTEIN (HUMAN) contains element L1 repetitive element; ZINC FINGER PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4047	9178	14319	0.64	2.8E-01	AB018428.1	NT	Cavia porcellus mRNA for glutathione S-transferase, complete cds
4062	9193		0.65	2.8E-01	AW002892.1	EST_HUMAN	W0210x1 NCI CGAP_GCDB Homo sapiens cDNA clone IMAGE:2480396 3'
4484	6583	14721	0.64	2.8E-01	AA284458.1	EST_HUMAN	z55712x1 NCI CGAP_GCDB Homo sapiens cDNA clone IMAGE:701681 6 similar to contains Ali repetitive element
4657	9774		0.73	2.8E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5012	10115	15246	5.24	2.8E-01	BF104760.1	EST_HUMAN	601822439F1 NIH MGIC_76 Homo sapiens cDNA clone IMAGE:4045818 6'
5012	10115	15247	5.24	2.8E-01	BF104760.1	EST_HUMAN	601822439F1 NIH MGIC_76 Homo sapiens cDNA clone IMAGE:4045818 6'
5088	10196			1.02	AB070899.1	EST_HUMAN	wat063x1 NCI CGAP_Gd11 Homo sapiens cDNA clone IMAGE:22297309 3' similar to contains L1.12 L1 repetitive element;
5205	10302	15638	0.81	2.8E-01	AV724733.1	EST_HUMAN	AV724733 HTBCCFC05 6'
567	6732		3.2	2.8E-01	U67138.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP180 mRNA, complete cds
572	5716		1.03	2.8E-01	L26145.1	NT	Prunus domestica nucleic acid, complete cds; seed protein, complete cds
1084	6223	11390	2.64	2.8E-01	AF168050.1	NT	Gutta gutta cycloide maturation factor (c-mef) gene, partial cds
1281	8410	11685	0.65	2.8E-01	BE313442.1	EST_HUMAN	601148753F1 NIH MGIC_19 Homo sapiens cDNA clone IMAGE:3163688 6'
1281	8410	11686	0.65	2.8E-01	BE313442.1	EST_HUMAN	601148753F1 NIH MGIC_19 Homo sapiens cDNA clone IMAGE:3163688 6'
1285	8424	11597	0.84	2.8E-01	D88550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1740	6867	12072	2.49	2.8E-01	AB060020.1	EST_HUMAN	QV70364-120200-065-B05 CT0364 Homo sapiens cDNA clone DKFZp586j2821
2009	7127	12368	1.22	2.8E-01	AL047820.1	EST_HUMAN	DKFZp586j2321_1' 588 (synonym: NR_1_T_GBC_Scates_NR_1_Homo sapiens cDNA clone IMAGE:28123333
2122	7237	12480	0.98	2.8E-01	AW511195.1	EST_HUMAN	Iw44003x1 Scates_NR_1_Homo sapiens cDNA clone IMAGE:28123333
2447	7661	12804	1.43	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2447	7551	12805	1.43	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2518	7622		1.06	2.8E-01	AL161688.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2628	7725	12878	1.16	2.8E-01	AB020976.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2840	8034		1.32	2.8E-01	AF179480.1	NT	Toxoplasma gondii 80kDa heat-shock protein (HSP80) mRNA, partial cds
2941	8095	13261	2.3	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH112)
2941	8095	13262	2.3	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH112)
3241	8391	13553	0.73	2.8E-01	4603812	NT	Hom sapiens coagulation Factor V procoagulant, labile factor (F5) mRNA
3380	8595	13572	0.88	2.8E-01	AP000604.1	NT	Pynococcus halophilus OT3 genomic DNA, 777001-89400 nt. position (4/7)
3971	9105	14253	1.57	2.8E-01	AE001180.1	NT	Bacillus burgdorferi (section 68 of 70) of the complete genome
4098	9226		0.62	2.8E-01	AE004480.1	NT	Pseudomonas aeruginosa PA01, section 11 of 529 of the complete genome
4170	9298		2.1	2.8E-01	AI090888.1	EST_HUMAN	civ4g10x1 Scates_NHT Homo sapiens cDNA clone IMAGE:1840226 3' similar to contains Ali repetitive element; contains element MfER22 repetitive element;
4434	9553	14698	0.94	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Mage9 gene, Cathepsin, NAD(P) steroid dehydrogenase and Zinc finger protein 185

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4439 9593	14700	282	2.6E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)	
4750 9883	15012	0.98	2.6E-01	D15050.1	NT	Human mRNA for transcription factor AREB3, complete cds	
4750 9883	15013	0.98	2.6E-01	D15050.1	NT	Human mRNA for transcription factor AREB3, complete cds	
4781 8904	16044	0.9	2.6E-01	AF072238.1	NT	Hepatitis G Virus isolate 80 (SGNAE12) polyprotein precursor, gene, partial cds	
4787 8910	16051	2.63	2.6E-01	AF030164.1	NT	Bovine endocrinus 3, complete genome	
4830 8942	16084	1.1	2.6E-01	EF528188.1	EST_HUMAN	602042801FT NCI CGAP_Bm57 Homo sapiens cDNA clone IMAGE:4180129 5' disect1_x1 Scores_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:18708628 3' similar to contains Ali repetitive elementcontains element LTR6 repetitive element;	
4855 8987	16112	2.48	2.6E-01	AI272689.1	EST_HUMAN	Reittus nonnegotius CDK104 mRNA	
476 6643	10784	2.44	2.7E-01	Y17324.1	NT	zC9b10.s1 Scores_Total fetus_Nb21F8_8w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Ali repetitive element	
610 5770	10889	3.75	2.7E-01	AA460061.1	EST_HUMAN	Ipsamia purpurea transposable element Tp100 gene for transposase, complete cds	
1285 6394	11688	2.01	2.7E-01	AB004906.1	NT	Giembla SR2 gene	
1633 6762	12073	1.82	2.7E-01	ZP8815.1	EST_HUMAN	zD22h10.r1 Scores_Heart_NbH18W Homo sapiens cDNA clone IMAGE:31443 5'	
1742 6869	12073	2.26	2.7E-01	W58087.1	EST_HUMAN	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P40; NUCLEOPROTEIN P10]	
1783 6912	12120	1.11	2.7E-01	PO3341	SWISSPROT	Felina immunodeficiency virus env gene, isolate TTCC088P1U (M88), partial	
2124 7633	12707	1.03	2.7E-01	AF047575.1	NT	fel3c11.x2 NCI CGAP_Lu26 Homo sapiens cDNA clone IMAGE:20468398 3' similar to contains element L1 repetitive element;	
2347 7454	12707	3.72	2.7E-01	Y173888.1	NT	Felidae immunodeficiency virus env gene, isolate TTCC088P1U (M88), partial	
2432 7636	12789	2.19	2.7E-01	AI310858.1	EST_HUMAN	fel3c11.x1 Scores_Total fetus_Nb21F8_8w Homo sapiens cDNA clone IMAGE:20468398 3' similar to contains element L1 repetitive element;	
2853 8107		0.77	2.7E-01	BF082284.1	EST_HUMAN	CIM-H10875-05030-385-005 H10875 Homo sapiens cDNA clone IMAGE:24628283	
3986 9120	14287	1.94	2.7E-01	AI928016.1	EST_HUMAN	wr92811x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:24628283	
3986 9130	14274	0.68	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (eEE6) gene, partial cds	
3986 9130	14276	0.68	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (eEE6) gene, partial cds	
4002 9135	14278	2.24	2.7E-01	L77669.1	NT	- Homo sapiens DiGeorge syndrome critical region, telomeric end	
4885 8977	16123	0.66	2.7E-01	27516.1	NT	Tritium testisnum (W6866) gene, complete cds	
6023 10126		3.3	2.7E-01	AW869131.1	EST_HUMAN	RCH-C7286-230200-016-003 C70286 Homo sapiens cDNA	
469 7891	10777	3.04	2.6E-01	PT78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IX-2	
480 5649		1.08	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds	
1400 8528	11707	1.48	2.6E-01	BE885087.1	EST_HUMAN	801510688F1 NIH_MG3C_71 Homo sapiens cDNA clone IMAGE:3012345 6'	
1447 8575	11761	1.26	2.6E-01	AB013280.1	NT	Glycine max pseudogene for Bd 30K	
1803 7022	12241	4.04	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2	
1803	70222	4.04	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2	

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2084	7200			4.41	2.6E-01 AW73162.1	EST_HUMAN	bb04d10_x1 NIH_NIGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:MS60722 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:MI4889_cds1 Mouse surfeit locus surfeit 3 protein gene
2448	7552			2.33	2.6E-01 Y12898.1	NT	B_martinius fbd. gene
2617	7621			4.2	2.6E-01 BE72440.1	EST_HUMAN	6011261016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2880043 5'
3065	8216			1.12	2.6E-01 AW874631.1	EST_HUMAN	EST388835 MAGE resequencing, MAGM Homo sapiens cDNA
3588	8709	15870	0.82	2.6E-01 M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds	
3621	8760	15917	2.13	2.6E-01 AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5	
4076	92016	14341	0.69	2.6E-01 AW889510.1	EST_HUMAN	EST371580 MAGE resequencing, MAGF Homo sapiens cDNA	
4128	9254	14363	16.62	2.6E-01 BE080598.1	EST_HUMAN	QV1-B1063C04040-132-403 BT1030 Homo sapiens cDNA	
4334	9456	14683	1.08	2.6E-01 AF176283.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene	
4470	9589	14728	0.67	2.6E-01 AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds	
4470	9589	14729	0.67	2.6E-01 AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds	
4521	9539	14788	1.38	2.6E-01 AA457617.1	EST_HUMAN	6880070.1 Stratagene fetal retina B372022 Homo sapiens cDNA clone IMAGE:338477 5'	
4816	9734	14871	2.81	2.6E-01 U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhcb3'1) mRNA, complete cds	
4883	9789	14844	1.44	2.6E-01 AF142703.1	NT	Ophiopisthe radiatae matruse-like protein (matr) gene, complete cds; chloroplast gene for chloroplast product	
4956	10084	15203	3.82	2.6E-01 H04682.1	EST_HUMAN	JF516571.1 Scores placenta NB24P Homo sapiens cDNA clone IMAGE:1622288 5'	
238	5431	10570	1.47	2.5E-01	4502286 NT	Homo sapiens ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA	
239	5431	10570	1.65	2.5E-01	4502286 NT	Homo sapiens ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA	
252	5443		4.63	2.5E-01 M26501.1	NT	Sterifast (P. ochraceus) cytoplasmatic actin gene, complete cds	
833	5985	11152	1.13	2.5E-01 U069984.1	NT	Mus musculus ICR/Swiss glycerateidyne 3'-phosphate dehydrogenase (Gapd-S) gene, complete cds	
1081	62012		0.83	2.5E-01 AE002158.1	NT	Ureaplasma urealyticum section 57 of 58 of the complete genome	
1122	62530	114226	10.46	2.6E-01 188837.1	EST_HUMAN	ye11g7.1 Stratagene lung (F33721) Homo sapiens cDNA clone IMAGE:1174638 6'	
1388	6510		0.98	2.5E-01 AB025343.1	NT	Olea europaea OEW mRNA for lipid synthase, complete cds	
1741	6868		3.12	2.6E-01	4885406 NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA	
1891	7828	12230	1.19	2.6E-01 BE688604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA	
1891	7828	12231	1.19	2.5E-01 BE688604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA	

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2384 7490			2.19	2.6E-01	AED00676.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2467 7571			1.12	2.6E-01	AA251987.1	EST_HUMAN	25111a12.1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:984862 5'
3394 85318			3.28	2.6E-01	AY873471.1	EST_HUMAN	EST388464 IMAGE resequencing, MGC Homo sapiens cDNA
3522 85833	13830	1.17	2.6E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds	
3538 89778	13830	6.55	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29	
3824 8950	14108	1.49	2.6E-01	AI741483.1	EST_HUMAN	wg11c07.1x Scares_NSF_F8_SW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2384780 3'	
3824 8960	14108	1.49	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.1x Scares_NSF_F8_SW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2384780 3'	
4043 9174			0.84	2.6E-01	P322323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4286 94117			0.79	2.5E-01	Q03314	SWISSPROT	RHB PROTEIN
4714 98330			1.19	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4721 9835	14979	3.61	2.5E-01	AF007768.1	NT	Chordataeae funiformis drosophila associated protein 2 (DAP2) mRNA, complete cds	
4749 9862	15011	1.83	2.6E-01	AEG04416.1	NT	Vibrio cholerae chromosome II, section 73 of 83 of the complete chromosome	
4771 9884			3.4	2.5E-01	AI230113.1	NT	Mus musculus synaptosomal V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
6203 10300	15437	24.69	2.6E-01	U97888.1	NT	Arabidopsis thaliana FKBP6 binding protein FKBP22 (ROF1) gene, complete cds	
552 5717	10849	0.74	2.4E-01	AA533316.1	EST_HUMAN	en7004.81 ScaresNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:162023 3'	
849 6000	11172	2.08	2.4E-01	BF78124.1	EST_HUMAN	6012c42f1 NIH_3T3 G-81 Homo sapiens cDNA clone IMAGE:1271578 6'	
1303 8438	11613	13.62	2.4E-01	AA289880.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and ZTFL1 gene	
1308 8438	11614	13.62	2.4E-01	AA289880.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and ZTFL1 gene	
1394 6522	11701	1.03	2.4E-01	Y17283.1	NT	Homo sapiens FLI-1 gene, partial	
1882 6082			7.18	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1806 7026	12245	0.88	2.4E-01	AF251708.1	NT	Zacry's drummades fructos-1,6-bisphosphatase mRNA, complete cds	
2242 7553	12810	1.8	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome	
2510 7813	12883	1.72	2.4E-01	Z36534.1	NT	D. discoideum (Ax3-K) pona gene	
2723 7818	13074	1.33	2.4E-01	XT1783.1	NT	S. pombe swi8 gene	
2747 7841	13068	3.47	2.4E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome	
3110 8263			2.69	2.4E-01	U72728.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pac) genes, complete cds
3126 8276	13434	1.77	2.4E-01	X74208.1	NT	H. sapiens AGT gene, part fragment of intron 4	
3741 8879	14030	0.82	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome	
4004 9197			0.68	2.4E-01	D29850.1	NT	Rattus norvegicus mRNA for alphaB oncostatin-related protein, complete cds
4882 9363	15140	9.08	2.4E-01	BE1600080.1	EST_HUMAN	QV1-H10412-02040-136-b10 HT0412 Homo sapiens cDNA	
387 6556	10700	0.87	2.3E-01	S75898.1	NT	aromatase [Porphobilinogen deaminase, ovary, mRNA, 3188 nt]	
636 6797		5.1	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 61 of the complete genome	

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## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit No.	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
668	6826	10984	17.78	2.3E-01	U675986.1	NT		Methanococcus jannaschii section 138 of 150 of the complete genome
895	8083	11248	3.03	2.3E-01	BE311893.1	EST_HUMAN	601142073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:35958118 5'	
1524	6651	11837	1.01	2.3E-01	68777880	NT	Mus musculus vacuolar protein sorting 4b (yeast) mRNA	
1842	8770	11984	2.22	2.3E-01	Y10887.2	NT	Mus musculus cdna gene, exon 1, partial	
2039	7168		1.14	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEF gene	
2428	7528	12780	1.37	2.3E-01	BE297718.1	EST_HUMAN	601165622F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:35931016 6'	
2812	7711	12884	1.05	2.3E-01	M1319.1	NT	Human erythropoietin gene, complete cds	
2784	8523	11702	2.19	2.3E-01	AB016033.1	NT	Marmosatilla agavevirens GyrB gene for DNA gyrase subunit B, partial cds, strain JFO 14857 no18d08 s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to ccmbr_Alu repetitive element contains element TIR repetitive element	
2832	8088	13263	0.87	2.3E-01	AA601378.1	EST_HUMAN	Y21567.31 Scores placenta Nb24F1 Homo sapiens cDNA clone IMAGE:130357 3'	
3093	8209		5.29	2.3E-01	R21732.1	EST_HUMAN	Y87710.71 Scores fetal liver spleen NFLS Homo sapiens cDNA clone IMAGE:213283 5'	
3382	8457	13688	0.8	2.3E-01	H68936.1	EST_HUMAN	Homo sapiens arachidonate (16-lipoxygenase) (ALOX15) mRNA	
3489	8530	13797	0.84	2.3E-01	4502054	NT	GSTA5-glutathione S-transferase Yc2 subunit (5' region, intron 1 [rat], Muris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]	
3818	8855	14103	1.02	2.3E-01	S82821.1	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA	
3908	9044		6.06	2.3E-01	7662133	NT	Y1767.11 Scores placenta Nb24F1 Homo sapiens cDNA clone IMAGE:148017 5'	
4327	9449	14582	0.7	2.3E-01	RB2252.1	EST_HUMAN	Mus musculus retina (Ren-16) gene, promoter region	
4378	8500		1.33	2.3E-01	L78789.1	NT	Synecystis sp. PCC6803 complete genome, 1/2-1-133859	
4428	9548	14690	0.7	2.3E-01	D80899.1	NT	Homo sapiens mitogen-activated protein kinase p32delta (PRKMK13) mRNA, complete cds	
4465	9584	14722	2.1	2.3E-01	AF082559.1	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA	
4527	9846	14782	6.45	2.3E-01	5031984	NT	6053 10155 16226 0.91 EST_HUMAN 601189163F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126368 5'	
6171	10269	15410	1.05	2.3E-01	AE000240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome	
6195	10282	15429	0.58	2.3E-01	U45324.1	NT	Human Kruppel-related 3 (HNR3) gene, exons 1-3	
85	5284		0.72	2.2E-01	A10521B0.1	EST_HUMAN	ccf14810.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672280 3' similar to TR-013040 Q13040 ATP-BINDING CASSETTE PROTEIN :	
1680	6709	11900	2.93	2.2E-01	AF187850.1	NT	Homo sapiens PPAR delta gene, promoter region	
2014	7131		2.57	2.2E-01	AF171501.1	NT	Trimeresurus melaleucus cobra gene, mitochondrial gene for mitochondrial product	
2082	7198	12443	1.53	2.2E-01	M34840.1	NT	Fresh-water sponge Ennf1 alpha collagen (COLF1) gene	
2381	7487	12741	2.76	2.2E-01	BF077338.1	EST_HUMAN	602086808F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4249689 5'	
2649	7652	12801	1.39	2.2E-01	BE618258.1	EST_HUMAN	6011426229F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:359581190 5'	
2649	7652	12902	1.39	2.2E-01	BE618258.1	EST_HUMAN	6011426229F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:359581190 5'	
2848	8003	13163	4.77	2.2E-01	BE155825.1	EST_HUMAN	PM2-FTT0353-281/289-003-a12 HT0353 Homo sapiens cDNA PM2-FTT0353-281/289-003-a12 HT0353 Homo sapiens cDNA	
2848	8003	13184	4.77	2.2E-01	BE155825.1	EST_HUMAN		

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Single Exon Probes Expressed in BT474 Cells

Probe Seq ID	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit No.	Top Hit Accession	Top Hit Database Source	Top Hit Descriptor
2888	8040			1.5	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3373	8518			2.23	2.2E-01	AL161682.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3781	8028			1.47	2.2E-01	AF158728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4185	9311			0.92	2.2E-01	AF118102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4195	8320			5.31	2.2E-01	AF155142.1	NT	Mus musculus mitoGK kinase 3 (Milk3) and two pore domain K+ channel subunit (Kcnk8) genes, complete cds
4237	8382	14494		2.75	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Makk1) mRNA, complete cds
4237	9362	14495		2.75	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Makk1) mRNA, complete cds
4353	9465	14591		1.02	2.2E-01	U01307.1	NT	Human sRNA (BC200 beta) pseudogene
4353	9466	14692		1.02	2.2E-01	U01307.1	NT	Human sRNA (BC200 beta) pseudogene
4477	8587	14736		0.95	2.2E-01	Z54148.1	NT	Boabuts bp26 gene
4784	8937	9127		1.27	2.2E-01	D50504.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4790	9012	15053		3.51	2.2E-01	AA211216.1	EST_HUMAN	zBTG05.1 Stratagene HNT neuron (8837233) Homo sapiens cDNA clone IMAGE:9488688 5'
6026	10127			1.41	2.2E-01	L13289.1	NT	Mus musculus Vinculin gene, exon 3
6038	10169	15338		1.03	2.2E-01	BE141035.1	EST_HUMAN	MFD-HT0037-20109-002-c10 HT0037 Homo sapiens cDNA
6115	10218			0.95	2.2E-01	S57565.1	NT	Histamine H2-receptor [Rats, Genomic, 1828 nt]
6145	10245	15333		1.83	2.2E-01	4502988	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
6164	10291	15428		0.98	2.2E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
5220	10297	15434		1.8	2.2E-01	HE05648.1	EST_HUMAN	y42H9.1 Severe fetal liver spleen tNFLS Homo sapiens cDNA clone IMAGE:208001 5' similar to gb:Z14116 m1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
972	8119	11289		1.38	2.1E-01	AA568289.1	EST_HUMAN	lmm3161.31 NCI CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1081804
976	6121	11291		0.97	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
1126	6282			2.16	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 46 of 85 of the complete genome
1201	6334	11603		1.11	2.1E-01	6734288	NT	Mus musculus Interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1201	6334	11504		1.11	2.1E-01	6764289	NT	Mus musculus Interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1816	7035	12256		1.10	2.1E-01	AA809824.1	EST_HUMAN	ck73e02.51 NCI CG4 Homo sapiens cDNA clone IMAGE:1518610 3' similar to dbK02765 COMPLEMENT C3 PRECURSOR (HUMAN);
2139	7253	12499		1.88	2.1E-01	BF6865073.1	EST_HUMAN	602088128F1 NIH MGCG_81 Homo sapiens cDNA clone IMAGE:427503 5'
2880	8044	18209		1.83	2.1E-01	6912446	NT	Homo sapiens potassium voltage-gated channel, subfamily H (��-related), member 4 (KCNH4), mRNA
3785	8522			6.31	2.1E-01	9838861	NT	Beta vulgaris mitochondrial, complete genome
4028	9169	14302		1.27	2.1E-01	P11676	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180

**Table 4**  
**Single Exon Probes Expressed in BT474 Cells**

Probe Seq ID No:	Exon Seq ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Value	BLAST E	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4028 8169	14303		1.27	2.E-01	P11676	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE-180	Homo sapiens mRNA for KIAA1215 protein, partial cds
4356 8477			1.69	2.E-01	AB03390441.1	NT		Homo sapiens HSP47 gene, complete cds
4649 9687	14899		2.37	2.E-01	AB010273.1	SWISSPROT	ALPHA-2A ADRENOCEPTOR (ALPHA-2AAR)	
5056 10158	15289		1.15	2.E-01	Q01338	SWISSPROT		Homo sapiens static acid-binding immunoglobulin-like lectin-9 (SIGLEC9) gene, complete cds
6158 10259			0.68	2.E-01	AF139027.1	NT		Gelius gratus mRNA for arena, complete cds
197 5392	10536		1.81	2.E-01	AB017437.1	NT		Homo sapiens CGI-18 protein (LOC51008), mRNA
532 5693			2.13	2.E-01	7705621	NT		Ocuminculus germline IgH heavy chain V-H pseudogenes, allele type V-H2
687 6854	10889		1.44	2.E-01	M77085.1	NT		Mus musculus Major Histocompatibility Locus class II region
811 6964	11128		1.69	2.E-01	AF027885.1	NT		Synaptosomal sp. PCG853 complete genome, 7/27, 781449-820816
1012 6165	11321		0.63	2.E-01	D69205.1	NT		Homo sapiens chromosome 21 segment HS21 C013
1128 9263	11427		2.67	2.E-01	AL169213.2	NT		Homo sapiens rat 1 gene
1268 6387	11584		1.19	2.E-01	AJ132089.5	NT		PMI-H70422-281/289-002-c06 HT0422 Homo sapiens cDNA
1312 6442	11619		1.56	2.E-01	AW384797.1	EST_HUMAN		Plum pox virus strain M, complete genome, isolate P_S
1471 6593			1.61	2.E-01	AJ248957.1	NT		Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1497 6824	11812		2.89	2.E-01	4803408	NT		Homo sapiens mRNA, chromosome 7 specific transcript KIAA0506
1687 6895	11882		4.68	2.E-01	AB007874.1	NT		Homo sapiens sodium/calcium exchanger mRNA, partial cds
1572 6700	11888		1.65	2.E-01	AF280700.1	NT		Human bradykinin B1 receptor (bradyb1) gene, complete cds
1710 6838	120339		1.27	2.E-01	U22346.1	NT		Homo sapiens Jagged2 gene, complete cds; and unknown gene
1732 6859					AF111170.3	NT		Methanococcus jannaschii section 67 of 150 of the complete genome
1769 6895					2.1	2.E-01	U67625.1	
1897 7016	12236		1.08	2.E-01	AF8971330.1	EST_HUMAN	6011449441E NIH MGIC_85 Homo sapiens cDNA clone IMAGE:3853330 5'	
1897 7016	12237		1.08	2.E-01	AF8971330.1	EST_HUMAN	6011449441F1 NIH MGIC_85 Homo sapiens cDNA clone IMAGE:3853330 5'	
2327 7436			1.03	2.E-01	XP282877.1	NT		H.sapiens N-ac-D-glucosidase transporter regulator gene
3555 8696			0.84	2.E-01	AW288005.1	EST_HUMAN	XP1510221 NCL_CGAP_H9N9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element MER21 repetitive element;	
3684 8623	13979		0.64	2.E-01	P24641	SWISSPROT	CED-11 PROTEIN	
3689 8628			0.71	2.E-01	6680787	NT		Mus musculus bone morphogenic protein 8 (Bmp8), mRNA
3927 8083	14221		0.83	2.E-01	Z48908.1	NT		Sus scrofa
4003 9138	14279		0.78	2.E-01	X63397.1	NT		Ciperellia capC gene
4409 8528	14669		0.74	2.E-01	AF242431.1	NT		Mus musculus neuronal apoptosis inhibitor protein 6 (Nrip6) gene, complete cds; and Nap3 gene, exons 2-9 and 11-16
4538 8598			7.82	2.E-01	BE226165.1	EST_HUMAN	QV4-EN0032-180501-223-e03 EN0032 Homo sapiens cDNA	
5022 10124	15256		5.56	2.E-01	8922080	NT		Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5087 10187	15328		0.88	2.E-01	Y18216.1	NT		Homo sapiens putative psihBD pseudogene for hprt karytin, exons 1 to 9

Table 4  
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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5169 10287	15408		48.35	2.0E-01	Y14880_1	NT	Actinobacter baumannii fur gene
108 6310			7.75	1.8E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arnt), mRNA
349 6532	10871		4.93	1.8E-01	AF004863.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
6555 5810	10953		1.43	1.9E-01	[U]32581_2	NT	Homo sapiens lamphodota protein kinase C-interacting protein mRNA, complete cds
6535 5810	10954		1.43	1.9E-01	[U]32581_2	NT	Homo sapiens lamphodota protein kinase C-interacting protein mRNA, complete cds
692 5823	10861		5.59	1.8E-01	BE070801_1	EST_HUMAN	RC3-BT0502-251189-01-001 BT0502 Homo sapiens cDNA
683 5823	10981		4.32	1.8E-01	BE070801_1	EST_HUMAN	RC3-BT0502-261189-01-001 BT0502 Homo sapiens cDNA
987 6133			1.34	1.8E-01	7305180	NT	Mus musculus interferokin 2 receptor, gamma chain (IKB2G), mRNA
1105 6243	11407		7.57	1.8E-01	AA358813_1	EST_HUMAN	EST67784 Fatal lung    Homo sapiens cDNA 5' end
1378 6507	116889		1.73	1.9E-01	AF0061282.1	NT	Sorghum bicolor 22 kDa kifin cluster
1445 6573			2.28	1.9E-01	AF184823.1	NT	Plasmodium vivax neutrophilic binding protein-2 (top-2) gene, complete cds
2381 7468	12723		1.77	1.8E-01	8922353	NT	Homo sapiens hepatocyte nuclear factor 2 (HNF1058), mRNA
2888 8042	13208		4.43	1.8E-01	U563058.1	NT	Stigmatodon hispidus p53 gene, partial cds
2904 8057			5.64	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
2912 8128	13280		0.97	1.9E-01	U25148.1	NT	Rattus norvegicus brush border myosin-H (BBM), mRNA, partial cds
3379 8321	13885		3.67	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3461 8803	13787		4.34	1.8E-01	IR16497.1	EST_HUMAN	Y42H10.1 Scores fetal liver spleen (FLS) Homo sapiens cDNA clone IMAGE:1286476
3783 8920	14071		0.77	1.9E-01	AF2284017.1	NT	Rattus norvegicus arylalkylamine N-acetyltransferase gene, complete cds
3887 9102	14250		4.13	1.9E-01	AB005784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4050 9191	14332		1.39	1.9E-01	AW784108.1	EST_HUMAN	CKR3-CT0315-21189-045-511 CT0315 Homo sapiens cDNA
4209 9334	14468		1.02	1.9E-01	BE32493.1	EST_HUMAN	IMR-FN010-280700-007-004 FN0010 Homo sapiens cDNA
4448 9557	14708		0.89	1.9E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4988 10104			0.98	1.8E-01	AF228642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
30 5241	10357		2.94	1.8E-01	U73200.1	NT	Mus musculus p116RP mRNA, complete cds
257 7887	10586		1.87	1.8E-01	AB022090.1	NT	Mus musculus Ccr5 gene for chaperonin containing TCP-1 gamma subunit, partial cds
368 5548	10692		1.14	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
743 5901	11055		0.7	1.8E-01	AB021490.2	NT	Oryza latipes gene for membrane glutamyl cyclase Olig1, complete cds
983 6129	11287		0.65	1.8E-01	AI012212.1	EST_HUMAN	wd71012.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1092 6280	11394		1.22	1.8E-01	AF000580.1	NT	Dicystostelium discoideum plasmid Dcp5, complete genome
1292 6421	11596		6.95	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1618 6645	11681		1.83	1.8E-01	6753947	NT	Mus musculus guanylyl nucleotide binding protein 1 (Gbp1), mRNA
1518 6645	11832		1.83	1.8E-01	6753947	NT	Mus musculus guanylyl nucleotide binding protein 1 (Gbp1), mRNA
1853 6978			1.09	1.8E-01	4505038	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1877	6997		1.21	1.8E-01	AI733708.1	EST_HUMAN	0922d1036 NCI_CGAP_K13 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:0765938 O765936 GAMMA BUTYROBETAINE HYDROXYLASE;
1918	7037	12257	1.29	1.8E-01	AB051897.1	NT	Mus musculus Scyta8, Scyta9, Scyta9-esp, Scyta5 genes for small inducible cytokine A8 precursor, small inducible cytokine A9 precursor, Scyta16 pseudogene, small inducible cytokine A8 precursor, complete cds
2653	7761		1.44	1.8E-01	AV935728.1	EST_HUMAN	Q73-D0018-081-289-038-804 D70018 Homo sapiens cDNA
2863	8018		1.78	1.8E-01	AF184589.1	NT	Jonatidium aciculatum LEAFY protein (LEAFY2) gene, partial cds
2888	8022	13189	1.54	1.8E-01	AV182300.1	EST_HUMAN	X415e3_x1 Scytes_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2558766 3'
3101	8264	13404	2.1	1.8E-01	AV985178.1	EST_HUMAN	Q70-BN0041-070300-147-004 BN0041 Homo sapiens cDNA
3348	8493	13660	0.63	1.8E-01	BF163582.1	EST_HUMAN	6016081723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3'
3604	8743	13897	0.78	1.8E-01	HP3369.1	EST_HUMAN	X45e61_x1 Scytes placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Aliu repetitive element
3604	8743	13898	0.78	1.8E-01	HP3369.1	EST_HUMAN	X45e61_x1 Scytes placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Aliu repetitive element
4309	9431		0.89	1.8E-01	D377854.1	NT	Bovine NB25 mRNA for MHC class II (Bc1A-DQB), complete cds
4528	9847	14793	6.51	1.8E-01	AL161656.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 88
4738	9851	14989	2.65	1.8E-01	AB051897.1	NT	Mus musculus Scyta8, Scyta9, Scyta9-esp, Scyta5 genes for small inducible cytokine A8 precursor, small inducible cytokine A9 precursor, Scyta16 pseudogene, small inducible cytokine A5 precursor, complete cds
4774	9887	15033	1.05	1.8E-01	S92179.1	NT	S. tuberosum mRNA for alcohol dehydrogenase
4837	9949	16093	50.8	1.8E-01	AA1383750.1	EST_HUMAN	E5T7176 Testis I Homo sapiens cDNA 5' end
6027	10129	15258	1.83	1.8E-01	AW814270.1	EST_HUMAN	MIR3-ST0203-151289-112-q00 S70203 Homo sapiens cDNA
6041	10143	16273	0.89	1.8E-01	AI792382.1	EST_HUMAN	sm2Bq077_5' Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1760028 5'
5078	10180	15316	10.32	1.8E-01	AF181268.1	NT	Mesocerfetus auratus Na+-lurocholate cotransporting polypeptide mRNA, partial cds
5092	10182	16332	0.81	1.8E-01	AI459881.1	EST_HUMAN	E57604_x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134690 3'
6133	10233	16389	11.74	1.8E-01	AJ132844.1	NT	Broad bean with virus 2 genes encoding 118kDa protein, 104kDa protein, large coat protein, small coat protein
6133	10233	16370	11.74	1.8E-01	AJ132844.1	NT	Broad bean with virus 2 genes encoding 118kDa protein, 104kDa protein, large coat protein, small coat protein
575	5739	10866	1.83	1.7E-01	BE385184.1	EST_HUMAN	E61274604F1 NH_MGC_20 Homo sapiens cDNA clone IMAGE:3815768 5'
800	5959	11122	2.09	1.7E-01	XE53330.1	NT	P.dumerili histone gene cluster for core Histones H2A, H2B, H3 and H4
662	6110		1.5	1.7E-01	P385616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE)(NF-L)
1983	7100		1.85	1.7E-01	AI7256051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product

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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2823 7979	13138	2.4	1.7E-01	AF000716.1	NT		Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapt) gene, complete cds, and YRAL_VIBCO gene, partial cds
2823 7979	13139	2.4	1.7E-01	AF000716.1	EST HUMAN		Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapt) gene, complete cds, and YRAL_VIBCO gene, partial cds
2892 8046	13211	1.38	1.7E-01	AA338909.1	EST HUMAN		EST14851 Endometrial tumor Homo sapiens cDNA 5' end
2865 8119	13282	1.14	1.7E-01	AJ238736.1	NT		Naja naja naja cdk-1 gene, exons 1-3
2865 8119	13283	1.14	1.7E-01	AJ238736.1	NT		Naja naja naja cdk-1 gene, exons 1-3
9091 8234	13384	1.61	1.7E-01	AF081614.1	NT		Tetrix canadensis tRNA synthetase diiphosphate synthase mRNA, complete cds
9347 8482	13659	0.61	1.7E-01	NE5763.1	EST HUMAN		J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3428 8570	13730	1.32	1.7E-01	AJ269505.1	NT		Anelaphus sp. ORF4 (partial), ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3911 8047	14208	6.39	1.7E-01	AJ235377.1	NT		Homo sapiens derivative 11 breakpoint fragment partial intron 10 of the ALL-1/MLLHRX gene fused to intron 5 of the AF-4/FEL1 gene
4533 8851		1.76	1.7E-01	AJ269506.1	NT		Schistoscoeca gigantea alpha repetitive DNA
4806 8818	16059	1.16	1.7E-01	AI247685.1	EST HUMAN		qf57608_x1_Scares_fetal_liver_spleen_1NFL_S_1 Homo sapiens cDNA clone IMAGE:18489008 3' similar to contains ORF, ORF1, ORF2 repetitive element;
5103 10204		1.17	1.7E-01	AF072725.1	NT		Zearumus strobli branching enzyme IIb (ze) gene, complete cds
5138 10238	15374	0.62	1.7E-01	BF030010.1	EST HUMAN		6015257-1 NIH_MSC_58 Homo sapiens cDNA clone IMAGE:3827197 5'
121 6321	10465	1.23	1.8E-01	AF217632.1	NT		Homo sapiens myotrophin kinase gene, exon 6 and 7
678 7869	10978	1.16	1.8E-01	AF31497.1	EST HUMAN		AF76172.1 Scares placenta NB2H1P Homo sapiens cDNA clone IMAGE:1856589 6'
1519 6846	11833	1.19	1.8E-01	AA5468863.1	EST HUMAN		AF28d12.61 NCI_CQAP_Co11 Homo sapiens cDNA clone IMAGE:1014839 3'
1637 6884	11850	3.14	1.8E-01	AF289117.1	NT		Homo sapiens homeobox protein OTZ2 gene, complete cds
1929 7048	12269	1.14	1.8E-01	P22058	SWISSPROT		AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2363 7839	12725	1.35	1.8E-01	X64232.1	NT		H. sapiens mRNA for novel T-cell activation protein
2385 7481	12744	1.94	1.8E-01	AL161633.2	NT		Arabidopsis thaliana DNA chromosome 4, contig fragment 1 No. 33
2858 8013	13176	33.76	1.8E-01	AF185589.1	NT		Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2858 8013	13177	33.76	1.8E-01	AF185589.1	NT		Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3813 8752	13908	1.03	1.8E-01	AJ003165.1	NT		Populus trichocarpa cv. Trichobet AB3 gene
3813 8762	13909	1.03	1.8E-01	AJ003165.1	NT		Populus trichocarpa cv. Trichobet AB3 gene
3976 9109		2.81	1.8E-01	AE004419.1	NT		Vibrio cholerae chromosome II, section 70 of 63 of the complete chromosome
4305 9427	14862	10.51	1.8E-01	AF178680.1	NT		Homo sapiens apelin gene, complete cds
4435 9554		2.61	1.8E-01	AW668601.1	EST HUMAN		EST1380877 MAGE resequences, MAGU Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4443	9502		4.45	1.6E-01	9753319 NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA	
4022	10032	15173	1.22	1.6E-01	AA088343.1	EST_HUMAN	Mus musculus cDNA clone (#897204) Homo sapiens cDNA clone IMAGE:611361 3' similar to TRE221865
4952	10080	15168	1.54	1.6E-01	AJ006386.1	NT	ZB41008 38 855 BP SEGMENT OF CHROMOSOME XIV.
4952	10080	16189	1.54	1.6E-01	AJ006388.1	NT	Lycopodium esculentum RsaI fragment 2, satellite region
5101	10201	15339	1.02	1.6E-01	AL353984.1	EST_HUMAN	DKFZ443401729_11434 (synonym: hest3) Homo sapiens cDNA clone DKFZ443401729 5'
6101	10201	15340	1.02	1.6E-01	AL353984.1	EST_HUMAN	DKFZ443401729_11434 (synonym: hest3) Homo sapiens cDNA clone DKFZ443401729 5'
5186	10283	16420	0.97	1.6E-01	AL161684.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
2445	10575	1595	1.59	1.6E-01	BE710087.1	EST_HUMAN	IL3+TT0619-040700-197-E006 HT00619 Homo sapiens cDNA
2445	10578	10578	1.59	1.6E-01	BE710087.1	EST_HUMAN	IL3+TT0619-040700-197-E005 HT00619 Homo sapiens cDNA
585	7864		2.03	1.6E-01	AV711688.1	EST_HUMAN	AT711688 DCAI008 5'
783	5598	11098	1.83	1.6E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1083	6231	11395	0.84	1.6E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EG3G522 myosin heavy chain, 3'UTR
1089	6238	11399	2.29	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1114	6252		1.53	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1218	63161	11520	1.03	1.5E-01	AW198616.1	EST_HUMAN	AK29d11.XT NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:26960985 3'
1279	8498	11592	3.97	1.5E-01	D28535.1	NT	Human gene for dihydroxyacetone phosphate succinyltransferase, complete cds (exon 1-15)
1279	8498	11563	3.97	1.5E-01	D28535.1	NT	Human gene for dihydroxyacetone phosphate succinyltransferase, complete cds (exon 1-16)
1492	6819	11809	1.88	1.6E-01	AF117340.1	NT	Mus musculus MAP Kinase Kinase 1 (Mkk1) mRNA, complete cds
2079	8033		1.19	1.6E-01	AW672516.1	EST_HUMAN	XW82d122 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X55072_mer1
3007	8161	13318	0.88	1.6E-01	MS1441.1	NT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3334	8480	13846	4.18	1.5E-01	AAC85049.1	EST_HUMAN	oc88d05.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3350	8495	13863	0.61	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN).
3350	8495	13864	0.61	1.5E-01	Z23104.1	NT	L_stagialis mRNA for G protein-coupled receptor
3736	8874	14025	2.63	1.5E-01	U08884.1	NT	Mus musculus IC17Smiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S1) gene, complete cds
3752	8889	14040	1.34	1.5E-01	710335B NT	Homologous protein, mRNA	Homologous protein, mRNA
3848	8882	14137	2.23	1.5E-01	AW685983.1	EST_HUMAN	HJ10583_XL_Scarce_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28814113'
4024	8166	14300	0.88	1.5E-01	AW366959.1	EST_HUMAN	RC22+TT1049-1810859-012-c08 HT0149 Homo sapiens cDNA
4154	9280	14416	8.83	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4693	9809	14956	1.65	1.5E-01	BF687685.1	EST_HUMAN	020267182P1 NIH_M3C_57 Homo sapiens cDNA clone IMAGE:4066223 5'

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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4718	7769	19021	2.25	1.6E-01	BF695381.1	EST_HUMAN	6020832691F1 NIH_MG3C_81 Homo sapiens cDNA clone IMAGE:4247537 5
4738	3871	15021	1.18	1.6E-01	BE173798.1	EST_HUMAN	CMV-H1T0568-280/200-245-b10 H1T0565 Homo sapiens cDNA
4758	3871	15022	1.18	1.6E-01	BE173798.1	EST_HUMAN	CMV-H1T0568-280/200-245-b10 H1T0565 Homo sapiens cDNA
4885	100093	15224	1.21	1.6E-01	AL161560.2	NT	Arabidopsis thaliana DNA clone IMAGE:4241685 4, contig fragment No. 60
297	6485		0.88	1.4E-01	AF058663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8S5P to TCRBV1S2A2 region
911	6091		2.65	1.4E-01	DY78583.1	NT	Xenopus laevis mRNA for DNA (cytosine-5-)methyltransferase, complete cds
1263	6392		2.4	1.4E-01	1731884.1	EST_HUMAN	xd6Ac01.61 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3
1760	6886		1.38	1.4E-01	6078880	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1763	6889	12093	1.83	1.4E-01	AE00710.1	NT	Thermotoga maritima section 22 of 138 of the complete genome
1988	7103		8.62	1.4E-01	AA720815.1	EST_HUMAN	ny72401.51 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3
2763	7847	13103	2.03	1.4E-01	AB634981.1	EST_HUMAN	wn74d01.1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441685 3
3875	8011	14167	1	1.4E-01	R592321.1	EST_HUMAN	yg57463.11 Soares infant brain NIB Homo sapiens cDNA clone IMAGE:41487 5
3876	8011	14168	1	1.4E-01	R592322.1	EST_HUMAN	yg57463.11 Soares infant brain NIB Homo sapiens cDNA clone IMAGE:41487 5
4145	9273	14410	8.95	1.4E-01	AI6890894.1	EST_HUMAN	ts56cd02x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3
4145	9273	14411	8.95	1.4E-01	AI6890894.1	EST_HUMAN	ts56cd02x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3
4216	8340	14472	3.21	1.4E-01	AE00710.1	NT	Thermotoga maritima section 22 of 138 of the complete genome
4648	9768	14611	0.78	1.4E-01	6453881	NT	Human ciliophorus phosphodiesterase 4A, cAMP-specific (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA
320	6508	10844	1.71	1.3E-01	4758487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
320	6508	10845	1.71	1.3E-01	4758487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
527	5593	10825	2.28	1.3E-01	AB013139.1	NT	Homo sapiens gene for NB51, complete cds
635	5798	10930	0.94	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Gilfingerton03/UK RNA for capsid protein (ORF2), strain HUNLV/Gilfingerton03/UK
635	5798	10931	0.94	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Gilfingerton03/UK RNA for capsid protein (ORF2), strain HUNLV/Gilfingerton03/UK
845	63938	11167	0.82	1.3E-01	X53330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
893	6046	11216	1.34	1.3E-01	AF138618.1	NT	Rattus norvegicus A-Kinase anchor protein mRNA, complete cds
1028	6169	11334	1.59	1.3E-01	AL117078.1	NT	Bombyx cineraria strain T4 cDNA library under conditions of nitrogen deprivation
1128	6265		2.22	1.3E-01	AL115285.1	NT	Bombyx cineraria strain T4 cDNA library under conditions of nitrogen deprivation
1218	6350	11519	2.48	1.3E-01	AV712487.1	EST_HUMAN	AV712487 DCA/Hcna cDNA clone DCAAF-F05 5
1465	6582		0.98	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1863	7080	12304	1.49	1.3E-01	AL117078.1	NT	Bostrychoplites cinereus strain T4 cDNA library under conditions of nitrogen deprivation
2287	7377		1.09	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-181089-032412 S10173 Homo sapiens cDNA
2360	7487		1.82	1.3E-01	AE001016.1	NT	Archaeobdulus fulgidus section 91 of 172 of the complete genome

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit No.	Top Hit Accession	Top Hit Database Source	Top Hit Descriptor
2548	7651	12800	1.78	1.3E-01	M86918.1	NT		Carexius burrusus keratin type I mRNA, complete cds
3338	8484	13650	1.12	1.3E-01	AF188778.1	NT		Homo sapiens transcription factor 1 (GTF-M protein), M4 protein, JM11 protein, JM10 protein, A2; differentiation-dependent protein, triplex DNA domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha 2$
3482	8574	13734	0.9	1.3E-01	M21572.1	NT		Bovine branched chain alpha-keto acid dihydrolyase mRNA, complete cds
3702	8840	13894	1.39	1.3E-01	AP000001.1	NT		Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (17)
3702	8840	13895	1.39	1.3E-01	AP000001.1	NT		Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (17)
3709	8847	14001	0.7	1.3E-01	AB032159.1	NT		Homo sapiens DD4 gene for dihydrodol dehydrogenase 4 (AKR1C4), exon 2
3781	8918	14069	0.67	1.3E-01	6978840	NT		Rattus norvegicus Fibronogen, gamma polypeptide (Fg9), mRNA
3963	9098			1.48	1.3E-01	AL1616812	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 77
4025	5796	10930	0.77	1.3E-01	AJ277696.1	NT		Human calicivirus H1/L1/N1/Gattington/B3/UK RNA for capsid protein (ORF2), strain H1/N1/V/Gattington/B3/UK
4026	5788	10831	0.77	1.3E-01	AJ277696.1	NT		Human calicivirus H1/N1/V/Gattington/B3/UK RNA for capsid protein (ORF2), strain H1/N1/V/Gattington/B3/UK
4109	8237			1.01	1.3E-01	AF020713.1	NT	Bacteriophage SPB2 complete genome
4130	8258			3.02	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081289-038-est3 DT0018 Homo sapiens cDNA
4137	8265	14404	1.97	1.3E-01	AF026806.1	NT		Schistosoma mansoni fibroblast alkaline phosphatase mRNA, complete cds
4167	8259	14419	17.16	1.3E-01	AW273741.1	EST_HUMAN	XV231021 Soares_NFL_T_GBC_ST_Homo sapiens cDNA clone IMAGE:2813865-3.	
4264	8389	14526	0.08	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD_Homo sapiens cDNA clone NPDAZ025'	
4284	8389	14527	1.08	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD_Homo sapiens cDNA clone NPDAZ025'	
4291	9413			1.43	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4458	8577	14716	0.69	1.3E-01	M21672.1	NT		Bovine branched chain alpha-keto acid dihydrolyase mRNA, complete cds
4503	8627	14770	2.33	1.3E-01	BE212339.1	EST_HUMAN	60112606EF1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:28900883 5'	
4815	10025			0.97	1.3E-01	Y12584.1	NT	H.sapiens gene encoding translin, exon 3
381	6590	10735	12.88	1.2E-01	AI421744.1	EST_HUMAN		ANNEAU V (HUMAN), f38bb022,x1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:20585539 3' similar to g30U00760_m1
423	6210			1.77	1.2E-01	U68912.1	NT	Dichotomium discoidatum ORF DG116 gene, partial cds
648	5711			2.49	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1386	6614	11685	2.43	1.2E-01	AU148146.1	EST_HUMAN	AU148146 NT2RM4 Homo sapiens cDNA clone NT2RM40016811 3'	
1388	6514	11686	2.43	1.2E-01	AU148146.1	EST_HUMAN	AU148146 NT2RM4 Homo sapiens cDNA clone NT2RM40016811 3'	
1383	6521			2.74	1.2E-01	AV752249.1	EST_HUMAN	AV752249 cDNA clone IMAGE:14005534 3' similar to TRQ16871
1622	6649			1.04	1.2E-01	AA897474.1	EST_HUMAN	Q16571 ANTHMULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR.;

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT4) (NFAT4)							
1841	0769	11883	1.4	1.2E-01	Q14834	SWISSPROT	
1663	6781	11887	2.85	1.2E-01	AI285042.1	EST_HUMAN	q68f08_x1 NCI_CGAP_Es62 Homo sapiens cDNA clone IMAGE:16805653 3'
1770	6935		6.41	1.2E-01	I89211.1	NT	H.sapiens DNA for analogous retroviral like element
1923	7042		3.36	1.2E-01	AW442668.1	EST_HUMAN	UI-H-B13-46L>-10-L-J1.1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734654 3'
2164	7277	12824	1.94	1.2E-01	BF248480.1	EST_HUMAN	6018215877F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4048224 5'
2851	7654	12804	2.16	1.2E-01	AW898559.1	EST_HUMAN	QV3-BN0046-220300-12A-T10 BN0046 Homo sapiens cDNA
2657	7859	12812	16.53	1.2E-01	BE2219989.1	EST_HUMAN	BE2219989_x1 NCI_CGAP_L124 Homo sapiens cDNA clone IMAGE:31178303 3'
2805	7881	13124	1.36	1.2E-01	U18016.1	NT	Human_E1A enhancer binding protein (E1A-F) mRNA, partial cds
2887	8014	13188	2.04	1.2E-01	AI20470.1	EST_HUMAN	680205_x1 Barnard et al HPLB7 Homo sapiens cDNA clone IMAGE:2336024 3' similar to qb:105095
2860	8054	13222	3.27	1.2E-01	MH9284.1	NT	Human creatine kinase-B mRNA, complete cds
2970	8130	13294	0.74	1.2E-01	K56882.1	NT	Wheat mRNA for a group 3 lats embryogenesis abundant protein (LEA)
3215	82683	13350	1.77	1.2E-01	AW370668.1	EST_HUMAN	QY1-BT0268-26108-021-d05_B10259 Homo sapiens cDNA
3240	8390		0.72	1.2E-01	U87800.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3460	86022		0.51	1.2E-01	I299118.1	NT	Bacillus subtilis complete genome (section 15 of 21) from 2785131 to 3013540
3507	8848	13814	1.26	1.2E-01	K56882.1	NT	Wheat mRNA for a group 3 lats embryogenesis abundant protein (LEA)
3607	88483	13816	1.25	1.2E-01	K56882.1	NT	Wheat mRNA for a group 3 lats embryogenesis abundant protein (LEA)
3651	88022		0.84	1.2E-01	I299118.1	NT	Bacillus subtilis complete genome (section 16 of 21) from 2785131 to 3013540
3750	8887		0.75	1.2E-01	BF128551.1	EST_HUMAN	601610188R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053658 3'
4168	8279	14414	1.91	1.2E-01	I254285.1	NT	P-clark1 mRNA; repeat region (ID 2M2R17)
4153	8279	14416	1.91	1.2E-01	I254285.1	NT	P-clark1 mRNA; repeat region (ID 2M2R17)
4739	8852		2.5	1.2E-01	I32873.1	NT	Arabidopsis thaliana homeodomain protein (CLABER12) gene, complete cds
5028	10131	15269	1	1.2E-01	BE173168.1	EST_HUMAN	MRO-H1T0559-24040-018-019 HT0559 Homo sapiens cDNA
5028	101311	15281	1	1.2E-01	BE173168.1	EST_HUMAN	MRO-H1T0559-24040-018-019 HT0559 Homo sapiens cDNA
5053	10165		1.01	1.2E-01	PI18468	SWISSPROT	HEMOLYSIN PRECURSOR
683	6728	10888	0.7	1.1E-01	AI581003.1	EST_HUMAN	In 18d08_x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2107883 3'
612	6772	10902	2.13	1.1E-01	AA1663006.1	EST_HUMAN	mm08g11_s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059820 3' similar to qb:X00885_ma1
1058	6197	11382	1.37	1.1E-01	BF0817308.1	EST_HUMAN	HEMOXYGENASE 1 (HUMAN);
1088	6225		1.4	1.1E-01	AL181556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1161	7910	11462	3.63	1.1E-01	AW972158.1	EST_HUMAN	EST3B142 MAGE sequences. MAGL Homo sapiens cDNA
1263	6883	11581	1.31	1.1E-01	DB40004.1	NT	Synecochysis sp. PCC8803 complete genome, 23/27, 2888/167-3002985
1635	6882	11848	2.07	1.1E-01	AU140363	EST_HUMAN	AU140363 PLACE2H Homo sapiens cDNA clone PLACE2000403 5'

Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
22292	7401		1.57	1.1E-01	8755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA
28119	7974	13133	1.1	1.1E-01	S62418.1	NT	Interleukin-12 p35 subunit [mice, Genomic, 700 nt, segment 4 of 6]
30005	81169	13316	0.89	1.1E-01	FC3263.1	EST_HUMAN	HSCIRF022 normalized brain cDNA clone Homo sapiens cDNA clone &lt;10023'
33223	8470		1.44	1.1E-01	8753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1D subunit (Caenva1b), mRNA
34022	8546	13705	2.31	1.1E-01	BE393186.1	EST_HUMAN	60130870F1 NIH_MGC_44_Homo sapiens cDNA clone IMAGE:3B27085 5'
34335	8575	13735	1.38	1.1E-01	X62195.1	NT	Cretinobindin nuclear gene on linkage group XIX
3472	8614	13781	0.63	1.1E-01	R86948.1	EST_HUMAN	Y052918.61 Scores fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:2004114 3' similar to contains Ali repetitive element,
35570	8711	13877	0.78	1.1E-01	Y07695.1	NT	Alimversus gene for transposase
36877	8828	13981	1.31	1.1E-01	X52708.1	NT	G. gallus gene encoding non-Histone chromosomal protein HMG-14b, exons 4 and 5
40883	9216	14348	0.85	1.1E-01	AW618412.1	EST_HUMAN	MR3-S-28010-025-007 ST10280 Homo sapiens cDNA
40890	9216	14949	0.86	1.1E-01	AW618412.1	EST_HUMAN	MR3-S-28010-025-007 ST10280 Homo sapiens cDNA
4226	9354		7.73	1.1E-01	AF157006.1	NT	Drosophila melanogaster Kardiotrophin protein (Ktr) mRNA, complete cds
4281	9388	14523	0.65	1.1E-01	AW802036.1	EST_HUMAN	L5-UHM070-02050-068-008 UM0070 Homo sapiens cDNA
4800	8813	15054	1.32	1.1E-01	Y07695.1	NT	Alimversus gene for transposase
50098	9219		0.6	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class II region:butyrophilin-like protein gene, partial cds; Notch4 PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
1204	6337		3.8	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEIC ACID PRECURSOR (DNASE) (ACID DNASE) (LYSOSOMAL DNASE II)
1278	8406	11579	2.88	1.0E-01	A1985499.1	EST_HUMAN	W08001 XI NCI_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:24985877 3' similar to contains MER7.13 MER7 repetitive element:
1399	6327	11708	1.81	1.0E-01	A1161604.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment 1 No. 18
3498	86319	13803	1.03	1.0E-01	BF033891.1	EST_HUMAN	601458301F1 NIH_MGC_58_Homo sapiens cDNA clone IMAGE:3855849 6'
36539	85337	13991	0.92	1.0E-01	BF238818.1	EST_HUMAN	60160848BF1 NIH_MGC_54_Homo sapiens cDNA clone IMAGE:4134071 6'
3813	8850	14087	0.88	1.0E-01	AF287081.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3813	8850	14088	0.88	1.0E-01	AF287081.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
38226	8902	14220	2.33	1.0E-01	BF238578.1	EST_HUMAN	QV2-NFT0048-1605010-3118-005 NT0048 Homo sapiens cDNA
45229	8946		0.61	1.0E-01	A1792349.1	EST_HUMAN	an32c04.36 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4680	9786	14841	1.02	1.0E-01	U60460.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
4903	10013	15157	2.26	1.0E-01	AW862344.1	EST_HUMAN	EST384414 MAGE sequences. MAGE_Homo sapiens cDNA
5108	10207	15344	1.08	1.0E-01	A1163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
2739	7833	13086	0.86	9.8E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-RII) mRNA, complete cds
2748	7842	13097	1.38	9.8E-02	BE545554.1	EST_HUMAN	60107218F1 NIH_MGC_12_Homo sapiens cDNA clone IMAGE:3456385 5'

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 Table 4 :  
 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2748	7842	130688	1.36	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:34568365 5'
3249	8386	135650	1.23	9.9E-02	AF096810.1	NT	Homo sapiens neuregulin III-epsilon gene, partial cds
562	5727		1.69	9.8E-02	X563838.1	NT	Oсетин RAM3/C gene for alpha-antitrypsin
3078	8231		1.57	9.8E-02	4504578 NT	Hom sapiens I factor (complement) (IF) mRNA	
3123	8275	134320	3.74	9.8E-02	AF184274.1	NT	Daurus carota leucanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4201	8326	144567	6.41	9.8E-02	AF257329.1	NT	Lepidosaphes maculatus beta-tubulin mRNA, complete cds
4201	8325	144568	6.41	9.8E-02	AF257328.1	NT	Lepidosaphes maculatus beta-tubulin mRNA, complete cds
1387	8486	11687	1.12	9.7E-02	AB005868.1	NT	Alce aristosensis mRNA for NADP-malic enzyme, complete cds
2241	7302	126699	1.38	9.7E-02	BE168860.1	EST_HUMAN	QY14-TT0516-070300-095-004 HT0516 Homo sapiens cDNA
38956	8031		3.61	9.7E-02	Q89785	SWISSPROT	CELL SURFACE A3 ANTIGEN PRECURSOR (GLYCOPROTEIN A3)
4322	9444	14577	3.44	9.6E-02	Z32886.2	NT	Protein mitchells fibrillar operon, strain H420
4887	10964	15225	1.27	9.6E-02	AW668320.1	EST_HUMAN	EST378563 MAGE sequences, MAGE1 Homo sapiens cDNA
4077	9237	14844	1.88	9.6E-02	AW892395.1	EST_HUMAN	CM2-EN0023-050200-087-7-2 BN0123 Homo sapiens cDNA
1847	8958	12188	2.28	9.4E-02	BF0701093.1	EST_HUMAN	602156982F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 6'
38688	8994	14151	5.14	9.4E-02	Z33059.1	NT	M.capitatum DNA for C0NTIG MC073
2958	8112		1.78	9.3E-02	4805280 NT	Hom sapiens BA11-associated protein 3 (BA1A3) mRNA	
30000	81155		6.69	9.3E-02	8912628 NT	Hom sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA	
3238	8389	13552	1.84	9.3E-02	BF573511.1	EST_HUMAN	60213086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 8'
4124	9252	143869	3.24	9.3E-02	BE391843.1	EST_HUMAN	60212816082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4124	9252	143950	3.24	9.3E-02	BE391843.1	EST_HUMAN	60212816082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4703	9819		1.91	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAU06 5'
227	6421	10568	7.03	9.2E-02	U60316.1	NT	Motulicum contagiosum virus subtype 1, complete genome
227	5421	10557	7.03	9.2E-02	U60316.1	NT	Motulicum contagiosum virus subtype 1, complete genome
227	6421	10558	7.03	9.2E-02	U60315.1	NT	Motulicum contagiosum virus subtype 1, complete genome
2209	7321		6.16	9.2E-02	R54156.1	EST_HUMAN	Ygb6707.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41618 6'
3168	8310	13470	3.52	9.2E-02	C28631	SWISSPROT	MAJOR EPIDERMIS-SPECIFIC PROTEIN E4 (EPIDERMAL PROTEIN BE-20)
3287	8438	13667	0.82	9.2E-02	AA534354.1	EST_HUMAN	MT79eM s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:8286136 3'
3575	8714		1.06	9.2E-02	6756215 NT	Mus musculus pre T-cell antigen receptor alpha (Prcse), mRNA	
4216	8341		0.84	9.2E-02	U29048.1	NT	Human hepatitis 1 strain KOS-88, latency-associated transcript, promoter region
4285	9407		0.73	9.2E-02	BE298722.1	EST_HUMAN	602044265F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:2660178 5'
4898	9728	14882	1.22	9.2E-02	X86402.1	NT	G.gallus Mla-CK gene
422	5209	10322	1.79	9.1E-02	X77685.1	NT	O.curicus k12 keratin gene
2391	7497	12749	2.89	9.1E-02	P78886	SWISSPROT	6-PHOSPHOFRUCTOKINASE (PHOSPHOHEXOKINASE)
3647	8788		0.84	9.1E-02	AW372868.1	EST_HUMAN	PM2-B1034B-161288-001-002 BT0348 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4483 9582	14720		1.35	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
743 6599	11052		5.28	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FB)
1645 6773	11685		4.28	9.0E-02	BE220482.1	EST_HUMAN	HIV-1 P8c085-08 from USA envelope glycoprotein (env) gene, partial cds HIV-1 P8c085-08 from USA envelope glycoprotein (env) gene, partial cds
2784 7858	13114		2.63	9.0E-02	AF138822.1	NT	Dicytostellum discoidin spore coat structural protein SP85 (cotE) gene, complete cds
3318 8485	13629		1.42	9.0E-02	AF2279135.1	NT	corticosteroid-binding globulin (Saimiri sciureus) cDNA clone IMAGE:3178842 3' similar to contains Alu repetitive element
4275 9398	14539		0.61	9.0E-02	SE89767.1	NT	corticosteroid-binding globulin (Saimiri sciureus) cDNA clone IMAGE:3178842 3' similar to contains Alu repetitive element
4276 9398	14539		0.61	9.0E-02	SE89757.1	NT	corticosteroid-binding globulin (Saimiri sciureus) cDNA clone IMAGE:3178842 3' similar to contains Alu repetitive element
4396 9593	14859		0.57	9.0E-02	P55298	SWISSPROT	LAMININ BETA-2/CHAIN PRECURSOR (SLAMININ)
4638 9750	14903		2.02	9.0E-02	Y057740.2	NT	Plasmidium falciparum P-type ATPase 3 gene
1448 6576	11762		2.13	8.9E-02	BF701693.1	EST_HUMAN	IMAGE:42858951 6
1448 6876	11763		2.13	8.9E-02	BF701693.1	EST_HUMAN	IMAGE:42858951 6
4117 9287			1.82	8.9E-02	AF285055.1	NT	Archium angustatum AtrenF02 protein (AtrenF02) gene, partial cds
4604 9722	14858		1.02	8.9E-02	AA424887.1	EST_HUMAN	IMAGE:768169 3
1382 6810	11691		1.57	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3880 8018	14173		0.89	8.8E-02	AA289728.1	EST_HUMAN	EST11685 Ustulus Homo sapiens cDNA 5' end
4009 9141			3.08	8.8E-02	000268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 133 KDA SUBUNIT (TAIFI-135) (TAIFI-130) (TAIFI130)
4217 8342			1.07	8.8E-02	4602804	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA genes, complete cds; and biglycan (BGN)
4278 8401			0.76	8.8E-02	4580423	NT	Homo sapiens paired box gene 8 (embtite, keratin) (PAX8), isoform b, mRNA genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
1659 6787	11982		1.11	8.7E-02	AI167281.1	EST_HUMAN	IMAGE:16811681 3'
3670 8808	13988		4.16	8.7E-02	U82865.2	NT	Homo sapiens zinc finger protein 82 (ZFP82), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN)
3670 8808	13907		4.16	8.7E-02	U82865.2	NT	Homo sapiens zinc finger protein 82 (ZFP82), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN)
4874 9790	14938		1.39	8.7E-02	AF786836.1	NT	Mus musculus JNK interacting protein 3a (Jip3) mRNA, complete cds
1259 6585	11582		5.65	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudoubosomal region; segment 22
2224 7336	12580		1.27	8.6E-02	BE408887.1	EST_HUMAN	IMAGE:3638843 6
3170 8321	13482		3.62	8.6E-02	LO5468.1	NT	Titanomassus vaginatus beta-tubulin (tub1) gene, complete cds

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Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Assessment No.	Top Hit Database Source	Top Hit Descriptor
3822 8761				3.88	8.6E-02 AF153382.1	NT	Dichotomellum discoloratum adenylyl cyclase (accA) gene, complete cds
6135 10235	15371	22		8.6E-02 AF060174.1	NT	Rattus norvegicus synaptic vesicle protein 2C (SV2C) mRNA, complete cds	
2373 7479	12733	1.4		8.5E-02 AE000682.1	NT	Halocynthia pyriformis section 130 of 134 of the complete genome	
2628 7847	12281	2.91		8.4E-02 W68390.1	EST_HUMAN	Zd4481171 Sorex_fetal_heart_NbH19W_Homo_sapiens cDNA clone IMAGE:349532 5'	
4331 9453	14887	0.85		8.4E-02 AF267213.1	NT	Cavia porcellus glucoprotein alpha-subunit mRNA, complete cds	
4231 9453	14588	0.95		8.4E-02 AF257213.1	NT	Cavia porcellus glucoprotein alpha-subunit mRNA, complete cds	
3879 8720	13878	6.98		8.3E-02 PT75394	SWISSPROT	HYPOTHETICAL LIPOPROTEIN M3509 HOMOLOG PRECURSOR	
1389 6517				4.18	8.2E-02 Y08170.2	NT	Gallus gallus mRNA for OBICAM protein gamma isoform
1609 6538	11823	2.08		8.2E-02 AF187077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds	
3045 8159		2.21		8.2E-02 AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006	
3780 8917		1.32		8.2E-02 AL161468.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10	
3882 9110	14264	1.18		8.2E-02 AL162016.2	NT	Homo sapiens chromosome 21 segment HS21C008	
4258 8383	14516	5.8		8.2E-02 P48920	SWISSPROT	LEUCOCYTE ANTIGEN CD87 PRECURSOR	
4259 8353	14517	5.8		8.2E-02 P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD87 PRECURSOR	
4258 8389	14618	5.8		8.2E-02 P48980	SWISSPROT	LEUCOCYTE ANTIGEN CD87 PRECURSOR	
6050 10162	16283	0.67		8.2E-02 AF240778.1	NT	Mus musculus peptidoglycan F (Pepf) mRNA, complete cds	
6065 10167	15301	3.12		8.2E-02 U76009.1	NT	Mus musculus zinc transporter (Znt-3) gene, complete cds	
1508 6635	11622	1.14		8.1E-02 AB017198.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mcaA, mcaB, mcaC, mcaD, mcaE, mcaG, mchA, mchB, and mchD genes), complete cds	
4831 10041	15180	0.68		8.1E-02 BF343921.1	EST_HUMAN	6020158085F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4161840 5'	
4831 10041	15181	0.68		8.1E-02 BF343921.1	EST_HUMAN	6020158085F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4161840 5'	
5 7881	10639	3.97		8.0E-02 AW954653.1	EST_HUMAN	EST3887-23 MAGE sequences, MAGC Homo sapiens cDNA	
1713 7823	12042	8.38		8.0E-02 D26535.1	NT	Human gene for dihydrofolate reductase, complete cds (exon 1-15)	
1713 7823	12043	8.36		8.0E-02 D26535.1	NT	Human gene for dihydrofolate reductase, complete cds (exon 1-15)	
1809 7028	12248	3.28		8.0E-02 BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-508 BT0347 Homo sapiens cDNA	
2448 7650		3.13		8.0E-02 BF246744.1	EST_HUMAN	6018655445F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075810 5'	
2865 8019	13185	0.87		8.0E-02 AL445087.1	NT	Thermoplasma acidophilum complete genome, segment 5/5	
3784 8861	14078	0.79		8.0E-02 AW966118.1	EST_HUMAN	EST378191 MAGE sequences, MAGI Homo sapiens cDNA	
4046 9177		0.69		8.0E-02 4503034 NT	Home sapiens cAMP responsive element binding protein-like 2 (CREB1) mRNA		
4743 9866	16004	1.18		8.0E-02 AL434202.1	EST_HUMAN	B319022X1 NC1_CQAP_Qas4 Homo sapiens cDNA clone IMAGE:21321143'	
4783 8866		6.97		8.0E-02 X72194.1	NT	Mus musculus gene for gelatinase B	
4858 10009	15154	0.65		8.0E-02 M28071.1	NT	Herpesvirus salmini transformation-associated protein (STP), and dihydrofolate reductase (DHFR) genes, complete cds, and small nuclear RNAs (uRNAs)	
2163 7266	12516	1.81		7.8E-02 BE2505098.1	EST_HUMAN	60084319F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859510 5'	

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2849	8103	13288	8.92	7.9E-02	AI682029.1	EST_HUMAN	er88cd8.x1 Barstead colon HPLC&lt;br&gt;60S RIBOSOMAL PROTEIN L38 (HUMAN);
3828	8965	14118	4.62	7.9E-02	6681044 NT		Mus musculus colony stimulating factor 1 receptor (Csf1), mRNA
3829	8965	14117	4.62	7.9E-02	6681044 NT		Mus musculus colony stimulating factor 1 receptor (Csf1), mRNA
4780	9895		1.37	7.9E-02	AB0068018.1	NT	Arabidopsis thaliana RXN24L mRNA, partial cds
4884	9995	15141	1.73	7.9E-02	L24757.1	NT	Human bone sialoprotein (BNSP) gene, exons 2, 3 and 4
4892	10003		4.83	7.9E-02	AW081738.1	EST_HUMAN	3b70a10x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581628 3'
1213	6346	11614	1.42	7.8E-02	A1793275.1	EST_HUMAN	cc65dd2_y6 NCI_CQAP_Lus Homo sapiens cDNA clone IMAGE:1670467 6' similar to contains L13 L1 repetitive element;
1213	6345	11515	1.42	7.8E-02	A1783275.1	EST_HUMAN	cc65dd2_y6 NCI_CQAP_Lus Homo sapiens cDNA clone IMAGE:1670467 6' similar to contains L13 L1 repetitive element;
6071	9863		3.27	7.8E-02	BE250D48.1	EST_HUMAN	600945055EF1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:2559653 5'
1406	7917	11712	1.02	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3374	8716		1.89	7.7E-02	AJ238668.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
3398	85113	13680	1.84	7.9E-02	BE514432.1	EST_HUMAN	601318428EF1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3834863 5'
3389	85339	13694	0.89	7.8E-02	AA286447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to protocadherin 43
786	6940	11098	1.54	7.8E-02	5902093 NT		Homo sapiens solute carrier family 6 (neurotransmitter transporter, glychire), member 9 (SLC6A9), mRNA
785	5940	11099	1.64	7.8E-02	6902083 NT		Homo sapiens solute carrier family 6 (neurotransmitter transporter, glychire), member 9 (SLC6A9), mRNA
1824	7043	12293	1.21	7.6E-02	AI1632782...	NT	Homo sapiens chromosome 21 cegtmatt HS21C078
477	5844	10785	1.44	7.4E-02	AV1838547.1	EST_HUMAN	RC5-LT054-250100-A011-H08 LT054 Homo sapiens cDNA
1473	6800		1.1	7.4E-02	AF050027.1	NT	Equine herpesvirus 4 strain NS80567, complete genome
2544	7647		1.03	7.4E-02	67765069 NT		Mus musculus p4reec-like homeodomain transcription factor 1 (Ptx1), mRNA
3550	8721	13879	1.02	7.4E-02	AI807685.1	EST_HUMAN	w423h01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2355388 3'
4672	9788	14833	1.11	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4753	9876	16027	2.6	7.4E-02	6978442 NT		Rattus norvegicus Activin receptor like kinase 1 (Acvr1), mRNA
4918	10029	15171	1.0	7.4E-02	6978482 NT		Mus musculus ubiquitin c-terminal hydrolase related polypeptides (Uchtp), mRNA
488	68538	10775	1.3	7.3E-02	BIG864961.2	EST_HUMAN	601583738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
488	56568	10773	1.3	7.3E-02	BIG84961.2	EST_HUMAN	601683738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
683	58441	10980	3.42	7.3E-02	AE001788.1	NT	Thermotoga maritima section 101 or 138 of the complete genome
1491	78119	11808	3.35	7.3E-02	AV800281.1	EST_HUMAN	CMB-NH1004-130300-284-908 NN1004 Homo sapiens cDNA
1868	78228		9.68	7.3E-02	AL168302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4983	10081		1.11	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds

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## Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
116	6318	10460	0.87	7.2E-02	AE009882.1	NT	Methanobacterium thermoautotrophicum from bases 1028165 to 1039834 (section 88 of 148) of the complete genome
116	6318	10461	0.97	7.2E-02	AE009882.1	NT	Methanobacterium thermoautotrophicum from bases 1028165 to 1039834 (section 88 of 148) of the complete genome
1486	6613	11800	2.02	7.2E-02	AL1683301.2	NT	Hom sapiens chromosome 21 segment HS21C101
1486	6613	11801	2.02	7.2E-02	AL1683301.2	NT	Hom sapiens chromosome 21 segment HS21C101
2520	7624			1.57	7.2E-02	UJ4794.1	NT
3862	8998	14185	0.84	7.2E-02	AW288322.1	EST_HUMAN	U1-H-BW0-af1-e-05-0-U1_s1 NCI CGAP_Sub8 Hom sapiens cDNA clone MAGE-2732049 3'
4323	9446	14578	5.25	7.2E-02	BF572307.1	EST_HUMAN	602077767F1 NIH_MGC_62 Hom sapiens cDNA clone MAGE-4251850 5'
1910	7029	12249	1.19	7.1E-02	Q02280.1	NT	Human immunodeficiency virus type 1 [D8] proximal structural capsid protein (gag) gene, partial cds
2284	7374			1.21	7.1E-02	AE004880.1	NT
2269	7378	'2628	4.24	7.1E-02	BF7208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Hom sapiens cDNA clone MAGE-4092881 5'
528	6932	10824	1	7.0E-02	Q07082	SWISSPROT	COLLAGEN ALPHA 1(XVII) CHAIN PRECURSOR
1514	6841			1.12	7.0E-02	XR86577.1	NT
3091	8168	13314	1.88	7.0E-02	AW138152.1	EST_HUMAN	U1-H-B11-ecy-c-07-0-U1_s1 NCI CGAP_Sub8 Hom sapiens cDNA clone MAGE-2716020 3'
3874	9010	14168	0.83	7.0E-02	AA1B15498.1	EST_HUMAN	ribosomal proteins L32 (HUMAN); alfa5ar12_s1 Scores: testis, JHT Hom sapiens cDNA clone 1375878 3' similar to gbk:K03002 60S
4018	9151	14283	1.05	7.0E-02	BE070284.1	EST_HUMAN	QY4-BT0407-280100-000-010 BT0407 Hom sapiens cDNA
4111	9239			0.82	7.0E-02	AW782822.1	EST_HUMAN
4183	8314	14449	1.07	7.0E-02	AF077821.1	NT	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
4807	10017	15161	7.25	7.0E-02	BF5281687.1	EST_HUMAN	6018761261F1 NIH_MGC_58 Hom sapiens cDNA clone MAGE-4050071 5'
5112	56778	10810	12.18	6.8E-02	AL1683210.2	NT	Hom sapiens chromosome 21 segment HS21C010
6112	56778	10811	12.18	6.8E-02	AL1683210.2	NT	Hom sapiens chromosome 21 segment HS21C010
1338	6468			1.33	6.9E-02	4507988	NT
3770	8807	14059	1.06	6.9E-02	Q053864	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT SS (NUCLEAR ANTIGEN 21D7)
3770	8807	14060	1.08	6.9E-02	Q053864	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT SS (NUCLEAR ANTIGEN 21D7)
1912	7031	12251	2.62	6.8E-02	AF058973.1	NT	Hom sapiens putative hepatic transcription factor (NBSCE14) gene, complete cds
3076	82228	13379	1.13	6.8E-02	AA781988.1	EST_HUMAN	al75ac06_s1 Scores: testis, NHT Hom sapiens cDNA clone 1376828 3'
3076	82228	13380	1.13	6.8E-02	AA781988.1	EST_HUMAN	al75ac06_s1 Scores: testis, NHT Hom sapiens cDNA clone 1376828 3'
3076	82228	13381	1.13	6.8E-02	AA781988.1	EST_HUMAN	al75ac06_s1 Scores: testis, NHT Hom sapiens cDNA clone 1376828 3'
4528	8844			0.62	6.8E-02	BE141076.1	EST_HUMAN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Sequence	Top Hit Descriptor
1643	6671		1.63	6.7E-02 AF115536.1	NT	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1 T1 allele, complete cds	
1800	7019	12239	1.1	6.7E-02 AI220285.1	EST_HUMAN	sp78e04.x1 Seares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:1841405 3'	
3697	8035	13888	4.17	6.7E-02 P7278	SWISSPROT	HOMEOBOX PROTEIN HOXA4 CHOXA)	
1355	8484	11684	2	8.6E-02 AI735509.1	EST_HUMAN	at1205.x1 Barstead aorta HFLRB6 Homo sapiens cDNA clone IMAGE:2354620 3' similar to SW.1.In1_NYCCO_P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG ;	
2163	7278	12523	1.63	6.6E-02 AI2382241.1	NT	Mus musculus Capn12 gene for capn12, exons 1-21, three alternative transcripts	
3445	8587	13750	8.86	6.6E-02 R84308.1	EST_HUMAN	Y118b10.x1 Seares placenta Nb24P Homo sapiens cDNA clone IMAGE:139578 3'	
3459	8601	13785	2.65	6.6E-02	7108357 NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA	
2459	8501	13768	2.68	6.6E-02	7108357 NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA	
4057	9187	14329	1.68	6.6E-02 AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced	
4983	10071	15207	0.78	6.6E-02 Q81703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (INTER-HEAVY CHAIN H2)	
4668	10071	15208	0.78	6.6E-02 Q81703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (INTER-HEAVY CHAIN H2)	
680	5749	10871	1.8	6.5E-02 BF027638.1	EST_HUMAN	601871048F1 NIH MGSC 20 Homo sapiens cDNA clone IMAGE:3854178 6'	
888	6135	11305	2.02	6.5E-02	7708088 NT	Homo sapiens E2F-like protein (LO651270), mRNA	
1398	6828	11705	3.1	6.5E-02 U47624.1	NT	Xenopus laevis alpha(E)-actinin mRNA, complete cds	
1748	8874	12079	1.22	6.5E-02 AE000784.1	NT	Aequorea coerulea section 98 of the complete genome	
673	5737	10884	1.39	6.4E-02 Y84549.1-	NT	Acanthaea precursor of peridinin-chlorophyll-a-protein (PCP) gene	
1748	8872	12078	1.04	6.4E-02 AE001777.1	NT	Thamnotoga maritima section 89 of the complete genome	
1748	6872	12077	1.04	6.4E-02 AE001777.1	NT	Thamnotoga maritima section 89 of the complete genome	
4871	8140	13304	1.09	6.4E-02	6098523 NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA	
1760	86892	12089	2.38	6.3E-02 AF108805.1	NT	Mus musculus major histocompatibility locus class Iii regions Hsc70t gene, partial cds; smRNP, G7A, NG23,	
35589	8729		2.12	6.3E-02 P37082	SWISSPROT	MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes	
4228	8363	14488	4.28	6.2E-02 AL161872.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68	
4315	8437		1.88	6.2E-02 AF271235.1	NT	Rattus norvegicus differentiation-associated Na+-dependent inorganic phosphate cotransporter (DNP1) mRNA, complete cds	
4558	8974		6.21	6.2E-02 Q82181	SWISSPROT	KD PROTEIN (S-JOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO52)	
253	5444	10588	3.71	6.1E-02 D18471.1	NT	Human mRNA, Xq terminal portion	
3906	9101		2.78	6.1E-02 U73323.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AtKC1) gene, complete cds	
4624	9742	14884	0.98	6.1E-02 AF19413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACCS3) gene, complete cds	
4624	9742	14885	0.98	6.1E-02 AF19413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACCS3) gene, complete cds	
5152	10232	15391	28.79	6.1E-02 Y12533.1	NT	S. scrofa mRNA for Mannose-mannosidase	
1268	8385	11669	1.23	6.0E-02 AE001777.1	NT	Thamnotoga maritima section 89 of the complete genome	

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Probe Seq ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit Description	
2837	7736	12889	1.12	6.0E-02	AW/9888348.1	EST_HUMAN	EST380824 MAGE sequences, MAGI Homo sapiens cDNA	
							Mesocetostides cord mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2	
2734	7823		1.27	6.0E-02	AB031289.1	NT		
2802	6302	10441	1.12	6.0E-02	AA188730.1	EST_HUMAN	ZP_786041 Strategaea Hela cell 63 83/7216 Homo sapiens cDNA clone IMAGE:026310 5'	
2802	6302	10442	1.12	6.0E-02	AA188730.1	EST_HUMAN	ZP_786041 Strategaea Hela cell 63 83/7216 Homo sapiens cDNA clone IMAGE:026310 5'	
3214	8366	13528	1.97	6.0E-02	AA372876.1	EST_HUMAN	EST84288 Colorectal carcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein	
3214	8365	13528	1.97	6.0E-02	AA372376.1	EST_HUMAN	EST84288 Colorectal carcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein	
5081	10182	15319	4.4	6.0E-02	AF148738.1	NT	Rattus norvegicus testis specific protein mRNA, complete cds	
228	5422	10559	4.39	6.8E-02	AW/934718.1	EST_HUMAN	RCU-DT0001-2801 W00-012-010 D7061 Homo sapiens cDNA	
2852	8108	13271	2.49	6.8E-02	AF180269.1	NT	Mus musculus p53 tumor-suppressor gene, exon 10 and 11, partial cds; alternatively spliced	
5100	10284	15403	0.67	6.8E-02	AW/028748.1	EST_HUMAN	wn34e02-X1 NCI CGAP_Or18 Homo sapiens cDNA clone IMAGE:2831450 3' similar to TR:083386 O65388 F12E1-2D PROTEIN.;	
							wn34e02-X1 NCI CGAP_Or18 Homo sapiens cDNA clone IMAGE:2831450 3' similar to TR:083386 O65388 F12E1-2D PROTEIN.;	
5168	10284	15404	0.57	6.8E-02	AW/028748.1	EST_HUMAN	O65388 F12E1-2D PROTEIN.;	
624	6082		4.73	6.8E-02	DE00110.1	NT	Thiobacillus ferrooxidans marC, marA genes and URF-1	
6802	11897		1.12	6.8E-02	Q81768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (KIFHC)	
1973	6802							
3640	6778	13934	1.68	5.8E-02	AE001776.1	EST_HUMAN	Themobius maritimus section 87 of 138 of the complete genome	
4332	9454	14589	4.08	5.8E-02	AW/051927.1	EST_HUMAN	wn24e02-X1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'	
4332	9454	14590	4.08	5.8E-02	AW/051927.1	EST_HUMAN	wn24e02-X1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'	
4620	6838	14784	5.07	5.8E-02	AI247405.1	EST_HUMAN	q565010_X1 Scores fetal liver spleen INFSL_S1 Homo sapiens cDNA clone IMAGE:1848897 3' similar to cbm113-42 COAGULATION FACTOR XI PRECURSOR (HUMAN);	
4620	6838	14785	5.07	5.8E-02	AI247505.1	EST_HUMAN	cbm113-42 COAGULATION FACTOR XI PRECURSOR (HUMAN);	
4546	8884		2.31	5.8E-02	AF058284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds	
5165	10285	16394	0.63	5.8E-02	U76897.1	NT	Rattus norvegicus insulin-regulated membrane protein peptidase tRPA mRNA, complete cds	
5168	10285	16432	1.41	5.8E-02	SE8289.1	NT	growth hormone (Syrian Golden hamster), mRNA, 809 nt	
							eu63805.61 NCI CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37422 CE08811:	
3029	8183	13338	1.34	5.7E-02	AB01844.1	EST_HUMAN	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds	
3043	8197	13353	1.42	5.7E-02	AF419417.1	NT	Chloromys trummi thymulin VIIa (ctt-7A), globin I (ctt-9.1), globin II (ctt-7A), non-functional globin XII (ctt-13RT), globin XI (ctt-12) and globin XI (ctt-11) genes, complete cds	
3685	8824		0.73	5.7E-02	AF001282.1	NT	EST370883 MAGE sequences, MAGI Homo sapiens, cDNA	
3779	8916	14068	2.05	5.7E-02	AW/88797.1	EST_HUMAN	NT	Hydroxylase rotundifolia ribosomal protein L16 (rpL16) gene, intron; chloroplast gene for chloroplast product

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
22665	7375		0.98	5.0E-02	BE504308.1	EST_HUMAN	6014945781F2 NIH_MG3_C_70 Homo sapiens cDNA clone IMAGE:3596610 5'
4610	9728	14884	1.2	5.0E-02	AB013100.1	NT	Lycopetolase epsilon-L-4-C56 mRNA for 4-aminocyclopropane-1-carboxylate synthase, complete cds
46855	9781	14925	1	5.0E-02	AA280599.1	EST_HUMAN	zg4501.51 NCI_CGAP_QCB1 Homo sapiens cDNA clone IMAGE:700416 3'
2616	7714	12887	3.87	5.0E-02	AF27869.1	NT	H_sapiens gene encoding La autoantigen
3200	8351	13514	4.24	5.0E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3c1B), mRNA
4180	9319	14450	1.05	5.0E-02	U41581.1	NT	Gallid herpesvirus mRNA fragment
1283	64222		2.32	5.4E-02	AF157623.1	NT	Homo sapiens HTRA dectin protease (PRSS11) gene, complete cds
2891	81449		0.78	5.4E-02	AL277468.1	NT	Oryza sativa ribis-1 gene for putative Bowman-Birk type trypsin inhibitor
3403	10315		8.25	5.4E-02	BE073468.1	EST_HUMAN	RCB-BT0539-140200-012-C03 BT0539 Homo sapiens cDNA
1055	61863	11360	1.75	6.3E-02	AV381248.1	EST_HUMAN	QV0-ST0213-021289-002-409 ST0213 Homo sapiens cDNA
1055	61869	11361	1.75	6.3E-02	AV381248.1	EST_HUMAN	QV0-ST0213-021289-002-409 ST0213 Homo sapiens cDNA
1521	68448	11835	3.37	5.3E-02	TA4739.1	EST_HUMAN	Y-STRH21r1 Stratiogene lung #337210 Homo sapiens cDNA clone IMAGE:119855 6' similar to gdi0101608
2488	7672	12825	1.3	5.3E-02	AA278640.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP1 ALPHA CHAIN (HUMAN);
2698	80622	13233	0.7	5.3E-02	ME59417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
2698	80622	13234	0.7	5.3E-02	ME59417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3131	82832	13498	4.27	5.3E-02	AA278640.1	NT	Pseudomonas putida tgsS gene
5073	10174	15309	10.8	5.3E-02	ME59483.1	NT	Mus musculus caudal-type homeobox-1 (Cdx-1) gene, complete cds
2261	7371		170.81	5.2E-02	ME51908	NT	Homo sapiens insulin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3090	8243	13392	2.34	5.2E-02	AA277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3090	8243	13393	2.34	6.2E-02	AA277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3912	80448	14207	0.7	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylic diiron protein (Crd1) mRNA, complete cds
4252	9377	14509	3.65	5.2E-02	U07192.1	NT	Human steroid hormone receptor Nor-1 mRNA, complete cds
2344	7451		0.89	6.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073_1 547 (synonym: fibf1) Homo sapiens cDNA clone DKFZp547D073_5'
4176	8302	14438	0.72	5.1E-02	AE01301.1	NT	Chlamydia trachomatis section 2B of the complete genome
482	68650	10788	1.14	6.0E-02	AF08804.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1207	6339	11509	14.54	6.0E-02	BB9104.1	NT	Bacillus subtilis complete genome (section 1 of 21); from 1 to 213080
1891	7108	12341	2.34	5.0E-02	PC02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-1/PRP-2/PRP-4) (PIF-PIF-S) (PROTEIN APPREIN C) [CONTAINS: PEPTIDE P-C]
2778	6134	11304	1.54	5.0E-02	U72742.1	NT	Oreobatus carniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3319	8468		1.4	5.0E-02	7305610	NT	Mus musculus Ure-5-like kinase 2 (C_elegans) (Uk2) mRNA
3581	8722		0.81	8.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 87 of 163 of the complete genome
3661	8800	13958	8.12	5.0E-02	U12769.2	NT	Anthonaea pectiniferae chitinase mRNA, complete cds

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Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T <sub>cap</sub> ) BLAST E Value	Top Hit No.	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
222	5416			32.48	4.9E-02	M14230.1	NT	Chicken 25-kDa vitamin D-dependent calcium-binding protein (CaBP-2B) mRNA, complete cds
387	5547	10580		3.03	4.9E-02	AF276948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
367	6547	10591		3.03	4.9E-02	AF276948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2838	7853	13151		0.74	4.9E-02	U32628.1	NT	Zea mays phytocare synthase (Y1) gene, complete cds
3273	8422	13583		1.76	4.9E-02	IP54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3578	8719	13876		0.61	4.9E-02	AA406914.1	EST_HUMAN	2778a03_61_Soares_tests_NH <sub>T</sub> Homo sapiens cDNA clone IMAGE:728428 3'
3578	8719	13877		0.81	4.8E-02	AA406914.1	EST_HUMAN	2778a03_61_Soares_tests_NH <sub>T</sub> Homo sapiens cDNA clone IMAGE:728428 3'
4808	8820	15061		5.76	4.9E-02	AW167821.1	EST_HUMAN	X58510_1x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:28632388 3'
4808	8820	16062		8.76	4.9E-02	AW167821.1	EST_HUMAN	X58510_1x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:28632388 3'
5176	10273			1.34	4.9E-02	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
328	6512	10580		1.18	4.8E-02	D16471.1	NT	Human mRNA_XQ terminated portion
329	6512	10850		2.98	4.8E-02	D16471.1	NT	Human mRNA_XQ terminated portion
488	5636	10783		9.88	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
								xx4902_61_Soares_senescence_fibroblasts_NbHSF_Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:NM00388 LUPUS_KU AUTOANTIGEN PROTEIN P86 (HUMAN)
2252	7392	128018		1.13	4.8E-02	W51983.1	EST_HUMAN	Tetrahymena rostrata histone H3I and histone H4II intergenic DNA
3193	8344	135058		1.77	4.8E-02	X17144.1	NT	S sorghum gene for skeletal muscle ryanodine receptor
4842	9760			1.06	4.8E-02	Z54280.1	NT	Streptococcus constellatus D-alanine-D-alanine ligase gene, partial cds
5109	10210	16347		0.61	4.8E-02	U91814.1	NT	Rattus norvegicus Nest (Nes) mRNA
4888	10102	16233		0.83	4.7E-02	GG81261	NT	PM0-HT0339-251169-003-005 HT0339 Homo sapiens cDNA
268	5458	10598		2.47	4.6E-02	BE163583.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
738	5894	11048		2.37	4.6E-02	AE000445.1	NT	am50d02_51_Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538878 3' similar to TRP80533
1286	6426			0.98	4.6E-02	AJ014255.1	EST_HUMAN	P90532_LIMA :contains element LTR1 repetitive element;
1388	8498	11079		2.37	4.6E-02	AV727059.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBW C01 5'
2482	7538	12818		1.62	4.6E-02	AW236023.1	EST_HUMAN	Xn2403_1x1 CGAP_K1011 Homo sapiens cDNA clone IMAGE:28694853 3' similar to SW:GRF1_HUMAN
2769	6498	10598		1.92	4.6E-02	BE153583.1	EST_HUMAN	Q12449_G-RICH SEQUENCE FACTOR-1;
3477	8134	13207		0.82	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251169-003-005 HT0339 Homo sapiens cDNA
4095	8224			0.99	4.6E-02	AF220356.1	NT	Mus musculus nucleolar RNA helicase II (dok2) gene, complete cds
446	5614	10760		2.59	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1221	6333	11522		0.94	4.5E-02	AF005750.1	NT	Marburg virus strain M/S Africa/Johannesburg/1975/Oxolin VP35 gene, complete cds
1221	63153	11523		0.94	4.5E-02	AF005730.1	NT	Marburg virus strain M/S Africa/Johannesburg/1975/Oxolin VP35 gene, complete cds
1816	6339	12166		3.29	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2100	7215	12462		2.27	4.5E-02	AE003984.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9703 8841		13996	4.16	4.E-02	AL169278.2	NT	Homo sapiens chromosome 21 segment HS21C078
217 6411			3.49	4.E-02	BE97273.1	EST_HUMAN	601652-64F1 NIH_MSC_S2 Homo sapiens cDNA clone IMAGE:3836388 6'
1026 6167	11333		2.5	4.E-02	L18285.1	NT	Drosophila melanogaster oxidoreductase (EXD) mRNA, complete cds
2057 7203			1.84	4.E-02	PS1688	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 228)
2463 7667	12820		1.02	4.E-02	AW875475.1	EST_HUMAN	QV2-PT10012-010300-4-070-0102 PT0012 Homo sapiens cDNA
3618 8757	13913		1.89	4.E-02	AF158180.1	NT	Mycoecoccus xanthus serine/threonine kinase Pkn10 (Pkn10) gene, complete cds
4696 9714	14850		1.03	4.E-02	AF108907.1	NT	Homo sapiens S184 gene, partial cds, PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds
4696 9714	14851		1.03	4.E-02	AF108907.1	NT	Homo sapiens S184 gene, partial cds, PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds
781 5836	11094		6.58	4.3E-02	AF003249.1	NT	Morone saxatilis myostatin heavy chain RNA (Fn34) mRNA, complete cds
3411 8654	12713		8.38	4.3E-02	AL168210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3658 8775			1	4.3E-02	AF0501588.1	NT	Homo sapiens promyelocytic leukaemia zinc finger protein (PLZF) gene, complete cds
823 6976	11140		1.39	4.E-02	AU123327	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 6'
887 6018			1.81	4.E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 6'
897 6047	11218		0.73	4.2E-02	AW003645.1	EST_HUMAN	Y034901.1 NCI_CGAP_Pt11 Homo sapiens cDNA clone IMAGE:2545634 3' similar to TRQ83281 Q83281 Y034901.1 NCI_CGAP_Pt11 Homo sapiens cDNA contains L1, L1 repetitive element; L1 RETROPOSON, ORF2 mRNA; contains L1, L1 repetitive element;
1734 6881			2.38	4.2E-02	AL445088.1	NT	Thiomoplasma acidophilum complete genome; segment 4/5
1768 6914	12121		1.13	4.E-02	PF23091	SWISSPROT	TRANSFORMING PROTEIN MAF
3841 8780	13935		2.72	4.2E-02	PF23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4451 9570			7.38	4.E-02	AV893484.1	EST_HUMAN	QV1-NN0012-180400-164-008 NN0012 Homo sapiens cDNA
3228 8378	13639		4.02	4.0E-02	AB040804.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3777 6914	14068		1.05	4.0E-02	L11810.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
1121 6259	11424		2.86	3.8E-02	BF5f16148.1	EST_HUMAN	UJ-HBV-~amx-h-09-0-U_61 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084154 3'
1351 6480	11659		2.91	3.8E-02	PF41047	SWISSPROT	FAS ANTIGEN LIGAND
1868 7082	12306		1.5	3.8E-02	AL403386.1	NT	H. musculus DNA for desmin-binding fragment DesD7
2865 7761			1.76	3.8E-02	4503862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
4110 9233	14375		1.12	3.8E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163) mRNA
4110 8238	14376		1.12	3.8E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163) mRNA
5119 10220	16354		0.51	3.8E-02	AW892417.1	EST_HUMAN	RCA-ST0258-171189-321-C08 ST0258 Homo sapiens cDNA
5139 10239	16376		1.02	3.8E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163) mRNA
5139 10239	16378		1.02	3.8E-02	8824019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163) mRNA
2110 7225			0.97	3.8E-02	AJ251973.1	NT	Homo sapiens partial stealth-1 gene

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Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4908 6139	10016 11309	16160 11309	0.88 4.31	3.8E-02 AU124122.1 3.7E-02 P19137	EST_HUMAN EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001698 5' SWISSPROT LAMININ ALPHAI-1 CHAIN PRECURSOR (LAMININ A CHAIN) wR85eB_XI_NCI_C3AP_Kid1 Homo sapiens cDNA clone IMAGE:2494502 3'	
2218 3022 3024	7330 8176 8178	12583 13333 13334	3.72 1.21 6.38	3.7E-02 AI884808.1 3.7E-02 P79044 3.7E-02 BF312883.1	EST_HUMAN EST_HUMAN EST_HUMAN	EOMEISODERMIN 601686239F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125538 5' Mus musculus probasium large conductance pH-sensitive channel, subfamily N, alpha member 3 (Kcnma3), mRNA	
3436 3171 3631	8378 8322 8770		1.05 1.38 0.77	60803541 NT 3.6E-02 AP000003.1 3.6E-02 X73221.1	NT NT NT	Pyrococcus horikoshii OT3 genomic DNA, 544-001-777000 nt; position (37) H. vulgaris Ss1 gene for sucrose synthase	
3639 889 1009	8778 6048 6153	13933 11217 11320	0.65 1.41 1.03	3.6E-02 AL096808.1 3.5E-02 U09588.1 3.5E-02 AF258417.1	NT NT NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens Dipturus melanostictus ligustrum mRNA, complete cds Homo sapiens microsatellite hydrolase (EPH-D1) gene, complete cds	
1579 1579	6708 6708	11898 11899	1.37 1.37	3.5E-02 BF078085.1 3.5E-02 BF078086.1	EST_HUMAN EST_HUMAN	602085138F1 NIH_M3C_83 Homo sapiens cDNA clone IMAGE:4248377 5' 602085138F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248377 5'	
4187	8313	14448	1.83	3.6E-02 AE00173.1	NT	The monotoga maritima a section 85 of 138 of the complete genome	
4289	8416	14560	1.16	3.6E-02 PE3780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CB1) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)	
5177	10274		0.97	3.5E-02 P47144	SWISSPROT	HYPOTHETICAL 80.7 kD PROTEIN IN SOD1-CPA2 INTERGENIC REGION	
576	5740	10887	1.05	3.4E-02 AI024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds	
578	5740	10888	1.05	3.4E-02 AI024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds	
577	5740	10887	4.5	3.4E-02 AI024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds	
577	5740	10888	4.5	3.4E-02 AI024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds	
1053	8184	11358	3.17	3.4E-02 AW274020.1	EST_HUMAN	NCBI0007_X1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814283 3' similar to SW:02111 HUMAN PS3801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR;	
1209	6341		8.4	3.4E-02 11346458	NT	Homo sapiens hypothetical protein FLJ15220 (FLJ15220) Homo sapiens cDNA clone IMAGE:31250 5' similar to contains yr2008_11 Stratagene lung (#S3721) Homo sapiens cDNA clone IMAGE:31250 5' similar to contains MER28 repetitive element	
2269	7476	12729	1.38	3.4E-02 T57160.1	EST_HUMAN		
3412	8555	13714	1.18	3.4E-02 AI163208.2	NT	Homo sapiens chromosome 21 segment HS21C008 ...	
3766	8883	14043	0.85	3.4E-02 BE88514.1	EST_HUMAN	RCG-FNI055-06070-011-410 FN0756 Homo sapiens cDNA	
3834	8030	14189	3.8	3.4E-02 AW784932.1	EST_HUMAN	RCG-UHM0015-21020-021-A10 FN0756 Homo sapiens cDNA	
4571	9889	14827	2.48	3.4E-02 X587088.1	NT	Mus musculus S-antigen gene promoter region	
5042	10144		2.26	3.4E-02 Q28457	SWISSPROT	LA PROTEIN IN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)	
5061	10163	15288	1.48	3.4E-02 AJ012468.1	NT	Catarractalis elegans mRNA for DYS-1 protein, partial	

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No	Top Hit Database Source	Top Hit Descriptor
370 5550			21.46	3.3E-02	AA398735.1	EST_HUMAN	Zf75508.61 Scareas_festis_NH1 Homo sapiens cDNA clone IMAGE:728188 3'
1188 6304	11470		9.4	3.3E-02	AB0368867.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1650 6778	11870		1.49	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle 1 (FLH) gene, complete cds
2077 7193			1.25	3.3E-02	RD8112.1	EST_HUMAN	y125c09.11 Scareas testis liver spleen NIH3T3 Homo sapiens cDNA clone IMAGE:127888 5'
2428 7632	12795		0.95	3.3E-02	6755882	NT	Mus musculus tumor rejection antigen gp38 (Trat) mRNA
3342 8489	13654		1.16	3.3E-02	HO2389.1	EST_HUMAN	Y35H02.11 Scareas placenta NCI-H1825P Homo sapiens cDNA clone IMAGE:150771 5'
4148 9778	11870		2.53	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle 1 (FLH) gene, complete cds
4448 95683	14707		2.2	3.3E-02	6755882	NT	Mus musculus tumor rejection antigen gp38 (Trat) mRNA
4779 98822	150339		0.59	3.3E-02	AW2716598.1	EST_HUMAN	pp040564-x1 NCI_C3A/P_HN11 Homo sapiens cDNA clone IMAGE:2742789 3'
127 6325	10471		1.73	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding l-lact acid transporter
1127 6264	11428		15.01	3.2E-02	AF0588276.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68a allele, complete cds
2108 7223			16.01	3.2E-02	AF0588276.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68a allele, complete cds
2802 63225	10471		0.63	3.2E-02	AW2716598.1	NT	LARGE TEGUMENT PROTEIN
3112 8265	13420		9.38	3.2E-02	BE887353.1	EST_HUMAN	Oryctolagus cuniculus gene encoding l-lact acid transporter
3683 8831	13986		1.21	3.2E-02	AL163203.2	NT	GD1442431F1 NIH_MCC_65 Homo sapiens cDNA clone IMAGE:33491727 5'
3683 90169	14224		0.66	3.2E-02	Z74103.1	NT	Homo sapiens chromosome 21 segment HS21C003
3683 90169	14225		0.63	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055C
4184 8319			14.19	3.2E-02	X94168.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4733 6846	14922		3.38	3.2E-02	AF1114182.1	NT	Saccharomyces cerevisiae matruse (mark) gene, chloroplast gene encoding chloroplast protein, partial cds
4824 10034			1.54	3.2E-02	AF108906.1	NT	Mus musculus MHC class III region RD gene, partial cds; BI, C2, G8, NG22, G9, HSP70, HSP70, HSP70, HSP70 genes, complete cds; G7A gene, partial cds; and unknown genes
1284 63153			2.27	3.1E-02	4505416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1306 64339	11615		1.45	3.1E-02	F18846	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GFA-LPH-3)
1876 7093			1.31	3.1E-02	Z50097.1	NT	Drosophila melanogaster mRNA for headcase protein
1835 6784			2.14	3.0E-02	AF187126.1	NT	Pityroderma minutum cytochrome oxidase I gene, partial cds, mitochondrial gene for mitochondrial product
3652 88593	13855		1.07	3.0E-02	AB4176.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3650 8769	13925		2.49	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II amidotransferase gene, complete cds
3728 88833			0.82	3.0E-02	AW320223.1	EST_HUMAN	QV2-ST0288-1502200-0-0-008 S10288 Homo sapiens cDNA clone
3920 90159			1.08	3.0E-02	AA384003.1	EST_HUMAN	EST74530 Pitressin
4681 8777			12.88	3.0E-02	AI240487.1	EST_HUMAN	QH1008_X1 Scareas_NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:18443143
5032 10134	15284		6.62	3.0E-02	AF281074.1	NT	Homo sapiens neutrophil 2 (NRP2) gene, complete cds, alternatively spliced

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**Single Exon Probes Expressed in**

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
28223 80777	13246	14294	3.22	2.5E-02	X69897.1	NT	H_catenaria mRNA for nucleophthalin chlrophytin a/c binding protein, Fcp1
4016 10308	14295	0.98	2.5E-02	BE701165.1	EST_HUMAN	FM2-AN0128-Q80700-001-012 NND028 Homo sapiens cDNA	
4019 10303	14459	0.88	2.5E-02	BE701165.1	EST_HUMAN	FM2-AN0128-Q80700-001-012 NND028 Homo sapiens cDNA	
4178 8304	14459	5.14	2.5E-02	AW592114.1	EST_HUMAN	H38108-x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28340163'	
5083 10312			11.72	2.5E-02	AI7542201.1	EST_HUMAN	CR21111.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMS3 cr211113'
169 6394	10568	0.68	2.4E-02	A1378582.1	EST_HUMAN	ts72507.x1 Scores_NHMPU_S1 Homo sapiens cDNA clone IMAGE:20701583'	
1811 6739	11833	1.88	2.4E-02	H65894.1	EST_HUMAN	y75f1.1 Scores fetal liver spleen INFSL Homo sapiens cDNA clone IMAGE:2111495'	
2038 7831	12385	0.98	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN_K-B ALPHA CHAIN PRECURSOR (H-2K(B))	
2038 7831	12388	0.98	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN_K-B ALPHA CHAIN PRECURSOR (H-2K(B))	
4347 9469	14868	1.58	2.4E-02	J05110.1	NT	T_thiomethyl calcium-binding 25 kDa (TCBP 26) protein mRNA, complete cds	
4495 8814	14754	1.38	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN_K-S ALPHA CHAIN PRECURSOR (H-2K(B))	
4495 9614	14755	1.38	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN_K-S ALPHA CHAIN PRECURSOR (H-2K(B))	
5175 10272		1.2	2.4E-02	AF18453.1	NT	Kidney virus reading frame 6 VP6 gene, complete cds	
1882 7002		2.4	2.3E-02	W05340.1	EST_HUMAN	ZB544808.x1 Scores_fetal lung NB1L8W Homo sapiens cDNA clones IMAGE:2892846	
1885 7014		3.48	2.3E-02	U84185.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4	
2330 7437	12630	1.98	2.3E-02	Z74283.1	NT	S_cerevisiae chromosome IV reading frame ORF YDI245c	
3659 8798	13854	6.18	2.3E-02	Z29377.1	EST_HUMAN	HSAAACADHP_Human feces/Brain/Whole tissue/Homo sapiens cDNA	
3684 8832		2.28	2.3E-02	L23428.1	NT	Canis beta-galactosidase-binding lectin (LGALS5) mRNA, 3' end	
4121 9249	14388	0.69	2.3E-02	L24789.1	NT	Celitus grilus connexin 45.8 (Cx45.8) gene, complete cds	
4121 9249	14387	0.59	2.3E-02	L24789.1	NT	Celitus grilus connexin 45.8 (Cx45.8) gene, complete cds	
4398 9518	14859	1.03	2.3E-02	AM899107.1	EST_HUMAN	CNA4-AN0080-280400-160-004 NND0080 Homo sapiens cDNA	
4427 8547	14888	0.9	2.3E-02	BE835226.1	EST_HUMAN	CR3-4110118-01080-0118-007 NT0118 Homo sapiens cDNA	
4427 8547	14687	0.9	2.3E-02	BE835226.1	EST_HUMAN	CM3-AN10118-01080-0118-007 NT0118 Homo sapiens cDNA	
4428 10309	14688	0.75	2.3E-02	AW583693.1	EST_HUMAN	xs25d08-x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:27708713'	
4428 10309	14689	0.75	2.3E-02	AW583693.1	EST_HUMAN	xs25d08-x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:27708713'	
4867 8885	14824	2.62	2.3E-02	BF026487.1	EST_HUMAN	601672278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:38553885'	
4867 9885	14825	2.62	2.3E-02	BF026487.1	EST_HUMAN	601672278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:38553885'	
5132 10232	15387	0.73	2.3E-02	AF257110.1	NT	Rattus norvegicus glutamine nucleotide binding protein gamma subunit 11 mRNA, complete cds	
5132 10232	15388	0.73	2.3E-02	AF257110.1	NT	Rattus norvegicus glutamine nucleotide binding protein gamma subunit 11 mRNA, complete cds	
736 5892	11044	2.05	2.2E-02	AF018287.1	NT	Catombia liva nucleotida diphosphata kinase (NDPK) gene, nucleotida diphosphata kinase, complete cds	
1759 6885		1.44	2.2E-02	4557448	NT	Hom sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA	
1772 6898	12105	1.12	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	
1772 6893	12109	1.12	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	

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 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
20111	7128	12365	1.12	2.2E-02	Z82001_1	NT	S_pneumoniae popA gene and open reading frames
3416	8559		1.84	2.2E-02	AA577785_1	EST_HUMAN	nt_245d4.81 NCI CGAP_Gastri Homo sapiens cDNA clone IMAGE:1084782 3'
3624	8763			4.07	2.2E-02	AF083094_1	NT
							Infectious burst disease virus segment B strain ILA VP1 gene, complete cds
3882	8888	14122	1.16	2.2E-02	AW601317_1	EST_HUMAN	PM0-BT0340-170100-004503 B10340 Homo sapiens cDNA
3893	9028	14188	0.88	2.2E-02	Z74283_1	NT	S_cerevisiae chromosome IV reading frame ORF_YOL245c
4585	9703		1.36	2.2E-02	P16759	SWISSPROT	HYPOTHETICAL PROTEIN_1_U121
5049	10150	15280	0.92	2.2E-02	Z73597_1	NT	S_cerevisiae chromosome XVI reading frame ORF_YOL241c
6172	8029	14188	2.31	2.2E-02	Z74283_1	NT	S_cerevisiae chromosome IV reading frame ORF_YOL245c
4118	5588		4.02	2.1E-02	AV761502_1	EST_HUMAN	AV761502 MDS MDSADG01 6'
449	6516		6.76	2.1E-02	AF029728_1	NT	Dichrostatium discoidatum histidine kinase C (dhkC) mRNA, complete cds
							Basidio subtilis oakLM cluster, Oak< (cont), Oak (cont), and spore coat protein OakM (cont) genes, complete cds
1207	6398	11570	6.19	2.1E-02	U72073_1	NT	
1782	6918	12126	1.15	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN_B2A
1782	6918	12427	1.15	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN_B2A
1782	6918	12126	1.15	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN_B2A
2777	6594	11092	3.07	2.1E-02	N28288_1	EST_HUMAN	YAC3707.71 Scarece melanocyte 2NBBM Homo sapiens cDNA clone IMAGE:264541 5'
3128	7148	12389	4.84	2.1E-02	BE072548_1	EST_HUMAN	PM2-BT0548-120100-001-f1 B10548 Homo sapiens cDNA
3128	7148	12387	4.84	2.1E-02	BE072548_1	EST_HUMAN	PM2-BT0548-120100-001-f11 B10548 Homo sapiens cDNA
3571	8712	13872	1.16	2.1E-02	AA481271_1	EST_HUMAN	ZB8389.1 Scarece boar_fetus_N22fF8_3w Homo sapiens cDNA clone IMAGE:788121 6'
4102	8231	14388	0.8	2.1E-02	Z74283_1	NT	S_cerevisiae chromosome IV reading frame ORF_YOL245c
4286	9408	14544	0.7	2.1E-02	BF349561_1	EST_HUMAN	6020163106F1 NCI CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4181161 6'
4423	8549	14682	1.79	2.1E-02	U44914_1	NT	Battella burgdorferi plasmid cp22-2, espC and espD genes, complete cds, and unknown genes
4433	8532	14695	1.33	2.1E-02	A1768127_1	EST_HUMAN	wg814d11_x1 Scarece_NSF_F8_g1N_Ot_P_A_P_S11 Homo sapiens cDNA clone IMAGE:2371569 3'
4472	8661		15.42	2.1E-02	Y192123_1	NT	Homo sapiens putative pthHbA pseudogene for hair keratin, exons 2 to 7
4849	9551		1.54	2.1E-02	Y192123_1	NT	Homo sapiens putative pthHbA pseudogene for hair keratin, exons 2 to 7
4877	9783	14839	4.85	2.1E-02	Y08501_1	NT	A_thaliana mitochondrial genome, part A
4898	8814	14982	0.72	2.1E-02	AA685737_1	EST_HUMAN	eg56g12.81 Gaster_Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4788	8801	15042	0.67	2.1E-02	AI822432_1	EST_HUMAN	wh54at5_x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
17	5228	10340	1.16	2.0E-02	BF002952_1	EST_HUMAN	7681068_x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3309968 3' similar to contains MER1.13 MER1 repetitive element
18	6229	10341	7.62	2.0E-02	AW895885_1	EST_HUMAN	QV4-NN0038-270400-187-h58 NND038 Homo sapiens cDNA
256	5447	10585	2.69	2.0E-02	8753835	NT	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
283	5491	10623	2.38	2.0E-02	AA465638_1	EST_HUMAN	aa165b10_x1 Scarece_NhMPu_S1 Homo sapiens cDNA clone IMAGE:813307 6'
789	6883	11113	1.41	2.0E-02	8753835	NT	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA

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Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1088	6227	11392	1.21	2.0E-02	AL098805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 11 [p36.33] of Homo sapiens
1202	6335	11503	1.33	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10370 (FLJ10370), mRNA
1202	6335	11508	1.33	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1883	7033	12221	1.29	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
1883	7033	12222	1.29	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10489 (FLJ10489), mRNA
2759	7853		2.22	2.0E-02	AL161632.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3051	5223	10340	1.17	2.0E-02	BF002832.1	EST_HUMAN	IMAGE:3308998 3' similar to contains MER1.13 MER1 repetitive element;
3122	8274		1.44	2.0E-02	7305674	NT	Mus musculus retina domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sem6b), mRNA
3212	8383		1.23	2.0E-02	AF208568.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF2 mRNA, complete cds
3981	9115	14263	1.19	2.0E-02	MI16095.1	NT	P_vulgaris hydroxypyridine-rich glycoprotein (HRGP) mRNA, 3' end
6039	10183		2.7	2.0E-02	AL271985.1	EST_HUMAN	IMAGE:11886078 3' Q936G3_X1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:94188 similar to contains L1_H1_L1 nt 9407..51 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:94188 similar to contains L1_H1_L1 repetitive element;
691	5949	10891	1.77	1.9E-02	AA572764.1	EST_HUMAN	EMPTY SPICES HOMEOPTIC PROTEIN SWISSPROT
1628	6767	11681	0.85	1.8E-02	PI18488	NT	Empty splices HOMEOPTIC PROTEIN
2033	7161	12359	1.63	1.8E-02	AL1683103.2	NT	Homo sapiens chromosome 21 segment HS21C103
2033	7161	12361	1.63	1.8E-02	AL1683103.2	NT	Homo sapiens chromosome 21 segment HS21C103
2870	8024	13190	7.47	1.8E-02	AA715856.1	EST_HUMAN	IM0456.51 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
2870	8073	13243	1.57	1.8E-02	AL648669	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone GLOBLH07 3'
3695	8734		1.05	1.9E-02	NS2230.1	EST_HUMAN	Y2BBD22.81 Scores_3 multiple_sclerosis_2NtMSP Homo sapiens cDNA clone IMAGE:3839564 5'
3695	8820		9.11	1.8E-02	BE738088.1	EST_HUMAN	6015728825_NIH_MSC_57 Homo sapiens cDNA clone IMAGE:1697280 3' similar to contains Alu repetitive element;
3695	8833	13987	0.72	1.8E-02	AL301183.1	EST_HUMAN	Q940C7_X1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1697280 3' similar to contains Alu repetitive element;
4021	9163	14287	1.39	1.9E-02	AF141840.1	NT	Myoepithelial tumor VilM1 precursor (VWA1) and VlbA2 precursor (VWA2) genes, partial cds.
4165	9291	14428	1.59	1.9E-02	PO9081	SWISSPROT	HOMEOPTIC BICOID PROTEIN (PRD-4)
4165	9291	14429	1.59	1.9E-02	PO9081	SWISSPROT	HOMEOPTIC BICOID PROTEIN (PRD-4)
4514	9832	14777	2.89	1.9E-02	AI452889.1	EST_HUMAN	Y4804.31 Scores_NSF_F8_9W_O1_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
4699	7581	12832	2.69	1.9E-02	AL1616550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
343	6626	10862	2.13	1.8E-02	AW771104.1	EST_HUMAN	hr52c0.5_X1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER20 repetitive element;
1162	6297	11483	1.42	1.8E-02	X17684.1	NT	H.franckei mRNA for myelin basic protein (MBP)

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Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2840	7738	12881	1.28	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3195	8349		0.89	1.8E-02	AL065829.1	EST_HUMAN	test2at09x1 Soares cDNA clone IMAGE:2080288 3'
4083	9194		1.06	1.8E-02	AA861446.1	EST_HUMAN	AK24h04_61 Soares cDNA clone IMAGE:1406835 3'
4408	9628	146683	1.25	1.8E-02	AW9308383.1	EST_HUMAN	Q14-D7021-301289-071-b11 DT021 Homo sapiens cDNA
897	6057	11226	1.22	1.7E-02	BE394889.1	EST_HUMAN	ED3103268F_NIH_MGC_44 Homo sapiens cDNA clone IMAGE:363218D 5'
1801	6926	12138	1.37	1.7E-02	AW573183.1	EST_HUMAN	Hs24-03x1 Soares cDNA clone IMAGE:2833740 3' similar to contains L1.L1 repetitive element;
1801	6926	12139	1.37	1.7E-02	AW573183.1	EST_HUMAN	Hs34-03x1 Soares cDNA clone IMAGE:2833740 3' similar to contains L1.L1 repetitive element;
1891	7001		1.44	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2102	7217		6.4	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitogenin/29, complete cds
2899	8120	13284	1	1.7E-02	AL147815.1	EST_HUMAN	cpb220-8x1 Soares, preprint, uterus, NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3497	8638		4.28	1.7E-02	AW827388.1	EST_HUMAN	hmp45a04_x1 NCI CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER18_b1 MER18 repetitive element;
4140	9288		1.01	1.7E-02	AA668618.1	EST_HUMAN	ec1b104_a1 Strategate open (#437217) Homo sapiens cDNA clone IMAGE:8556927 3' similar to contains Alu repetitive element/contains element MER24 repetitive element;
4172	9289		2.34	1.7E-02	RD2596.1	EST_HUMAN	ye8688r1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:1248475
4432	8951	14694	0.62	1.7E-02	AI305278.1	EST_HUMAN	gnt0807_x1 NCI_CGAP_L15 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gp-X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4502	9821	14783	1.68	1.7E-02	AW573183.1	EST_HUMAN	Hs34e00-8x1 Soares cDNA clone IMAGE:2833740 3' similar to contains L1.L1 repetitive element;
4682	9798	14943	2.08	1.7E-02	VO0841.1	NT	Messenger RNA for arcticfish ( <i>Lophius americanus</i> ) somatosatin II
4782	9895		6.03	1.7E-02	AI015076.1	EST_HUMAN	ox51e02_61 Soares, testis, NT Homo sapiens cDNA clone IMAGE:1640858 3'
5163	10253	15392	0.62	1.7E-02	A1251973.1	NT	Homo sapiens partial elastin-1 gene
5110	5676		1.55	1.6E-02	AL021828.1	NT	Mycobacterium tuberculosis H37Rv complete genome segment 137/162
1689	6788	11894	0.68	1.6E-02	Y18889.1	NT	Treponema pallidum 1882_1fB3 and fID genes for flagellin subunit proteins and CAP protein homologues
2230	7342	12595	1.45	1.6E-02	Q84178	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASTYN) (ESTERASE-22)
2230	7342	12590	1.45	1.6E-02	Q84178	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASTYN) (ESTERASE-22)
2606	7705	12881	1.4	1.6E-02	AA484872.1	EST_HUMAN	ms81d08_x1 NCI CGAP_Emt Homo sapiens cDNA clone IMAGE:910887
2856	7763		1.13	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA01834 protein, partial cds
2889	8144	13306	0.66	1.6E-02	AF112282.1	NT	Leucine sp. isolate IBd cytochrome oxidase III gene, partial cds; mitochondrial gene
3312	8653	13919	4.35	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3626	8952	14112	0.91	1.6E-02	AL165301.2	NT	Mus musculus chromosome 21 segment HS21C101
4148	9274			2.14	1.6E-02 AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIF-C1, Fas-binding protein, BINQ1, tapasin, RatGDP-like, KE2, BINQ4, beta 1,3-galactosyl transferase, and RP918 genes, complete cds; Secern2 gene, partial
4276	8389	14540	1.02	1.6E-02 AW8756407.1	EST_HUMAN	QV2-PFT0012-140100-4-030-007 PT00012 Homo sapiens cDNA	
750	5903			33.34	1.6E-02 8923734	NT	Homo sapiens transcription factor (HSFA1A)30894, mRNA
2127	7241	12483	1.83	1.6E-02 N38521.1	EST_HUMAN	Y271607.11 Scores fetal liver spleen INFES Homo sapiens cDNA clone IMAGE:2432626.3'	
2164	7267	12616	1.33	1.6E-02 AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80	
3038	8187	13342	1.72	1.6E-02 AL0086216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48	
3053	8187	13343	1.72	1.6E-02 AL0086216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48	
3705	8843	13983	0.9	1.6E-02 BF0928442.1	EST_HUMAN	MR4-TR0115-08030-201-012 TR0115 Homo sapiens cDNA	
416	5694			1.4E-02 AL002230.2	NT	Chlamydomonas pneumoniae ARS9, section 58 of Bd of the complete genome	
1119	9257	11421	3.44	1.4E-02 770580	NT	Homo sapiens NESH protein (LOC51225), mRNA	
1280	6389			2.71	1.4E-02 132600.1	NT	Haemophilus influenzae Rd section 116 of 163 of the complete genome
1302	6432			2.7	1.4E-02 U67778.1	NT	Xenopus laevis neurogranin related 1b (XANGNR-1b) mRNA, complete cds
1403	6531			2.39	1.4E-02 AF216854.1	NT	Homo sapiens headpin gene, complete cds
1632	6859			0.97	1.4E-02 AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH116
3197	8349	13510	2.4	1.4E-02 AF160869.2	NT	Bifidobacterium longum Natto+ antigen (nbb), tyrosine decarboxylase, and alpha-glucosidase (agl)	
3370	8624	13687	0.67	1.4E-02 AW074212.1	EST_HUMAN	XP05070521 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575763.3	
3468	8808	13772	6.86	1.4E-02 AL161686.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82	
3468	8808	13773	5.85	1.4E-02 AL161598.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82	
3505	8848	13812	1.17	1.4E-02 4503828	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA	
3833	8772	13928	7.72	1.4E-02 6898518	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA	
4486	8885	14723	6.9	1.4E-02 AW862688.1	EST_HUMAN	EST374761 MAGE Homeoboxes, MAGG Homeoboxes cDNA	
4486	8885	14724	6.9	1.4E-02 AW862688.1	EST_HUMAN	EST374761 MAGE resequences, MAGG Homeoboxes cDNA	
4847	9859	16102	6.85	1.4E-02 BE735142.1	EST_HUMAN	6016674031F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280.6	
4847	9859	16103	6.85	1.4E-02 BE735142.1	EST_HUMAN	6016674031F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280.6	
1876	6398		0.83	1.3E-02 BE739203.1	EST_HUMAN	601568462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828335.6	
1959	7076	12298	1.32	1.3E-02 AL168201.2	NT	Homo sapiens chromosome 21 segment HS21C001	
3189	8349	13511	1.67	1.3E-02 BE7697081.1	EST_HUMAN	602128475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203.6	
3188	8349	13612	1.67	1.3E-02 BE7697081.1	EST_HUMAN	602128475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203.6	
3942	9078		1.27	1.3E-02 AF169288.1	NT	Mus musculus beta-secretogranin gene, complete cds	

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No	Top Hit Database Source	Top Hit Descriptor
210	5404		0.71	1.E-02	K87344.1	NT	H_sapiens cDNA, DMB, HLA-Z1, IPP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 8, 13 and 14 genes
352	5534	10973	3.5	1.E-02	AAD59289.1	EST_HUMAN	Scenes retina N2b-4fR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element 286501.1
452	5820	10783	2.68	1.E-02	P268838	SWISSPROT	L1 repetitive element; HYPOTHETICAL 17.1 KD PROTEIN IN PUR6 3REGION
737	5683	11045	0.77	1.E-02	AI163222.1	EST_HUMAN	Scenes testis_NHt Homo sapiens cDNA clone IMAGE:1734070 3' similar to contains L1, H1 L1 repetitive element;
2157	7270	12519	1.14	1.E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2160	7273	12521	1.21	1.E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2420	7626	12778	0.87	1.E-02	AW172350.1	EST_HUMAN	X87609.1 Scenes NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2457	7561	12813	1.27	1.E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018.
3076	8279		6.89	1.E-02	AA0755418.1	EST_HUMAN	2m8Ba03.1 Streptococcus overman cancer f837218 Homo sapiens cDNA clone IMAGE:846020 5'
3272	8421	13682	1.85	1.E-02	RE22805.1	EST_HUMAN	Y11608.81 Scenes placenta NB2aP Homo sapiens cDNA clone IMAGE:138903 3'
4852	8964	16109	0.89	1.E-02	6764867	NT	Mus musculus interferon regulatory factor 5 (Ifi5), mRNA
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H2A-H) gene, Ror2 gene, and sodium phosphate transporter (NPT2) gene, complete cds
4883	10004	15148	1.89	1.E-02	U91328.1	NT	Cytochrome p450 2D6 mRNA, partial cds
5024	10126		1.27	1.E-02	AB019788.1	NT	AT731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5068	10170	15305	1.77	1.E-02	AV731704.1	EST_HUMAN	Zn981.61 Strategene neuroepithelium (#337231) Homo sapiens cDNA clone IMAGE:530924 3'
1273	8402	11576	1.05	1.E-02	AA0703864.1	EST_HUMAN	H.sapiens LTPA gene, exon 4
1721	6848	12052	1.35	1.E-02	AF73491.1	NT	H.sapiens LTPA gene, exon 4
1721	8848	12053	1.35	1.E-02	X73491.1	NT	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL.
2032	7150	12289	2.99	1.E-02	BF346283.1	EST_HUMAN	RC3-S10167-1/2020-01-15-811 ST0187 Homo sapiens cDNA
2849	7898		3.8	1.E-02	N89523.1	EST_HUMAN	2m40695.1 Scenes fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:280540 5'
3609	8850	13817	2.38	1.E-02	AI1632508.1	EST_HUMAN	DK7ZP688E0924. s1 888 (synonym: Fats1) Homo sapiens cDNA clone DK7ZP688E0924
4082	9211		0.64	1.E-02	AV813706.1	EST_HUMAN	MR3-C70178-111089-013-510 CT0178 Homo sapiens cDNA
4788	8911	15052	2.21	1.E-02	ALD48383.2	EST_HUMAN	RCD-FN0025-250500-021-012 FN0025 Homo sapiens cDNA
6	6217	10331	7.57	1.0E-02	AW846120.1	EST_HUMAN	601BA087R1 NH_JMG_74 Homo sapiens cDNA clone IMAGE:933889 3'
3062	8216	13369	2.62	1.0E-02	BE835556.1	EST_HUMAN	MIR-C70060-081098-5110 CT0060 Homo sapiens cDNA
3245	8395	13557	1.16	1.0E-02	BE868899.1	EST_HUMAN	HA09221 Human fetal liver cDNA library Homo sapiens cDNA
3493	8634		0.64	1.0E-02	AW84621.1	EST_HUMAN	Mus musculus corticotropin releasing hormone receptor 2 (Crrt2), mRNA
3869	8956	14162	0.78	1.0E-02	AI086886.1	EST_HUMAN	6753521 NT
4744	9887	15605	4.26	1.0E-02	6753521	NT	

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Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exam Seq ID No:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4813	6925	15088	5.68	1.0E-02	P985897.1	EST_HUMAN	Y754h01_r1_Scares_fetal_liver_spleen_1NF1S_Homo_sapiens_cDNA_clone IMAGE:1888633 5'
8394	6044	11216	3.28	9.0E-03	AI7986126.1	EST_HUMAN	W42f08x1_NCI_CGAP_Kid11_Homo_sapiens_cDNA_clone IMAGE:2383483 3' similar to contains element MER22 MER22 repetitive element;
1268	6397		1.47	9.0E-03	BE781889.1	EST_HUMAN	G01410242f1NH_MGC_87_Homo_sapiens_cDNA_clone IMAGE:3973348 5'
1480	6818	11807	1.58	9.0E-03	AED01270.1	NT	Tropomodulin section 86 of 87 of the complete genome
23372	7478	12732	1.4	9.0E-03	AL1161658.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
2871	8025	13191	0.8	9.0E-03	AI251744.1	EST_HUMAN	Q18069x1_Scares_NFL_T_GBC_S1_Homo_sapiens_cDNA_clone IMAGE:1854281 3'
2871	8025	13192	0.8	9.0E-03	AI251744.1	EST_HUMAN	Q18069x1_Scares_NFL_T_GBC_S1_Homo_sapiens_cDNA_clone IMAGE:1854281 3'
3845	8784	139838	0.62	9.0E-03	J05184.1	NT	S.acidocaudatus thermopsin gene, complete cds
4972	10080	18217	1.14	9.0E-03	BE047984.1	EST_HUMAN	tz24e10.y1_NCI_CGAP_Bm62_Homo_sapiens_cDNA_clone IMAGE:2281468 5'
501	5099		2.57	8.0E-03	AA722907.1	EST_HUMAN	Zfsecd3.s1_Scares_phenyl_dihydronaphthalene IMAGE:413598 3' similar to contains Ali repetitive element;
830	6137	11306	83.35	8.0E-03	AF108656.1	NT	Homo_sapiens_adenylosuccinate lyase gene, complete cds
2140	7254	12500	1	8.0E-03	AL163283.2	NT	Homo_sapiens_chromosome 21 segment HS21 C088
29283	8082		0.97	8.0E-03	U47048.1	NT	Escherichia coli mitochondrial 24 region, DNA binding protein (mtbA), immunity protein (mtfI), mtrooch 24 (mttS), and mtrooch transport protein (mtfA, mtfB) genes, complete cds
9340	8498	13652	0.8	8.0E-03	AI1131018.1	NT	Homo_sapiens_SCL gene locus
38653	8792	13947	1.28	8.0E-03	PS28264	SWISSPROT	HYPOTHETICAL_1270_KD PROTEIN IN RAD24-BMH INTERGENIC REGION
38653	8792	13948	1.28	8.0E-03	PS28264	SWISSPROT	HYPOTHETICAL_1270_KD PROTEIN IN RAD24-BMH INTERGENIC REGION
4362	9484	14825	4.21	8.0E-03	EF5363227.1	EST_HUMAN	CMA-NN0118-30050-223-205 NN0119_Homo_sapiens_cDNA_Proline-rich_wickerhamii_263-11 complete mitochondrial DNA
5164	10254	163159	0.94	8.0E-03	JU02970.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
632	5849	10982	12.77	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
692	5849	10993	12.77	7.0E-03	AF097183.1	NT	Glycine max glutathione S-transferase GST_21 mRNA, partial cds
878	6124	11294	5.37	7.0E-03	AF243378.1	NT	AV731712_HTF_Homo_sapiens_cDNA_clone HITFAZP-10 5'
1117	6255	11419	2.78	7.0E-03	AV731712.1	EST_HUMAN	FORKHEAD BOX PROTEIN D3 (HNF3FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORK-HEAD HOMOLOG 2) (HFH-2)
1373	6601		1.02	7.0E-03	Q61080	SWISSPROT	NUCLEAR FACTOR 3 FORK-HEAD HOMOLOG 2 (HFH-2)
1402	6530	11709	3.16	7.0E-03	AA688298.1	EST_HUMAN	ab78b018.1_Stratagene fetal retina S37202_Homo_sapiens_cDNA_clone IMAGE:353145 3'
1517	6844	11830	2.52	7.0E-03	AW303559.1	EST_HUMAN	x221b02x1_Scares_NFL_T_GBC_S1_Homo_sapiens_cDNA_clone IMAGE:2813739 3'
1763	6878	12084	1.23	7.0E-03	AW890656.1	EST_HUMAN	ES7362826_NAGE_resequences, MAGA_Homo_sapiens_cDNA
1763	6878	12086	1.23	7.0E-03	AW890556.1	EST_HUMAN	ES7362826_NAGE_resequences, MAGA_Homo_sapiens_cDNA
2238	7828	12809	1.38	7.0E-03	PG4929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3544	8885	13847	0.73	7.0E-03	AI1150273.1	EST_HUMAN	gr34h02x1_Scares_leads_NHT_Homo_sapiens_cDNA_clone IMAGE:1761956 3'
3747	8886	14036	0.72	7.0E-03	AW444683.1	EST_HUMAN	UI-H-B13-akb-c-10-o-UJ_s1_NCI_CGAP_Sub5_Homo_sapiens_cDNA_clone IMAGE:2733691 3'

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Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3789	8923	14076	0.88	7.0E-03	AF196344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4572	9690		1.42	7.0E-03	AW030888.1	EST_HUMAN	Hs38a05_Y_NCI_CQAP_GU1 Homo sapiens cDNA clone IMAGE:28668938 5'
4674	10082		2.18	7.0E-03	AL1632782	NT	Homo sapiens chromosome 21 segment HS21 C018
5086	10186	15324	1.02	7.0E-03	BE044191.1	EST_HUMAN	hs36b08_X1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:30398073 similar to TR:OS3434
6038	101881	16325	1.02	7.0E-03	BED44191.1	EST_HUMAN	hs33h03_X1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:30398073 similar to TR:OS3434
1244	6375	11650	9.28	8.0E-03	AW511148.1	EST_HUMAN	hs22a05_X1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28102243 similar to SW_PXR_HUMAN_076489_ORPHAN NUCLEAR RECEPTOR PXR;
1244	6375	11551	9.29	8.0E-03	AW511148.1	EST_HUMAN	hs22a05_X1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28102243 similar to SW_PXR_HUMAN_076489_ORPHAN NUCLEAR RECEPTOR PXR;
2857	8012	13174	1.7	8.0E-03	AA759135.1	EST_HUMAN	hs78e11_1.01 Scores_tests_NHT Homo sapiens cDNA clone 1321772 3'
2857	8012	13175	1.7	8.0E-03	AA759135.1	EST_HUMAN	hs78e11_1.01 Scores_tests_NHT Homo sapiens cDNA clone 1321772 3'
9228	8379		2.39	8.0E-03	HT76800.1	EST_HUMAN	yt77h04J1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
9288	8435		1.13	8.0E-03	AF196338.1	NT	Notocampus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial product
3363	8608	13875	1.21	8.0E-03	US09890.1	NT	Fugu rubripes zinc finger protein, isocobolin, fatty acid binding protein, sepiapterin reductase and vasodolin genes, complete cds
3362	8608	13876	1.21	8.0E-03	US09890.1	NT	Fugu rubripes zinc finger protein, isocobolin, fatty acid binding protein, sepiapterin reductase and vasodolin genes, complete cds
3533	8875		1.12	8.0E-03	W37685.1	EST_HUMAN	2013a1_1.1 Scores_periphytid_tumot_NbHPA_Homo sapiens cDNA clone IMAGE:322172 5'
3637	8776	13931	4.08	8.0E-03	BF510988.1	EST_HUMAN	UH-B114_4pm-c-08-D1J51_NCI_CGAT_S1s8_Homo sapiens cDNA clone IMAGE:3087764 3'
3671	8810	13988	0.92	8.0E-03	EE077358.1	EST_HUMAN	RC1-BT0808-280400-014-a07_B10618_Homo sapiens cDNA
3758	8895	14045	1.2	8.0E-03	6754028	NT	Mus musculus glucosamine-6-phosphate deaminase (Gpd), mRNA
3893	8032	14192	1.21	8.0E-03	AW847284.1	EST_HUMAN	RCA-C10204-240588-021-h10_C10204_Homo sapiens cDNA
3829	8046		0.8	8.0E-03	BE250108.1	EST_HUMAN	6003642804AF1_NIH_MGC_15_Homo sapiens cDNA clone IMAGE:2869515 6'
4342	9464		2.01	8.0E-03	AI016833.1	EST_HUMAN	ov35e11_X1 Scores_tests_NHT Homo sapiens cDNA 5' end similar to EST containing AU repeat
4684	9780	14924	9.05	8.0E-03	AA329242.1	EST_HUMAN	EST27118_Cerebellum II Homo sapiens cDNA 5' end similar to EST containing AU repeat
688	6828	10987	1.88	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB, anti-methyl-tRNA synthase, complete cds; complete ORFA, and gpE-like protein, complete cds
668	6628	10988	1.88	6.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB, anti-methyl-tRNA synthase, complete cds; complete ORFA, and gpE-like protein, complete cds

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
669	5828	10867	2.65	6.0E-03	U25105.1	NT	Chlamydia trachomatis partial ORF; amineacyl-tRNA synthetase, complete cds; complete ORFA, and gtpE-like protein, complete cds
669	5828	10988	2.65	5.0E-03	U25105.1	NT	Chlamydia trachomatis partial ORF; amineacyl-tRNA synthetase, complete cds; complete ORFA, and gtpE-like protein, complete cds
1113	6251	11416	0.99	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH13
2842	7740	12983	1.64	6.0E-03	AB033008.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2801	8086	13224	0.76	6.0E-03	U2266057.1	EST_HUMAN	601194786F_1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538769 6'
3114	8267	13423	3.72	5.0E-03	T87623.1	EST_HUMAN	XCB1f08.81 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:223953 3'
3133	8284		2.08	6.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3145	8288	13455	1.14	5.0E-03	RT71794.1	EST_HUMAN	X88902.81 Scores breast 2NIBH Best Homo sapiens cDNA clone IMAGE:153686 3'
3281	8410		0.99	6.0E-03	AJ287357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
9878	8816	13971	3.65	6.0E-03	AF417449.2	NT	Pseudogene scores strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
9759	8877	14028	0.7	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
3944	9080		1.49	5.0E-03	AA288675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 6' end
4281	9404	14543	0.68	5.0E-03	HT8355.1	EST_HUMAN	JW79101.1 Scores fetal liver spleen 1NFL Homo sapiens cDNA clone IMAGE:240088 5'
4282	9877	14028	0.77	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4580	9898	14835	1.3	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4887	9803	14950	1.53	5.0E-03	AI752387.1	EST_HUMAN	cm15e02_x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH-TBC_cm15e02_hancom
231	5425	10563	8.16	4.0E-03	AW500198.1	EST_HUMAN	U1H-F5N0-akc-H-04-U1T1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:30768831 6'
319	6505	10843	1.71	4.0E-03	RA48482.1	EST_HUMAN	Y8510d.61 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:359983 3'
442	6610	10756	0.82	4.0E-03	P64675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
601	6763	10891	4.31	4.0E-03	AAQ29839.1	EST_HUMAN	cn765112.61 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:15622698 3'
878	6028	11201	1.78	4.0E-03	RA48482.1	EST_HUMAN	Y8510d.61 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:369988 3'
912	6082		3.34	4.0E-03	AW749101.1	EST_HUMAN	RC3-B70383-110100-012-101 BT0383 Homo sapiens cDNA
1152	6288	11453	23.83	4.0E-03	AA098977.1	EST_HUMAN	2612807.1 Stratagene cDNA (R9317204) Homo sapiens cDNA clone IMAGE:510988 5'
1171	6309	11473	1.43	4.0E-03	AW794740.1	EST_HUMAN	RCS-LJM0014-170400-023-G01 UMD014 Homo sapiens cDNA
1307	8437	11612	1.15	4.0E-03	AA284874.1	EST_HUMAN	25528e07.1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701738 5'
1689	6727		1.29	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB03 5'
1755	6881	12087	2.28	4.0E-03	U53472.1	NT	Rattus norvegicus type I astrocyte and olfactory-limbic associated protein A1-46 mRNA, complete cds
2013	7130	12358	5.61	4.0E-03	AA059777.1	EST_HUMAN	2612807.1 Strategene cDNA (R9317204) Homo sapiens cDNA clone IMAGE:510988 5'
2228	7340		1.8	4.0E-03	BE410586.1	EST_HUMAN	601304161F_1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3698510 5'
2265	7365	12821	1.19	4.0E-03	AW794740.1	EST_HUMAN	RCS-LJM0014-170400-023-G01 UMD014 Homo sapiens cDNA

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2637	7640	12888	1.09	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 8 (DUSP8), ribosomal protein L18a (RPL18a), Ca2+-/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
2637	7640	12889	1.09	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 8 (DUSP8), ribosomal protein L18a (RPL18a), Ca2+-/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
2682	7760	12889	2.57	4.0E-03	AJ277985.1	NT	Homo sapiens polyglutamine-containing C14orf4 gene
2682	7760	13000	2.57	4.0E-03	AJ277985.1	NT	Homo sapiens polyglutamine-containing C14orf4 gene
2687	7764	13003	1.11	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3210	8351	13523	1.16	4.0E-03	BE154134.1	EST_HUMAN	PM1-HIT0340-151-288-003-h08 HIT0340 Homo sapiens cDNA PM1-HIT0340-151-288-003-h08 HIT0340 Homo sapiens cDNA
3210	8351	13524	1.16	4.0E-03	BE154134.1	EST_HUMAN	PM1-HIT0340-151-288-003-h08 HIT0340 Homo sapiens cDNA PM1-HIT0340-151-288-003-h08 HIT0340 Homo sapiens cDNA
3567	8658	13824	0.74	4.0E-03	AW188428.1	EST_HUMAN	X585DA-X1 NC_ CGAP_Co18 Homo sapiens cDNA clone IMAGE:2685279 3'
3567	8658	13825	0.74	4.0E-03	AW188428.1	EST_HUMAN	X585DA-X1 NC_ CGAP_Co18 Homo sapiens cDNA clone IMAGE:2685278 3'
3970	9104			1.84	4.0E-03	AJ011712.1	NT
6187	10284			1.18	4.0E-03	O38821	SWISSPROT ATP SYNTHASE A CHAIN (PROTEIN 8)
369	6549	10683	2.01	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
880	6030	11202	11.35	3.0E-03	AF011920.1	NT	ncJ793d5-a1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:782884 similar to contains Abu repetitive element
1674	6903	11688	3.31	3.0E-03	AA468110.1	EST_HUMAN	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
2270	7390		4.86	3.0E-03	Z32521.1	NT	ncJ793d5-a1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:782884 similar to contains Abu repetitive element
2381	8115		1.73	3.0E-03	Y08006.1	NT	S.cerevisiae (cv. H38) mRNA for thiosphosphate isomerase
3065	8298	13383	4.44	3.0E-03	BE3179286.1	EST_HUMAN	Arabidopsis thaliana rpl31l gene
3130	8291	13437	2.62	3.0E-03	AW802687.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608633 5'
3359	8549	13702	1.58	3.0E-03	U34606.1	NT	[II-2-LN-0076-240320-058-D03 UMD076 Homo sapiens cDNA
3408	8551		7.13	3.0E-03	Y12500.1	NT	Nitis musculus alpha-(XVII) collagen (COL18A1) gene, exon 1 and 2
3690	9085	14239	6.58	3.0E-03	AV782392.1	EST_HUMAN	C.elegans smd-6 gene
3690	9085	14240	5.98	3.0E-03	AV782392.1	EST_HUMAN	AV782392 MDS Homo sapiens cDNA clone MDSSG01 5'
4011	9144	14284	1.37	3.0E-03	AT792278.1	EST_HUMAN	Ent04fb9.y6 Gossypium tumor Homo sapiens cDNA clone IMAGE:1185688 5'
4122	9250		1.24	3.0E-03	Z32521.1	NT	S.cerevisiae (cv. H38) mRNA for thiosphosphate isomerase
4374	9485	14639	13.02	3.0E-03	AJ011422.1	NT	Rattus norvegicus gdf11 gene
4492	9611	14751	4.98	3.0E-03	AJ538141.1	EST_HUMAN	xu8 P10_H3 concat Homo sapiens cDNA 3'
4801	9914	15055	3.48	3.0E-03	AI732754.1	EST_HUMAN	ab18ab5-x5 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Abu repetitive element
4823	9935	16076	7.71	3.0E-03	BE781945.1	EST_HUMAN	601482715F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:36385483 5'

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5123 10224	16359	1	3.0E-03	4508414	NT	Homo sapiens RAP1. GTPase activating protein 1 (RAP1GAP1) mRNA	
5123 10224	16360	1	3.0E-03	4608414	NT	Homo sapiens RAP1. GTPase activating protein 1 (RAP1GAP1) mRNA	
5159 10259	16398	0.82	3.0E-03	SS2213.1	NT	COD16-hulectoyne integrin alpha chain [Human, Germline; 104 nt segment 23 of 31]	
5174 10271	15412	1.32	3.0E-03	AW237754.1	EST HUMAN	xm8168.1x NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2686803 3'	
513 5679 10812	0.77	2.0E-03	0046852	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)		
613 6679 10813	0.77	2.0E-03	0046852	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)		
788 7801	10.75	2.0E-03	170874.1	EST HUMAN	jd1683.11 Scores feed liver spleen INF LS Homo sapiens cDNA clone IMAGE:108341 5'		
1372 6530 11683	2.03	2.0E-03	MC20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7		
1375 6533 11685	1.9	2.0E-03	AA661605.1	EST HUMAN	nu8501.81 NCI CGAP Ahr1 Homo sapiens cDNA clone IMAGE:1217593		
1384 6512 11683	6.44	2.0E-03	AF284448.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds		
1500 6627 11814	1.55	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)		
1631 6653 11844	1.78	2.0E-03	4557838	NT	Homo sapiens procollagen-lysine, 2-oxyglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA		
1631 6653 11845	1.78	2.0E-03	4657838	NT	Homo sapiens procollagen-lysine, 2-oxyglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA		
1604 6732	5.07	2.0E-03	P28440	SWISSPROT	COLLAGEN ALPHABETA(V) CHAIN PRECURSOR		
1781 6807 12116	1.08	2.0E-03	AA450138.1	EST HUMAN	2x22a10.1 Scores_total_fetus_N2BF8_8w Homo sapiens cDNA clone IMAGE:789114 5'		
1889 7113 12349	1.27	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds		
2543 7846	4.07	2.0E-03	AW137762.1	EST HUMAN	U1H-B11-adl-g-10-p-U1.51 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2217101 3'		
3398 8542 13701	3.39	2.0E-03	AA450138.1	EST HUMAN	2x42a10.1 Scores_total_fetus_N2BF8_8w Homo sapiens cDNA clone IMAGE:789114 5'		
3404 8847 13708	0.98	2.0E-03	B1F68855.1	EST HUMAN	60218336073 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'		
3843 8762 13936	5.49	2.0E-03	K87344.1	NT	H sapiens DNA, DMB, HLA-Z1, IFF2, LNF2, TAP1, LMP7, TAP2, DOB, DQ82 and RING8, 9, 13 and 14 genes		
4089 9217 14353	1.68	2.0E-03	PD3374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP35]		
4197 8322	9.07	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds		
4405 9128 0.98	2.0E-03	AW287380.1	EST HUMAN	U1H-BW0-en-5-33-0-U1.81 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:2730413 3'			
4519 9837 14782	2.13	2.0E-03	L42512.1	NT	Drosophila melanogaster short sighted class 2 (sts) mRNA, complete cds		
4519 9837 14783	2.13	2.0E-03	L42512.1	NT	Drosophila melanogaster short sighted class 2 (sts) mRNA, complete cds		
4678 9194	1.47	2.0E-03	R87773.1	EST HUMAN	jd45e02.01 Scores adult brain N2b4IB65Y Homo sapiens cDNA clone IMAGE:1808890 3'		
6005 10110 15239	0.74	2.0E-03	AF003528.1	NT	Homo sapiens X-linked antiidiopathic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions		
6013 10116 15248	1	2.0E-03	D38157.1	NT	Equine rotavirus RNA 5 for NSP1, complete cds, strain: H2		
5013 10116 15249	1	2.0E-03	D38157.1	NT	Equine rotavirus RNA 5 for NSP1, complete cds, strain: H2		

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
438	6607	10761	1.84	1.0E-03	I58471.1	EST_HUMAN	y58cd01_x1 Scores_ pitressin gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
630	6982	11160	1.37	1.0E-03	AI720263.1	EST_HUMAN	ss70b03_x1 Barsteed otoan HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR-Q13825
630	6982	11161	1.37	1.0E-03	AI720263.1	EST_HUMAN	ss70b03_x1 Barsteed otoan HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR-Q13825
1036	6234	11397	3.44	1.0E-03	AI885788.1	EST_HUMAN	Q13825_x1 AU-BINDING PROTEINENOL-COA HYDRATASE ;
1118	6254	11418	2.38	1.0E-03	AI954572.1	EST_HUMAN	Wk88601_x1 NCI_CGAP_Fanti Homo sapiens cDNA clone IMAGE:2422258 3'
1168	6303	11469	1.32	1.0E-03	AI892816.1	EST_HUMAN	wk88601_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:23538440 3' similar to contains Abu repetitive element
2021	7138	12378	2.71	1.0E-03	PF47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSINT (HMWWII)
2137	72497	12497	1.87	1.0E-03	JJ131016.1	NT	Homo sapiens SCL gene locus
2850	8104	13269	1.23	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1281 protein, partial cds
3174	8325	13488	2.18	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3174	8325	13487	2.13	1.0E-03	P18915.	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (SALIVARY CARBONIC ANHYDRASE)
3284	8433	13636	0.8	1.0E-03	PO8647	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
35820	85772	13837	0.8	1.0E-03	U68961.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
35820	85772	13838	0.8	1.0E-03	U68961.1	NT	Human MUC2 gene, promoter region
3842	8781		1.48	1.0E-03	AB044400.1	NT	Homo sapiens STMN gene for synaptic vesicle mannosidase transporter, exons 14, 15
3898	8034	14180	1.14	1.0E-03	AW170592.1	EST_HUMAN	xn63d01_x1 Scores_NH3eC_cervical tumor Homo sapiens cDNA clone IMAGE:2698381 3' similar to
3907	8043	14203	0.65	1.0E-03	749848.1	NT	contests TAR1_H TAR1 repetitive element ;
4412	8532	14671	2.51	1.0E-03	EE839162.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR148w
4455	9574	14713	3.89	1.0E-03	BE244536.1	EST_HUMAN	RC1-TN10128-1608004-021-011 TN0128 Homo sapiens cDNA
4683	9751	14898	0.8	1.0E-03	U29449.1	NT	TCBAP1D4609 Pedoblasto pro-B cell acute lymphoblastic leukemia Bayef-HGSC project TCBAP1D4609
4782	8905	15045	2.14	1.0E-03	AI073485.1	EST_HUMAN	Caenorhabditis elegans spliced Leader RNA (SL3 alpha), (SL4), and (SL5) genes
4782	8905	15046	2.14	1.0E-03	AI073485.1	EST_HUMAN	rrv45cd04_x1 Scores_ testis NHT Homo sapiens cDNA clone IMAGE:640262 3'
4783	9903		5.88	1.0E-03	EE154087.1	EST_HUMAN	crv45cd04_x1 Scores_ testis JHT Homo sapiens cDNA clone IMAGE:1640262 3'
6030	10162	16295	10.91	1.0E-03	Q48409	SWISSPROT	PMID:110339-200409-010-D02 HT0330 Homo sapiens cDNA
6198	10283	16430	2.16	1.0E-03	AV297269.1	EST_HUMAN	U-H-BW-0-4-0-0-U-11 NCI CGAP_Subs Homo sapiens cDNA clone IMAGE:2731838 3'
1498	6825		1.19	8.0E-04	Q84849.1	NT	Xlaevis mRNA for CASR protein
4161	9277		6.04	8.0E-04	PO8547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4730	8843	14989	2.63	8.0E-04	U28185.1	NT	Homo sapiens orphan protein (PRP) gene, complete cds
1841	6962	12185	1.06	7.0E-04	J41825.1	NT	Homo sapiens CTP7 gene, 5' end
2376	7482	12736	1.02	7.0E-04	U28185.1	NT	Homo sapiens orphan protein (PRP) gene, complete cds
2875	7772	13029	3.11	7.0E-04	AL168210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3264	8413	13575	0.97	7.0E-04	48857D	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3831	8067	14223	1.49	6.0E-04	AL382525.1	EST_HUMAN	WIF1a11_X1 NCI_CGAP Kid12 Homo sapiens cDNA clone IMAGE24028763'
4198	9282	14418	3.13	6.0E-04	U45983.1	NT	Homo sapiens CCR8 alternative receptor (CMKBR8) gene, complete cds
4421	9541	14680	0.9	8.0E-04	EE178435.1	EST_HUMAN	RC2-LT0560-180200-011-009 HT0560 Homo sapiens cDNA
4421	9541	14881	0.9	8.0E-04	EE178435.1	EST_HUMAN	RC2-LT0560-180200-011-009 HT0560 Homo sapiens cDNA
6003	10103	10108	1.07	6.0E-04	LA40808.1	NT	Plasmoidium falciparum (strain D2) variant-specific surface protein (var-1) gene, complete cds
6180	10277	15415	1.88	6.0E-04	BE059228.1	EST_HUMAN	CM2-BT0568-230300-128-f01 D10588 Homo sapiens cDNA
6550	6811	10948	9.89	5.0E-04	010344	SWISSPROT	HYPOTHETICAL 29.3 kD PROTEIN (ORF82)
1616	6843		1.17	6.0E-04	AV785184.1	EST_HUMAN	Q00-CT0225-021089-030-007 CT0225 Homo sapiens cDNA (ORF82)
3395	8539	13698	1.31	5.0E-04	AA548831.1	EST_HUMAN	EST27611_X1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE1014764 3' similar to contains Alu repetitive element
390	6559		0.84	4.0E-04	BF241482.1	EST_HUMAN	Q01876834F1 NIH_MSC_55 Homo sapiens cDNA clone IMAGE4104897 5'
672	6831	10871	1.09	4.0E-04	U32748.1	NT	Hemophilus influenzae Rd section 83 of 163 of the complete genome
848	6980	11170	1.25	4.0E-04	AI720268.1	EST_HUMAN	Q13825_X1 Barsheid cDNA HPLRB7 Homo sapiens cDNA clone IMAGE2334039 3' similar to TR-Q13825
848	5999	11171	1.25	4.0E-04	AI720268.1	EST_HUMAN	Q13825_X1 Barsheid cDNA HPLRB7 Homo sapiens cDNA clone IMAGE2354039 3' similar to TR-Q13825
1477	6604	11780	2.44	4.0E-04	AV753358.1	EST_HUMAN	RC3-CT0224-190103-023-001 CT0224 Homo sapiens cDNA
2078	7192	12436	1.04	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
2582	7683	12947	1.2	4.0E-04	0866615	SWISSPROT	SERICIN2 (SILK GUM PROTEIN 2)
3143	8294	13462	3.12	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4300	8422	14684	3.09	4.0E-04	AA576331.1	EST_HUMAN	Rh10a1_X1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE351830 3' similar to gBM21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4300	9422	14555	3.09	4.0E-04	AA576331.1	EST_HUMAN	Rh10a1_X1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE361830 3' similar to gBM21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4510	9829	14773	2.08	4.0E-04	AA0386324.1	EST_HUMAN	Zn61 cde_s1 Strategene muscle 837209 Homo sapiens cDNA clone IMAGE562670 3'
5072	10173	16308	3.37	4.0E-04	EE560660.1	EST_HUMAN	Q01346886F1 NIH_MSC_8 Homo sapiens cDNA clone IMAGE3678910 3'
5184	10281	16419	1.78	4.0E-04	Q068848	SWISSPROT	RABPHILIN-3A
161	5348	10480	1.81	3.0E-04	AL119423.1	EST_HUMAN	DKFZp761J221_1761 (synonym: tamy2) Homo sapiens cDNA clone DKFZp761J221 5
182	6387	10530	1.82	3.0E-04	F49269	SWISSPROT	180 kD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
881	6031	11203	1.6	3.0E-04	U83891.1	NT	Human short chain ester CoA dehydrogenase gene, exons 1 and 2 Q228203.y1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2028187 5'
1852	6973	12164	1.38	3.0E-04	AI282100.1	EST_HUMAN	CG23622.X1 NCI CGAP_F28 Homo sapiens cDNA clone IMAGE:2110082 3'
1865	6985			2.63	3.0E-04	AI389874.1	EST_HUMAN
3280	8438	135598	3.58	3.0E-04	P25147	SWISSPROT	INTERNEALIN B PRECURSOR
3626	9072	14228	4.2	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4030	9181			1.29	3.0E-04	AJ271736.1	Hom sapiens Xq pseudautosomal region; segment 1/2
4059	9189			1.03	3.0E-04	BE140809.1	EST_HUMAN
4785	9898			4.72	3.0E-04	BE153778.1	EST_HUMAN
171	6386	10507	1.38	2.85	2.0E-04	AF217798.1	NT
478	5843	10786	2.85	2.0E-04	AI46707.1	EST_HUMAN	Home sapiens SCG10 like-protein, helicase-like protein NHL_M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
908	6058	11227	9.92	2.0E-04	AI86524.1	NT	Human dystrophin gene
908	6059	11228	8.82	2.0E-04	MB6524.1	NT	Human dystrophin gene
1181	6318			4.31	2.0E-04	AI286021.1	EST_HUMAN
1188	6322			4.79	2.0E-04	AL163203.2	NT
1848	6867			0.99	2.0E-04	AF224238.1	NT
2100	7279			0.89	2.0E-04	AA478980.1	EST_HUMAN
2639	7642	12891	2.6	2.0E-04	U68061.1	NT	Human dermal T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV16S1, TCRBV11S1A1T, HVB relt, HVB relt, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJS1, TCRBJS2,>
2958	8110	13273	0.83	2.0E-04	AI124829.1	EST_HUMAN	sm58c09_X1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1639760 8'
3318	8463	13629	0.683	2.0E-04	5174736	NT	Mus musculus S flanking region of Ptx3 gene
3417	8580			2.46	2.0E-04	BE0282317.1	EST_HUMAN
3888	8024	14182	0.97	2.0E-04	AW978441.1	EST_HUMAN	EST30550 MAGE resequences, MAGP Homo sapiens cDNA EST30550 MAGE resequences, MAGP Homo sapiens cDNA
4114	9242			6.91	2.0E-04	U01029.1	NT
4639	9767	14904	1.35	2.0E-04	H86256.1	EST_HUMAN	Phaeopus vulgaris nitrate reductase (PVNR2) gene, complete cds
4639	9737	14905	1.35	2.0E-04	H86256.1	EST_HUMAN	Y01011.11 Scorpio_jebea gland_N31PG Homo sapiens cDNA clone IMAGE:232558 5'
4784	9877			1.65	2.0E-04	U09226.1	NT
5040	10142	16272	1.69	2.0E-04	AB037897.1	NT	Gelius gelius proteasome 28 kDa subunit homolog mRNA, complete cds
787	5821	11078	1.21	1.0E-04	H99646.1	EST_HUMAN	Y02605.s1 Scorpio melanocyte 28 kDa cDNA clone IMAGE:282884 3' similar to contains L1.H1 repetitive element;

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
<b>RETROVIRUS-RELATED POLYPOLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]</b>							
1076	8218	11380	2.02	1.0E-04	FM13889	SWISSPROT	
1116	6253	11418	3.41	1.0E-04	AW0413847.1	EST_HUMAN	U+H-BIG-Sub1-Homo sapiens cDNA clone IMAGE2708825 3'
1115	6253	11417	3.41	1.0E-04	AW013847.1	EST_HUMAN	U+H-BIG-Sub1-Homo sapiens cDNA clone IMAGE2708825 3'
1337	6465		3.38	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
							Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GP-CR, putative phosphotyrosylformylpeptidylamidine synthetase, and LAMP (LAMP) genes, complete cds
1888	8787	11850	2.82	1.0E-04	AF148805.1	NT	
							Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GP-CR, putative phosphotyrosylformylpeptidylamidine synthetase, and LAMP (LAMP) genes, complete cds
1838	8767	11981	2.62	1.0E-04	AF148805.1	NT	
1872	6982	12247	1.68	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY38
32688	8417	13578	0.87	1.0E-04	Q8Z203	SWISSPROT	SPlicingosome ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A88)
3717	8855	14009	0.71	1.0E-04	AI440282.1	EST_HUMAN	tp0111.x1 NCI_CGAP_Gene Homo sapiens cDNA clone IMAGE2142689 3' similar to contains Alu repetitive element
40324	9165	14307	2.12	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4059	9180	14331	1.38	1.0E-04	AV847727.1	EST_HUMAN	AV847727 GLC Homo sapiens cDNA clone GLCBBD4 3'
5080	10181	16317	1.48	1.0E-04	7662015	NT	Homo sapiens KIAA0237 genes product (KIAA0237), mRNA
5080	10181	16318	1.48	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5084	10184	15922	0.92	1.0E-04	AI357156.1	EST_HUMAN	Q82H04_x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE2005976 3'
6202	10289	16495	0.97	1.0E-04	AW451457.1	EST_HUMAN	U+H-BIG-Sub1-Homo sapiens cDNA clone IMAGE2708828 3'
638	6853	10898	2.38	9.0E-05	AA718933.1	EST_HUMAN	aa44611.1 Socres_tests_NH1 Homo sapiens cDNA clone 12824498 3'
822	6976	11139	1.19	8.0E-05	AJ251646.1	NT	Plasmid mRNA for beta-1,3 glucanase (gns2 gene)
865	6016		7.43	8.0E-05	AJ251646.1	NT	Plasmid mRNA for beta-1,3 glucanase (gns2 gene)
2816	8070		0.77	8.0E-05	MR3575.1	NT	Human platelet-derived growth factor A chain (PDGF-A) gene, exists only
4460	8579	14718	0.71	8.0E-05	AW044605.1	EST_HUMAN	WY780411 Socres_NSE_F8_BW_OT_P_S1_Homo sapiens cDNA clone IMAGE2354638 3'
5201	10283	16493	0.88	8.0E-05	AJ36918.1	NT	Pig microsatellite DNA (CA repeat)
344	6527	10653	7.12	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220889-011-E04 CT0208 Homo sapiens cDNA
344	6527	10684	7.12	7.0E-05	AW847446.1	EST_HUMAN	RC3-CT0208-220889-011-E04 CT0208 Homo sapiens cDNA
666	9731	10899	1.01	7.0E-05	LA9075.1	EST_HUMAN	HU072014F Human foetal cDNA Homo sapiens cDNA clone EST_HFD072014
568	6731	10860	1.01	7.0E-05	LA49075.1	EST_HUMAN	HU072014F Human foetal cDNA Homo sapiens cDNA clone EST_HFD072014
1057	6168	11363	1.65	7.0E-05	Q22849	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2680	7777	13027	2.29	7.0E-05	AL168278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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 Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3137	82883	13445	6.82	7.0E-05	AB008680.1	NT	Dichotostellum dissoidium gene for TRFA, complete cds
4361	9473	14811	1.84	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2020	7137	12376	1.27	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2020	7137	12377	1.27	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2550	7653	12943	1.14	6.0E-05	AI85241.1	EST_HUMAN	W54hr08_X1_NCI_CGAP_GoHomo sapiens cDNA clone IMAGE:2308331 3' similar to gb:J03230 DNA TOPOISOMERASE (HUMAN);
2775	6836	10875	2.57	6.0E-05	AF031630.1	NT	Homo sapiens monocyte-leukophil elastase inhibitor gene, complete cds
1411	68383	11716	35.84	5.0E-05	AV392088.1	EST_HUMAN	QV4-ST0234-241198-040-h11 ST0234 Homo sapiens cDNA
1874	6894		1.42	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC56895) mRNA
3952	9097	14241	3.47	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
2768	6419		3.52	4.0E-05	U12821.1	NT	Human retin (REN) gene, 6' flanking region
4461	9580	14717	0.88	4.0E-05	P49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4461	9580	14718	0.88	4.0E-05	P49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4846	8958		1.17	4.0E-05	AF104488.1	NT	Cryptosporidium parvum isolate Zaire 16 kDa glycoprotein gp16 gene, partial cds
6004	10109	16238	0.82	4.0E-05	AF22123.1	NT	Drosophila melanogaster starless protein (star) gene, complete cds
6837	10977		0.84	3.0E-05	AI248861.1	EST_HUMAN	Qh8ac10_X1_Scarce_fetal_liver_spleen_INF1S_S1 Homo sapiens cDNA clone IMAGE:1849468 3' similar to
1080	6201	11365	1.2	3.0E-05	AV273891.1	EST_HUMAN	xx24g03_X1_Scarce_INF1T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3
1132	6269	11431	1.4	3.0E-05	BF0317898.1	EST_HUMAN	ES01461463FI_NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3885142 5'
1132	6269	11432	1.4	3.0E-05	BF0317898.1	EST_HUMAN	ES01461463FI_NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885142 5'
2682	7779	13029	1.13	3.0E-05	Q8Z234	SWISSPROT	SKELEMIN
4361	9483	14623	6.86	3.0E-05	BE168211.1	EST_HUMAN	PMI-H10521-1/2020-001-#10 H10521 Homo sapiens cDNA
4361	9483	14824	5.86	3.0E-05	BE168211.1	EST_HUMAN	PMI-H10521-1/2020-001-#10 H10521 Homo sapiens cDNA
4446	9584	14705	1.03	3.0E-05	AA368678.1	EST_HUMAN	ES178866 Placenta 11 Homo sapiens cDNA similar to similar to p53-associated protein
4446	9584	14706	1.03	3.0E-05	AA368678.1	EST_HUMAN	ES178866 Placenta 11 Homo sapiens cDNA similar to similar to p53-associated protein
4704	9820	14967	1.03	3.0E-05	P87488	SWISSPROT	CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ)
4804	5837	10977	0.62	3.0E-05	AI248061.1	EST_HUMAN	contains Aliu repetitive element/contains element KER repetitive element;
4811	6823	15084	0.88	3.0E-05	AU125721.1	EST_HUMAN	AU125721 NT2KMA Homo sapiens cDNA clone NT2RWA002075 5'
2304	7413	12883	1.03	2.0E-05	AI2386021.1	EST_HUMAN	Qh8ac11_X1_Scarce_INF1T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2547	7650	12890	1.02	2.0E-05	M13782.1	NT	Human adenosine deaminase (ADA) gene, complete cds
2874	7771		3.85	2.0E-05	AA160562.1	EST_HUMAN	2046a12.1 Stratagene hNT neuron (h83723) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Aliu repetitive element/contains element L1 repetitive element;

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## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3116 8258	13424	1.29	2.0E-05	BE068038.1	EST_HUMAN	RC3-BT0318-120200-014-h08 BT0318 Homo sapiens cDNA	
3330 8476	13639	0.68	2.0E-05	AF184814.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds	
3351 8498	13665	0.94	2.0E-05	AB9211.1	NT	H.sapiens DNA for endogenous retroviral like element	
3476 8817		0.62	2.0E-05	NC05445.1	NT	S. cerevisiae 12.9 Kbp fragment of the left arm of chromosome XV	
4584 9702	114841	0.63	2.0E-05	AI263349.1	EST_HUMAN	Q91360(B_XI_Scenes_NHINP0_51 Homo sapiens cDNA clone IMAGE:1832374 3' similar to contains MER18_b3 MER18 repetitive element;	
6010 10113		1.08	2.0E-05	L77669.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end	
2859 7848	13002	1.15	1.0E-05	AI1692382.2	NT	Homo sapiens chromosome 21 segment HS21C082	
3627 8768	13922	1.84	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lel-120 Suppressor of Hairyless (Su(H)) gene, exons 7-49, and partial cds, alternatively spliced	
3790 8927		0.89	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	
3940 9076	14230	9.21	1.0E-05	CB1274	SWISSPROT	MOSAIC PROTEIN IN GIN	
4144 8272	14409	1.21	1.0E-05	AI168203.2	NT	Homo sapiens chromosome 21 segment HS21C083	
4261 8876	14507	1.94	1.0E-05	AA431118.1	EST_HUMAN	2K68g04_x1 Scenes_beta_tetts_NH7 Homo sapiens cDNA clone IMAGE:781484 5'	
4820 8932	15073	1.81	1.0E-05	AW419134.1	EST_HUMAN	X94911_x1 NCL_CGAP_LG34.1 Homo sapiens cDNA clone IMAGE:2856848 3'	
4954 10062	16201	0.7	1.0E-05	Z18943.1	NT	H.sapiens repeat region	
2833 7731	12883	2.62	9.0E-05	AI583811.1	EST_HUMAN	173a08_x1 NCL_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246388 3'	
9059 8222	13379	4.49	9.0E-06	AI216983.1	EST_HUMAN	Q911b08_x1 Scenes_placenta_BiotinWorks_2NBHP850M Homo sapiens cDNA clone IMAGE:1759181 3'	
3594 6733		3.18	9.0E-06	MB1755.1	NT	Human deaminase/lysyl oxidate amidotransferase (AGXT) gene, exons 1 and 2	
2501 7841	12853	3.36	8.0E-08	AW352859.1	EST_HUMAN	RC3-C10283-20189-011-h11 CT0283 Homo sapiens cDNA	
880 6126		1.45	7.0E-08	AA589729.1	EST_HUMAN	AB081101_x1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:354251 3' similar to contains MIER20 11 MER20 repetitive element;	
1449 6877	11784	3.8	7.0E-08	7682177 NT	NT	Homo sapiens KIAA0565 gene product (KIAA0565), mRNA qri10g9_x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:1891288 3' similar to contains Alu repetitive element;	
2837 7892		8.1	7.0E-08	AI388252.1	EST_HUMAN		
3549 8690		1.44	7.0E-08	AA385842.1	EST_HUMAN	EST88205 Thyroid Homo sapiens cDNA 6' end similar to EST containing L1 repeat	
2883 8037	13202	1	6.0E-08	BE068189.1	EST_HUMAN	QY9-BT0318-010300-105-d11 BT0318 Homo sapiens cDNA	
3869 8808	13985	1.08	6.0E-08	BE069189.1	EST_HUMAN	QY9-BT0318-010300-105-d11 BT0318 Homo sapiens cDNA	
4718 8091	13232	1.93	6.0E-08	Q01466	SWISSPROT	OVARIAN_ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)	
4728 8839	14983	2.62	6.0E-08	AI040898.1	EST_HUMAN	Q018e02_x1 Scenes_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER12 MER8 repetitive element;	
646 5807	10941	6.07	4.0E-08	R16287.1	EST_HUMAN	YE48c03_x1 Scenes_infant_brain_NIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element;contains L1 repetitive element;	

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 Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
847	5698	11169	5.64	4.0E-08	AW103364.1	EST_HUMAN	x68g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element;
1339	6467	11647	2.81	4.0E-08	AI334828.1	EST_HUMAN	tb33e05.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2059168 3'
1339	6467	11648	2.61	4.0E-08	AI334828.1	EST_HUMAN	tb33e05.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2059168 3'
1485	6612	11789	1.68	4.0E-08	BF3656812.1	EST_HUMAN	QV2-NT0046-20080-250-H107 NT0046 Homo sapiens cDNA clone IMAGE:2058168 3'
2245	7358	128131	1.14	4.0E-08	AW016401.1	EST_HUMAN	U1H-B10-eat-4-05-D-U1.S1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710426 3'
3038	8190	13346	0.74	4.0E-08	AF188349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3871	8007	14163	1.07	4.0E-08	AW84285.1	EST_HUMAN	IL8-CT0214-160200-074-B03 CT0214 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element
4778	8889	15034	2.18	4.0E-08	AI886838.1	EST_HUMAN	W94c10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element
2146	7259	12605	0.98	3.0E-08	AA700562.1	EST_HUMAN	Z54b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432883 3' similar to contains L1_H1 repetitive element;
2145	7259	12506	0.66	3.0E-08	AA700562.1	EST_HUMAN	Z54b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432883 3' similar to contains L1_H1 repetitive element;
2247	7357		1.18	3.0E-08	AF202835.1	NT	Homo sapiens PPP120 mRNA, complete cds
2887	8041	13205	0.84	3.0E-08	AA868218.1	EST_HUMAN	ak48g11.s1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.3 LTR1 repetitive element;
3248	8898		2.34	3.0E-06	AI857778.1	EST_HUMAN	w22a05.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR-O60734 O60734 LINE-1 LIKE PROTEIN_U1 contains L1.12 L1 repetitive element;
3762	8899	14050	1.42	3.0E-08	BE047094.1	EST_HUMAN	hg84d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3782	8899	14051	1.42	3.0E-08	BE047094.1	EST_HUMAN	hg84d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124161 3'
4454	9573	14712	0.86	3.0E-08	T60268.1	EST_HUMAN	y07801.17 Strategies ovary (#307217) Homo sapiens cDNA clone IMAGE:77275 3' similar to contains L1 repetitive element
4535	8853	14788	3.81	3.0E-08	XK4816.1	NT	Homo sapiens gene for alpha-1-microglobulin-beta-kunitin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
1689	5934		2.1	2.0E-08	P54568	SWISSPROT	HOMEOPBOX PROTEIN GOOSECOID
1682	8711		4.44	2.0E-08	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
2367	7464	12720	2.70	2.0E-08	AI872138.1	EST_HUMAN	w64a63.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297088 3' similar to contains MER30.61 MER30 repetitive element;
2443	7547	12800	1.72	2.0E-08	PG0929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2634	7657	12885	1.17	2.0E-08	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3604	8845	13811	1.05	2.0E-08	AV857655.1	EST_HUMAN	AV857655 GLC Homo sapiens cDNA clone GLCFPB05 3'
3742	8890	14031	1.74	2.0E-08	AA173518.1	EST_HUMAN	#p2605.11 Strategies ovarian cancer (#897219) Homo sapiens cDNA clone IMAGE:595232 5'
3763	8890	14041	0.63	2.0E-08	AW450215.1	EST_HUMAN	U1-H-B13-eky-g-05-0-L1.S1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'

Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3767 8894	14044	1.44	2.0E-08	AB030898.1	NT	Mus musculus gene for odorant receptor A18, complete cds	
32 6243	10369	2.84	1.0E-08	OTRS052	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-ORGANIC CATION/DEPENDENT CARNITINE COTRANSPORTER)	
656 6817	10955	1.89	1.0E-08	AF084384.1	NT	Mus musculus DEAMINE protein (D5NME), mRNA, complete cds	
1464 6591	11779	1.35	1.0E-08	FP09125	SWISSPROT	NEUROZOTE SURFACE PROTEIN CNV2-8	
1585 6714	11804	1.22	1.0E-08	AA034141.1	EST_HUMAN	z08a12.51 Scores: fetal_liver_spineen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:429882 3' similar to contains Alt repetitive element	
1685 6714	11805	1.22	1.0E-08	AA034141.1	EST_HUMAN	z08a12.51 Scores: fetal_liver_spineen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:429882 3' similar to contains Alt repetitive element	
1687 6723		1.1	1.0E-08	F27626	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT	
1685 7112	12348	3.68	1.0E-08	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds	
1695 7112	12347	3.68	1.0E-08	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds	
4348 6470	14607	12.32	1.0E-08	U07661.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8804 Met protein (M8804 Met) gene, complete cds	
60389 10163	15327	1.04	1.0E-08	AL163285.2	NT	Home sapiens chromosome 21 segment HS21_C085	
60388 10183	15328	1.04	1.0E-08	AL163285.2	NT	Home sapiens chromosome 21 segment HS21_C085	
338 65339	10630	1.19	8.0E-08	AF003628.1	NT	Home sapiens Glycerate 3 (GPC3) gene, partial cds and flanking repeat regions	
338 65339	10631	1.19	9.0E-07	AF003528.1	NT	Home sapiens Glycerate 3 (GPC3) gene, partial cds and flanking repeat regions	
4736 9849	14986	4.46	8.0E-07	AL288598.1	EST_HUMAN	q182g07.1x1 Scores: NHPMPu_S1 Homo sapiens cDNA clone IMAGE:18788763'	
4736 9849	14986	4.46	8.0E-07	AL288598.1	EST_HUMAN	q182g07.1x1 Scores: NHPMPu_S1 Homo sapiens cDNA clone IMAGE:18788763'	
1915 7034	12254	2.17	6.0E-07	AY855598.1	EST_HUMAN	CN8-C10277-22/1089-024-011 CT0277 Homo sapiens cDNA	
2465 7669	12823	2.3	6.0E-07	AF018413.1	NT	Human HLA class III region containing tenascin-X genes, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (B), and complement component C2 (C2) genes,>	
3945 8081		1.72	6.0E-07	F41478	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION	
324 6509		1.21	5.0E-07	AI881883.1	EST_HUMAN	wt6410x1 NC1_CGAP_K1d11 Homo sapiens cDNA 5' end	
1059 6200		3.61	5.0E-07	AA380630.1	EST_HUMAN	EST688115 Supt cells Homo sapiens cDNA 5' end	
3003 81577		0.61	5.0E-07	AB31883.1	EST_HUMAN	wt6410x1 NC1 CGAP_K1d11 Homo sapiens cDNA clone IMAGE:23886847 3'	
4615 9733	14870	0.88	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds	
3974 9108	14257	1.94	4.0E-07	AW006602.1	EST_HUMAN	ws84h05.5 NC1 CGAP_Co3 Homo sapiens cDNA clone IMAGE:2501697 3'	
440 5609	10753	3.65	3.0E-07	U18718.1	NT	Human microtubule-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons	
681 6744	10872	3.16	3.0E-07	AJ271735.1	NT	Homo sapiens Xa pseudautosomal region, segment 1/2	
1383 6511	11692	1.46	3.0E-07	M699149.1	NT	Human polymorphic microsatellite DNA	

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**Table 4**  
**Single Exon Probes Expressed In BT474 Cells**

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1637	67683	12892	1.48	3.0E-07	M84687.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 alleles
2446	7649	12892	19.22	3.0E-07	BE005077.1	EST_HUMAN	MRD-BN0115-020300-001-41 BN0115 Homo sapiens cDNA
2446	7649	12893	19.22	3.0E-07	BE005077.1	EST_HUMAN	MRD-BN0115-020300-001-41 BN0115 Homo sapiens cDNA
3000	8160	13317	0.87	3.0E-07	T84704.1	EST_HUMAN	Y50512.1x Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:111685 5
3138	8289	13446	1.57	3.0E-07	P7879	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4695	98111	14989	7.38	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCCD01 3'
4728	9841	14988	0.72	3.0E-07	AI787236.1	EST_HUMAN	W86512.1x Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347867 3'
5046	10148	16277	1.3	3.0E-07	T57850.1	EST_HUMAN	yc14h09_s1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:80765 3 similar to gb:M62882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
6046	10148	15278	1.3	3.0E-07	T57850.1	EST_HUMAN	yc14h09_s1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:80765 3 similar to gb:M62882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
27	6238	10383	2.58	2.0E-07	AF262898.1	NT	Hom sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
149	6348	10488	10.59	2.0E-07	L77569.1	NT	Hom sapiens DiGeorge syndrome critical region, telomeric end
149	5346	10489	10.59	2.0E-07	L77569.1	NT	Hom sapiens DiGeorge syndrome critical region, telomeric end
177	5371	10512	133.71	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoskeletal(vascular) actin gene, complete cds
747	5903	11057	1.87	2.0E-07	AF003630.1	NT	Hom sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
747	5903	11058	1.67	2.0E-07	AF003630.1	NT	Hom sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
759	5914		1.19	2.0E-07	P11369	SWISSPROT	RETOVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
843	6091	11259	2.03	2.0E-07	AA223260.1	EST_HUMAN	yc080731 Strategene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:650866 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
944	6092	11280	4.36	2.0E-07	T83042.1	EST_HUMAN	yc15g04_s1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:80760 3' similar to contains L1 repetitive element;
1165	6300	11468	0.92	2.0E-07	Q28768	SWISSPROT	I/B AUTOANTIGEN
1614	8742	11687	2.37	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.6 KD PROTEIN C2F7.10 IN CHROMOSOME 1
8653	8864	13980	17.85	2.0E-07	AF126348.1	NT	Hom sapiens cavinolin 1 (CAV1) gene, exon 3 and partial cds
1103	8241		0.99	1.0E-07	AL163292.2	NT	Hom sapiens chromosome 21 segment HS21C082
2787	8655	11851	2.67	1.0E-07	P08266	SWISSPROT	GLYCOPROTEIN GPV
3726	6241		0.93	1.0E-07	AL163282.2	NT	Hom sapiens chromosome 21 segment HS21C082
4269	88583	14531	2.63	1.0E-07	AV718862.1	EST_HUMAN	AV718862 GLC Homo sapiens cDNA clone GLCFN04 6
4269	88583	14532	2.63	1.0E-07	AV718862.1	EST_HUMAN	AV718862 GLC Homo sapiens cDNA clone GLCFN04 5
4708	8824		1.46	1.0E-07	O76820	SWISSPROT	ZINC FINGER PROTEIN 189
604	7885		2.32	8.0E-08	AI011362.1	EST_HUMAN	wd16065x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2322973 3'

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 Table 4  
 Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1052	6183		0.77	8.0E-08	BE795469.1	EST_HUMAN	601580133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3843978 5'
3532	6874		1.6	8.0E-08	BE795469.1	EST_HUMAN	601580133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3843978 5'
77	6288	10428	2.83	7.0E-08	Q02357	SWISSPROT	KRFRIN 1 (ERYTHROCYTE ANKYRIN)
1370	6498	11081	30.42	7.0E-08	X04808.1	NT	rat mRNA for unknown protein L31
3563	8104	13084	0.17	7.0E-08	P163005	SWISSPROT	DYNEN HEAVY CHAIN (DYHC)
3563	8104	13085	0.7	7.0E-08	P163005	SWISSPROT	DYNEN HEAVY CHAIN (DYHC)
818	5971	11132	2.76	6.0E-09	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
818	6971	11133	2.76	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2343	7450	12705	2.87	6.0E-08	BE144988.1	EST_HUMAN	MRO-HT0168-191109-004-g09 HT0168 Homo sapiens cDNA
3034	8188	13344	0.85	6.0E-08	7682473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4223	6891	14484	1.03	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
81	5290	10430	2.3	5.0E-08	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C048
2217	7329	12982	1.58	5.0E-08	AA483851.1	EST_HUMAN	nt03099.e1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:949183 similar to contains Aliu repetitive element
1771	6897	12103	1.14	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1771	6897	12104	1.14	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2862	8007		1	4.0E-08	AL079881.1	EST_HUMAN	DKFZp434J0426 n-434 (synonym: ntbs3) Homo sapiens cDNA clone DKFZp434J0426 5'
203	8398		11.08	2.0E-08	AW302886.1	EST_HUMAN	x87068x1 NCI_CGAP_L128 Homo sapiens cDNA clone IMAGE:2787139 3'
226	6420		6.39	2.0E-08	AA425598.1	EST_HUMAN	zv48f07.1 Search total_seqs_Nb21f8_Bw Homo sapiens cDNA clone IMAGE:773817 5' similar to contains
493	5853	10789	8.75	2.0E-08	AF198349.1	NT	Alu repetitive element; contains element MER15 repetitive element;
658	8820	10867	8.78	2.0E-08	AW886438.1	EST_HUMAN	Galus gallus Dach2 protein (Dach2) mRNA, complete cds
659	6820	10958	9.78	2.0E-09	AW886438.1	EST_HUMAN	MRO-O1080-240200-001-g08 OT0080 Homo sapiens cDNA
891	6138		32.08	2.0E-08	BE280477.1	EST_HUMAN	MRO-O1080-240200-001-g08 OT0080 Homo sapiens cDNA
1348	6477	11657	2.11	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1752	6918		1.38	2.0E-08	BE734871.1	EST_HUMAN	601580133F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3846168 5'
1868	6868		3.08	2.0E-08	AW270271.1	EST_HUMAN	nt04311.x1 NCI_CGAP_HM11 Homo sapiens cDNA clone IMAGE:2743149 5'
2514	70718		1.67	2.0E-08	K00216.1	NT	Sheep His-tRNA-GUG
3192	8343	13508	5.72	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3192	8343	13507	5.72	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3838	8974		1.59	2.0E-08	AW873820.1	EST_HUMAN	RC3-970197-16109-012-h03 ST0197 Homo sapiens cDNA
4053	9184	14328	0.65	2.0E-08	UB26888.1	NT	products, complete cds
4384	8605		2.53	2.0E-08	AA458040.1	EST_HUMAN	aa2807.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.2 L1 repetitive element

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLA STE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4837	10047		2.73	2.0E-08	AW672881.1	EST_HUMAN	hs1708.42_NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:28168327 3' similar to contains Alt repetitive element
1653	6781	11973	4.03	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT T-BINDING ACTIVITY)
1653	6781	11974	4.03	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT T-BINDING ACTIVITY)
1785	6911	12119	1.03	1.0E-08	AF126348.1	NT	Hom sapiens cavinin (CAV1) gene, exon 3 and partial cds
2048	7169		1.82	1.0E-08	BE441659.1	EST_HUMAN	PN2-H70130-150898-001-f12 HT0130 Homo sapiens cDNA
3175	8326	13488	0.95	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5223 Pediatric pre-B cell acute lymphoblastic leukemia Bayfor-HGSC project=TCBA_Homo sapiens cDNA clone TCBAP1D5223
3175	8326	13489	0.95	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5222 Pediatric pre-B cell acute lymphoblastic leukemia Bayfor-HGSC project=TCBA_Homo sapiens cDNA clone TCBAP1D5222
4221	8846	14473	4.48	9.0E-09	AL168270.2	NT	Hom sapiens chromosome 21 segment HS21C070
4221	8846	14476	4.48	9.0E-09	AL168270.2	NT	Hom sapiens chromosome 21 segment HS21C070
3592	8731		1.83	7.0E-08	D88842.1	NT	Hom sapiens DNA for 3-hydroxy-CoA thioesterase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
3933	9117		0.83	7.0E-08	U50871.1	NT	Human familial Alzheimer's disease (S1M2) gene, complete cds
4966	10073	15211	6.03	6.0E-08	BE168421.1	EST_HUMAN	PM4-H70521-16020-00-1-05 HT0251 Homo sapiens cDNA
1423	6550	11731	2.7	5.0E-09	BE449284.1	EST_HUMAN	RC2-H70521-12020-00-14-H10 HT0252 Homo sapiens cDNA
1894	8884	12208	1.01	5.0E-09	AL168284.2	NT	Hom sapiens chromosome 21 segment HS21C084
5163	10261	15369	0.72	5.0E-09	AW605634.1	EST_HUMAN	RC4-H10251-14010-013-008 HT0251 Homo sapiens cDNA
6163	10261	15400	0.72	5.0E-09	AW605634.1	EST_HUMAN	RC4-H10251-14010-013-008 HT0251 Homo sapiens cDNA
519	5685		1.52	4.0E-09	AL168282.2	NT	Hom sapiens chromosome 21 segment HS21C082
888	8113		-2.38	4.0E-09	AL168285.2	NT	Hom sapiens chromosome 21 segment HS21C085
1481	66008	11784	3	4.0E-09	9558718	NT	Hom sapiens hypothetical protein (AF038169), mRNA
2407	7613	12763	23.69	4.0E-09	AA360878.1	EST_HUMAN	EST59385 Inf brain Homo sapiens cDNA 5' end similar to heat shock protein, 90% da
519	5685		1.52	4.0E-09	AL168282.2	NT	Hom sapiens chromosome 21 segment HS21C082
2331	7438	12691	2.77	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element;
3148	8269	13469	3.83	3.0E-09	AW286435.1	EST_HUMAN	ULH4BW0-ak-a-08-q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3168120 3' similar to contains MER18.3
\$310	8457	13619	0.84	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element;
3358	8603		0.61	3.0E-09	AA442272.1	EST_HUMAN	ZB3400.11 Socres, bestis NHT Homo sapiens cDNA clone IMAGE:757422
4072	9202		0.8	3.0E-09	X16874.1	NT	H.sapiens PADPRF-4 gene for NAD(X+) ADP-ribosyltransferase
4404	8624	14685	3.68	3.0E-09	AF175325.1	NT	Hom sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe seq ID NO:	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4436 9805	14743	1.47	3.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0833)	xv17h2_x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2853459 3' similar to SW.ELF_DROME
4754 8887	18016	0.98	3.0E-08	AW473832.1	EST HUMAN	P-300 PROTEIN GRAINY-HEAD;	
813 6988	0.64	2.0E-09	X1G514.1	NT	H.sapiens PADPRP1 gene for NAD(+)-ADP-ribosyltransferase		
1282 63971	11587	4.89	2.0E-09	AL185284.2	NT	Homo sapiens chromosome 21 segment HS21C084	
1871 6800			7.76	2.0E-09	AL118573.1	EST HUMAN	DKFZp61B1710_r1_781 (synonym Nam2) Homo sapiens cDNA clone DKFZp61B1710_6'
2307 7416 12688	8.31	2.0E-08	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0833)		
3910 8048 14205	3.18	2.0E-09	O80241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR		
1110 6248 11411	2.27	1.0E-08	50316241	NT	Homo sapiens CCAAAT-box-binding transcription factor (CBF2) mRNA		
1110 6248 11412	2.27	1.0E-08	50316242	NT	Homo sapiens CCAAAT-box-binding transcription factor (CBF2) mRNA		
1644 6772		0.85	1.0E-09	AJ228041.1	NT	Homo sapiens 869 kb coming between AML1 and CBF1 on chromosome 21q22; segment 1/3	
2886 8011 13173	1.65	1.0E-09	UB0017.1	NT	Homo sapiens basic leucine zipper factor 2 p44 (NP44) gene, partial cds, neuronal apoptosis inhibitor protein (napip) and survival motor neuron protein (smn) genes, complete cds		
2881 8046 13209	6.75	1.0E-08	M28689.1	NT	Homo sapiens nuclear phosphoprotein B23 (NP711) mRNA, complete cds		
2881 8046 13210	8.75	1.0E-08	M28689.1	NT	Homo sapiens nuclear phosphoprotein B23 (NP711) mRNA, complete cds		
3010 8184 13322	0.87	1.0E-09	BE536440.1	EST HUMAN	6010538012F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:34465177_5'		
4787 9880		5.33	1.0E-08	AA715287.1	EST HUMAN	Zf35503_s1 Soesne_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element	
6162 10202 15341	10.98	1.0E-09	T80216.1	EST HUMAN	repetitive element contains element MER22 repetitive element;		
1313 6443 11620	1.33	9.0E-10	AW887740.1	EST HUMAN	repetitive element contains element MER28 repetitive element;		
						yc22cc08_r1 Stratagene lung #807210 Homo sapiens cDNA clone IMAGE:811242 5' similar to contains Alu repetitive element	
2786 7962 13118	5.86	9.0E-10	AI870071.1	EST HUMAN	ye78h03_x1 Soesne_Deckgrafte_colo_Homo_sapiens cDNA clone IMAGE:2347263 3' similar to SW.R29_HUMAN P47814 60S RIBOSOMAL PROTEIN L29 contains element PTR5 repetitive element;		
142 6339 10483	8.3	8.0E-10	U63630.2	NT	Homo sapiens MCM4 (MCM4) end DNA-PKcs (PRKDC) genes, partial cds		
3324 8471 13833	0.83	8.0E-10	BE080748.1	EST HUMAN	QVI_Et0801-156200-071-f01_BT0321_Homo sapiens cDNA		
4173 9289 14434	3.5	8.0E-10	AA376832.1	EST HUMAN	EST80584 Small Intestine 1 Homo sapiens cDNA 5' end		
639 6858 11003	33.9	7.0E-10	7708225	NT	Homo sapiens TFA Inducible protein (LOC51588), mRNA		
639 6858 11004	33.8	7.0E-10	7708225	NT	Homo sapiens TFA Inducible protein (LOC51588), mRNA		
1634 6763 11958	1.88	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID RESTRICTED HOMOLOG OF SP100)		
2528 7831		5.19	7.0E-10	FP08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	
3050 82113 13368	2.31	7.0E-10	X00888.1	NT	H.sapiens DHFR gene, exon 3		
914 6084 11230	4.11	8.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf16 gene, C11orf18 gene and C11orf17 gene		

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe seq ID	Exon seq ID	ORF seq ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2639	7737	12890	1.07	6.0E-10	AI424405.1	EST_HUMAN	ED2d07_X1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:20865021 3'
4707	8823		2.83	6.0E-10	AW853778.1	EST_HUMAN	RC3-CT0254-031098-012-912 C70254 Homo sapiens cDNA
760	6916		4.22	6.0E-10	AL048804.1	EST_HUMAN	DKFZp434N219_T144 (synonym: Hbs3) Homo sapiens cDNA clone DKFZp434N219 5'
3457	8829	13783	1.18	5.0E-10	QD1033	SWISSPROT	[HYPOTHETICAL PROTEIN] 48 PROTEIN
4976	10084	18219	1.16	5.0E-10	AF181897.1	NT	Homo sapiens WRN(WRN) gene, complete cds
107	8311		2.24	4.0E-10	AI221083.1	EST_HUMAN	dp00902_X1 Soares_placenta_Biosystems_2NBHPat0W Homo sapiens cDNA clone IMAGE:1769049 3'
578	5742	10870	1.14	4.0E-10	AA516260.1	EST_HUMAN	mt8401.5f_NCI_CGAP_Q03 Homo sapiens cDNA clone IMAGE:924648 3'
1897	7114	12349	1.78	4.0E-10	AW684708.1	EST_HUMAN	hg58g03_X1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element
2538	7041	12890	2.55	4.0E-10	AL163303.2	NT	Homo sapiens chitosanase 21 segment HS2/C103
918	8085	11232	1.24	3.0E-10	N386113.1	EST_HUMAN	Y632018_S1 Soares melanocyte_2NBHPat0M Homo sapiens cDNA clone IMAGE:272053 3' similar to contains L111 L1 repetitive element;
1388	6487		4.99	3.0E-10	A70056f0.1	NT	Homo sapiens extracellular glycoprotein laminin precursor, gene, complete cds
34	5245	10381	1.68	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B)(CENP-B)
34	5245	10382	1.68	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B)(CENP-B)
1804	7023		2.47	2.0E-10	U86017.1	NT	Homo sapiens basic transcription factor 2 p44 (BTF2/p44) gene, partial cds, neuronal apoptosis inhibitor protein (nrip) and survival motor neuron protein (smn) genes, complete cds
2856	8709		0.93	2.0E-10	Bf675047.1	EST_HUMAN	6021386840f1 NIH MGIC_B3 Homo sapiens cDNA clone IMAGE:4273377 5'
1820	6748	11842	2.88	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCXA11 3'
2549	7049	*	2.2	1.0E-10	AW685201.1	EST_HUMAN	QVO-C70226-191193-08-08 CT0225 Homo sapiens cDNA
3482	8823	13780	1.95	1.0E-10	AW852912.1	EST_HUMAN	QV2-TT0063-161193-013-q10 TT0063 Homo sapiens cDNA
3527	8829		1.24	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_T143 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N1317 6'
3821	8829		1.14	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_T143 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N1317 6'
3980	8124		4.98	1.0E-10	AE213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds
4088	8228	14364	6.13	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+-Calmodulin-<dependent protein kinase (CaMKI), creatine transporter (CRTTR)
4089	8228	14366	5.13	1.0E-10	U52111.2	NT	CDM protein (CDM), extended dystrophy protein >
4105	8234	14372	1.92	1.0E-10	AB031069.1	NT	Homo sapiens PICC1 mRNA for protein containing CXXC domain 1, complete cds
4141	8269		2	1.0E-10	M306829.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1)mRNA, last exon

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 Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
269	6449	10838		0.82	BE146800.1	EST_HUMAN	IL2-HIT0203-291088-018-008 HT0203 Homo sapiens cDNA
2085	7210	12456		3.33	AI134395.1	EST_HUMAN	DKF2p547D225_1 r1 547 (synonym: fibr1) Homo sapiens cDNA clone DKF2p547D225 6'
2096	7210	12457		3.33	9.0E-11 AI134395.1	EST_HUMAN	DKF2p547D225_1 r1 547 (synonym: fibr1) Homo sapiens cDNA clone DKF2p547D225 5'
3384	8509	13877		2.63	9.0E-11 AI134395.1	EST_HUMAN	DKF2p547D225_1 r1 547 (synonym: fibr1) Homo sapiens cDNA clone DKF2p547D225 6'
3384	8509	13878		2.63	9.0E-11 AI134395.1	EST_HUMAN	DKF2p547D225_1 r1 547 (synonym: fibr1) Homo sapiens cDNA clone DKF2p547D225 5'
4949	10058	15185		1.24	9.0E-11 AI165246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3082	8246			7.83	8.0E-11 H19871.1	EST_HUMAN	y15f11.1.1 Scores adult brain N2b5HB65Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contain: L1 repetitive element;
4017	8750	14282		4.88	8.0E-11 N23712.1	EST_HUMAN	yW46506.1\$1 Welzmann Officium Epithelium Homo sapiens cDNA clone IMAGE:263289 3'
1460	6887	11775		1.38	7.0E-11 AA330542.1	EST_HUMAN	EST34582 Embryo, 8 week Homo sapiens cDNA 6' end
411	6579	10729		6.87	9.0E-11 M55270.1	NT	Human matn3 Gla protein (MGP) gene, complete cds
411	5579	10729		6.87	9.0E-11 M55270.1	NT	Human matn3 Gla protein (MGP) gene, complete cds
11	52222	10334		0.97	5.0E-11 AL1652283.2	NT	Homo sapiens chromosome 21 segment HS21C043
3348	52222	10334		1.38	5.0E-11 AI1652283.2	NT	Homo sapiens chromosome 21 segment HS21C043
4206	8381	14484		1.3	6.0E-11 P48034	SWISSPROT	ALDEHYDE OXIDASE
9189	10286	15422		0.86	5.0E-11 P43770.1	NT	Homo sapiens RNA for differentiation or sex determination
1408	65356			1.15	4.0E-11 AA136042.1	EST_HUMAN	ZD1612.1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2761	78456	13100		4.76	4.0E-11 BE288500.1	EST_HUMAN	601507831F1 NIH MGIC_71 Homo sapiens cDNA clone IMAGE:35098285 5'
2839	8083	13260		0.98	4.0E-11 AI165247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4689	9707	14845		0.88	4.0E-11 D44686.1	EST_HUMAN	HUMSUPY058 Human brain cDNA Homo sapiens cDNA clone 089
1602	66228	11816		9.87	3.0E-11 6678077 NT	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nm22), mRNA
4250	6375			1.22	3.0E-11 AA309248.1	EST_HUMAN	EST1B0120 Liver, hepatocellular carcinoma Homo sapiens cDNA clone IMAGE:6' end
861	6109	11273		1.33	2.0E-11 AI150502.1	EST_HUMAN	q38c04_x1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:1762102 3' similar to contains MER10.6'
1187	6321	11480		3.67	2.0E-11 R24807.1	EST_HUMAN	1543612.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 6'
1187	6321	11491		3.67	2.0E-11 R24807.1	EST_HUMAN	1543612.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 6'
1626	6764	11847		3.35	2.0E-11 L17492.1	NT	COR3beta (COR3beta) genes, complete cds
1626	6754	11948		3.35	2.0E-11 L17492.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and delta-globin receptor-like protein COR3beta (COR3beta) genes, complete cds
2728	7321	13076		1.04	2.0E-11 AF087813.1	NT	Human endogenous retrovirus HERV-P-T47D
3178	8330	13494		6.54	2.0E-11 P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPEPTIDE (VERSION 1)
3307	8454	13816		0.77	2.0E-11 AI478617.1	EST_HUMAN	Im54c09_x1 NCI CGAP J0d11 Homo sapiens cDNA clone IMAGE:2161838 3'
4422	9542			1.18	2.0E-11 BE068537.1	EST_HUMAN	RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4579 8697			0.85	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
4912 10022			2.2	2.0E-11	BE062568.1	EST_HUMAN	QV2-BT0258-2610B8-014-e01 BT0258 Homo sapiens cDNA
4992 10098	16223		0.91	2.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C078
5014 10117	16250		0.62	2.0E-11	AA307331.1	EST_HUMAN	EST178220 Cedon catchroma (HCC) cell line Homo sapiens cDNA 5' end similar to alpha-2-
673 68333	10973		0.63	1.0E-11	AJ131018.1	NT	Homo sapiens SC1 gene locus
784 68339	11097		1.43	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1220 68352	11521		2.28	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C078
1613 68440			1.47	1.0E-11	AF118914.1	NT	Homo sapiens PR03078 mRNA, complete cds
2031 7149	12383		1.31	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2118 7233	12476		1.45	1.0E-11	AF006573.1	NT	Homo sapiens homoeobox 12-homeobox gene, complete cds
3480 8021	13786		0.71	1.0E-11	BE006315.1	EST_HUMAN	CMD-BN0105-71050-282-e012 BN0105 Homo sapiens cDNA
2918 8072	13242		0.18	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR (LSN94)
4631 9749	14886		1.49	7.0E-12	Q06504	SWISSPROT	34 kD SPICULE MATRIX PROTEIN PRECURSOR (LSN94)
3534 8876	8876		0.63	6.0E-12	AV730554	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF08 5'
							nz88f11.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302673 3' similar to contains Aliu
4325 9447	14580		0.03	6.0E-12	AA732618.1	EST_HUMAN	repetitive element
1045 8189	11352		2.75	5.0E-12	T08573.1	EST_HUMAN	EST04462 Fetal brain, Strategens (cat#S36206) Homo sapiens cDNA clone HBFDY33
3371 85116	13683		1.09	6.0E-12	BE047779.1	EST_HUMAN	EE2265.s1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:22691217.5
3703 88446	14000		6.31	6.0E-12	AJ271798.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
241 5433	10672		3.41	4.0E-12	AA100328.1	EST_HUMAN	Z74911.81 Soares, fetal liver, spleen, INFILS_S1 Homo sapiens cDNA clone IMAGE:460576.3
2922 5433	10572		3.58	4.0E-12	AA701528.1	EST_HUMAN	Z74911.81 Soares, fetal liver, spleen, INFILS_S1 Homo sapiens cDNA clone IMAGE:460576.3
4590 9708	14848		0.72	4.0E-12	AI888984.1	EST_HUMAN	EE26105.s1 NCI CGAP_Lc24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TRQ13639 Q13639
							MARF1NER TRANSPOSEASE;
613 5773	10939		3.9	3.0E-12	AW341683.1	EST_HUMAN	hd1301.x1 Soares, INFIL_S1 Homo sapiens cDNA clone IMAGE:2809377 3' similar to TR-O14517
613 5773	10904		3.9	3.0E-12	AW341683.1	EST_HUMAN	hd1301.x1 Soares, INFIL_S1 Homo sapiens cDNA clone IMAGE:2809377 3' similar to TR-O14517
1669 6794	11989		1.46	2.0E-12	AW802131.1	EST_HUMAN	O14517 SMRP;
3448- 8590	19754		0.87	2.0E-12	8754405	NT	IL6-UJM077-1-12D400-065-e03 UM0771 Homo sapiens cDNA
4090 9218	14354		2.24	2.0E-12	JD1684.1	NT	Mus musculus keratin-associated protein 6.2 (Kcap6-2), mRNA
4090 9218	14355		2.24	2.0E-12	JD1684.1	NT	Rat U3A small nuclear RNA
4389 8519			2.08	2.0E-12	BE068509.1	EST_HUMAN	CM05-BT0281-Q31189-087-e03 BT0281 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
118	5319	10462	1.63	1.0E-12	AW627674.1	EST_HUMAN	hhg009_x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MER18.11
1888	7105		1.25	1.0E-12	AB71728.1	EST_HUMAN	wnf107_x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2438483 3' similar to contains L1.53_L1 repetitive element;
3042	8186	13351	0.92	1.0E-12	AF000981.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TY2) mRNA, partial cds
3042	8188	13352	0.92	1.0E-12	AF000981.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TY2) mRNA, partial cds
3852	8888	14143	27.54	1.0E-12	AU132248	EST_HUMAN	AU32248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3852	8888	14144	27.54	1.0E-12	AU132248	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 6'
3918	9054	14216	0.9	9.0E-13	AB026900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
716	8872	11019	4.71	8.0E-13	U28188.1	NT	Homo sapiens pitran protein (PFP) gene, complete cds
715	8872	11020	4.71	8.0E-13	U28188.1	NT	Homo sapiens basic transcription factor 2 p44 (BTF44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
1851	6072	12103	2.14	8.0E-13	U80017.1	NT	Homo sapiens chromosome 21 segment HS21_C007
2092	7207	12453	8.92	6.0E-13	AL163207.2	NT	Homo sapiens placenta Nb2-Hp Homo sapiens cDNA clone IMAGE:145759 5'
3303	8450		0.61	6.0E-13	R78338.1	EST_HUMAN	y8264.1 Scores placenta Nb2-Hp Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu Z177a
3378	8823		1.24	6.0E-13	AA436773.1	EST_HUMAN	repetitive element contains element MER22 repetitive element ;
1878	6898		8.69	4.0E-13	AW378614.1	EST_HUMAN	PL24HT0224-22109-00 ->11 H70224 Homo sapiens cDNA
2437	7841		1.19	4.0E-13	AF003529.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds end flanking repeat regions
175	5369		3.89	3.0E-13	AF003628.1	NT	Homo sapiens X-linked emphydric ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
868	6017		4.09	3.0E-13	AA430310.1	EST_HUMAN	zv0808.1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:781408 5'
2350	7457	12712	0.98	3.0E-13	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2452	7558		1.57	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21_C010
2823	7724	12877	2.84	3.0E-13	BP372862.1	EST_HUMAN	CN3-F1010-14070-242-h05 F70100 Homo sapiens cDNA
3169	8820		2.2	3.0E-13	AA745844.1	EST_HUMAN	cb1800231 NCI_CGAP_JG5 Homo sapiens cDNA clone IMAGE:19224095 3'
145	5342	10483	2.57	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTTR) CDM protein (CDM), adrenoleukodystrophy protein >
236	61239	10569	0.86	2.0E-13	U23889.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1274	6403	11577	13.67	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3263	8414	13576	1.13	2.0E-13	BF431889.1	EST_HUMAN	nb705_x1 Scores NSF_F8_9IV_OTPA_P_ST Homo sapiens cDNA clone IMAGE:3'

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Probe SEQ ID NO:	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3491	8532	13789	1.19	2.0E-13	AF10507.1	NT	Homo sapiens S164 gene, partial cds; and S171 gene, partial cds
4084	9213		1.65	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
289	5477	10619	1.12	1.0E-13	ST7412B.1	NT	[FGF-5=fibroblast growth factor 1] Human, Kidney, Genomic, 342 nt, segment 2 of 2
889	60339	11210	3.89	1.0E-13	A1007973.1	NT	Homo sapiens LGN1C2B gene
.1341	8469	11650	1.23	1.0E-13	x87344.1	NT	H_sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, DOB, DQE2 and RING3, 8, 13 and 14 genes
2017	7134	12372	8.68	1.0E-13	AA1720674.1	EST_HUMAN	miR192_5' NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR_6
4565	9883	14822	1.67	1.0E-13	BF340987.1	EST_HUMAN	4f24_c01_51 Scores_bests_NHT Homo sapiens cDNA clone 1581232 3' similar to contains MER19H MER19
331	6514	10651	3.32	9.0E-14	AA1781159.1	EST_HUMAN	4f24_c01_51 Scores_bests_NHT Homo sapiens cDNA clone 1581232 3' similar to contains MER19H MER19
332	5616	10652	2.67	9.0E-14	AA1781169.1	EST_HUMAN	4f24_c01_51 Scores_bests_NHT Homo sapiens cDNA clone 1581232 3' similar to contains MER19H MER19
2471	7576		1.95	9.0E-14	AW881577.1	EST_HUMAN	RC4-C70322-080100-013-009 CT03221 Homo sapiens cDNA
2553	7656	12807	0.89	9.0E-14	A133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2553	7656	12803	0.89	9.0E-14	A133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2717	78112	13067	3.37	9.0E-14	AB038162.1	NT	Homo sapiens TFF gene cluster for trypsin cofactor, complete cds
3087	8240	13389	4.51	9.0E-14	AW513268.1	EST_HUMAN	xc54h05_x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707653 3'
3223	5614	10651	0.72	9.0E-14	AA1781159.1	EST_HUMAN	4f24_c01_51 Scores_bests_NHT Homo sapiens cDNA clone 1581232 3' similar to contains MER19H MER19
3775	8812	14065	9.58	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4722	8836	14980	1.8	9.0E-14	A1002153.1	NT	Squid ocellus gene for seminal vesicle secreted protein semenopelin 1
3478	8819		1.27	8.0E-14	BE468268.1	EST_HUMAN	1271c09_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
3928	9084		3.4	8.0E-14	R176269.1	EST_HUMAN	yf72e03_x1 Scores_placenta Nb2H P Homo sapiens cDNA clone IMAGE:144798 3'
1639	7822		3.39	7.0E-14	AW151673.1	EST_HUMAN	xf87e10_x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10_12
365	6845	10687	11.15	8.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
815	6775	10908	4.88	5.0E-14	Q83120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) CANALICULAR MULTIDRUG RESISTANCE-PROTEIN
5035	10137	16270	1.38	5.0E-14	AW073781.1	EST_HUMAN	xd03805_x1 NCI_CGAP_Gui Homo sapiens cDNA clone IMAGE:2876165 3' similar to contains L1_12_L1
1124	7909		1.65	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR

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Probe seq ID No:	Exon seq ID No:	ORF seq ID NO:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1883	7008	122293	4.63	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3733	8871		0.65	4.0E-14	AJ046802.1	EST_HUMAN	ZNF611 Scores 3.9 segment 1 iterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5' Y73C12.61 Scores 3.9 segment 1 iterus_NbHPU Homo sapiens cDNA clone IMAGE:270100 3' similar to Wt1 L1 L3 L1 repetitive element;
4283	8892	14630	0.95	4.0E-14	NA68328.1	EST_HUMAN	R_novelous mRNA for CPG2 protein
851	6099	11267	1.10	3.0E-14	X95469.1	NT	Xp45f12.1x1 NCI_CGAP_HN11_Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element/contains element MER9 repetitive element;
4905	10015	15159	0.65	3.0E-14	AW265364.1	EST_HUMAN	Homo sapiens Xq1 pseudautosomal region; segment 2/2
388	5557	10701	2.38	2.0E-14	AJ271738.1	NT	Homo sapiens Xq1 pseudautosomal region; segment 2/2
388	5557	10702	2.38	2.0E-14	AJ271738.1	NT	Homo sapiens chromosome 21 segment HS21C103
688	7897	10887	0.97	2.0E-14	AL1683303.2	NT	Homo sapiens chromosome 21 segment HS21C048
2365	7471		1.07	2.0E-14	AW372868.1	EST_HUMAN	RCSE-B10377-0912B0377-031-D12 BT0377 Homo sapiens cDNA Rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2441	7545		0.88	2.0E-14	7657129	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
2636	7734		1.07	2.0E-14	PI08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1088	6208	11371	2.48	1.0E-14	AL168246.2	NT	Homo sapiens chromosome 21 segment HS21C048
1414	6841	11719	5.78	1.0E-14	AL168268.2	NT	Homo sapiens chromosome 21 segment HS21C088
1414	6841	11719	5.78	1.0E-14	AL168268.2	NT	Homo sapiens chromosome 21 segment HS21C088
2002	7119	12356	22.17	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
2167	7280	12523	2.48	1.0E-14	AL168303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2388	7492	12745	23.8	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2910	8064	13236	1.11	1.0E-14	PI05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3148	8297	13459	6.64	1.0E-14	BF535227.1	EST_HUMAN	RC2-C70432-31070-013-e09_1 CT0432 Homo sapiens cDNA
3146	8297	13457	5.64	1.0E-14	BF535227.1	EST_HUMAN	RC2-C70432-31070-013-e09_1 CT0432 Homo sapiens cDNA
3883	8898	14163	1.84	1.0E-14	A4882884.1	EST_HUMAN	aa88c12.61 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:971950 3'
4452	8571	14710	1.81	1.0E-14	AW276852.1	EST_HUMAN	Xp38h10.x1 NCI_CGAP_Luc28 Homo sapiens cDNA clone IMAGE:2753069 3'
1589	8718	11907	1.49	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type T (PTPRT), mRNA
2772	5647		1.52	8.0E-15	BE281482.1	EST_HUMAN	601148632F1 NIH MG-19 Homo sapiens cDNA clone IMAGE:3160223 5'
885	6141	11310	7.37	6.0E-15	AJ271738.1	NT	Homo sapiens Xq1 pseudautosomal region; segment 2/2
409	5577	10723	5.23	5.0E-15	AL168208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3450	8892		1.01	5.0E-15	AW26587.1	EST_HUMAN	U1-HBW0-9jb-g-10-0-U1 s1 NCI CGAP_Subb Homo sapiens cDNA clone IMAGE:2731219 3'
426	5213	10325	2	4.0E-15	AL168303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4191	8317		5.22	3.0E-15	N88452.1	EST_HUMAN	ANF(CARDIOLATIN)

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
247	6438	10573	4.77	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, end partial cds, alternatively spliced
368	65448	10883	3.68	2.0E-16	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, end partial cds, alternatively spliced
368	65448	10883	3.56	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, end partial cds, alternatively spliced
2352	7459	12714	1.04	2.0E-15	BE350127.1	EST_HUMAN	htrg01_x1 NCI_CGAP_Kd13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29_ls3 MER29 repetitive element;
2352	7459	12715	1.04	2.0E-15	BE350127.1	EST_HUMAN	htrg01_x1 NCI_CGAP_Kd13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29_ls3 MER29 repetitive element;
3494	8835	13801	0.61	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, end partial cds, alternatively spliced
3494	8835	13802	0.61	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, end partial cds, alternatively spliced
4592	8710	2.63	2.0E-16	AI806395.1	EST_HUMAN	Wf078_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q81043 Q26103_NINEIN_;	
2738	7830		2.48	1.0E-16	AI689884.1	EST_HUMAN	htrg01_x1 NCI_CGAP_L1224 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13538 Q13539 MARINER TRANSPOSEASE_;
2883	8137	13302	1.71	1.0E-15	BE045594.1	EST_HUMAN	hk4002_x1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2889162 5'
3120	8272	13423	1.41	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4337	8459	14597	0.6	1.0E-16	BE182698.1	EST_HUMAN	RC3-HT0840-100500-0422-h05 HT0840 Homo sapiens cDNA
2844	7742	12895	1.04	9.0E-16	CQ9610	SWISSPROT	DYNEN ALPHA CHAIN, FLAGELLAR OUTER ARM
4481	8600	14739	1.04	9.0E-16	4803168	NT	Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
2126	7240		3.12	6.0E-16	AW97261.1	EST_HUMAN	EST384702 IMAGE_resequencing, MAGI Homo sapiens cDNA
1603	8630	11817	1.38	6.0E-16	AJ281154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogenes
2841	7739	12892	1.28	5.0E-16	AA92178.1	EST_HUMAN	ot8004_s1 Scores_biot_f8_Bw Homo sapiens cDNA clone IMAGE:1623078 3' similar to G11111 contains element L1 repetitive element;
2359	7466	12721	1.04	4.0E-16	AV787168.1	EST_HUMAN	QV1-1JM0036-200300-115-002 UM0036 Homo sapiens cDNA
2359	7466	12722	1.04	4.0E-16	AV787168.1	EST_HUMAN	QV1-1JM0036-200300-115-002 UM0036 Homo sapiens cDNA
3439	8831	13741	3.97	4.0E-16	Q16853	SWISSPROT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4113	8241	14977	5.45	4.0E-16	BE088875.1	EST_HUMAN	PMA-B-BT0650-010400-0022-809 BT0650 Homo sapiens cDNA
4113	8241	14373	5.45	4.0E-16	BE088875.1	EST_HUMAN	PMA-B-BT0650-010400-0022-809 BT0650 Homo sapiens cDNA
4926	10036		1.02	4.0E-16	AV730833.1	EST_HUMAN	AV730833 HTF Homo sapiens cDNA clone HTFA_XE09 5'

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## Single Exon Probes Expressed in BT474 Cells

Probe seq ID NO.	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
128	5326	10472	1.01	3.0E-16 AW022862.1	EST_HUMAN	EST	Human Fetal Cochlea cDNA clone IMAGE:2486378 3'
129	5326	10473	1.01	3.0E-16 AW022862.1	EST_HUMAN	EST	Human Fetal Cochlea cDNA clone IMAGE:2486378 6'
465	5843		1.3	3.0E-16 AL04445.1	EST_HUMAN	EST	DKFZp634P037_1 434 (synonym: hsaS3 Homo sapiens cDNA clone DKFZp634P037 5'
475	5842		2.42	3.0E-16 AF35448.1	NT	NT	Homo sapiens TSX (TSN) pseudogene, exon 6
1465	8592	11780	1.85	3.0E-16 Q28983	SWISSPROT	ZONADHESIN PRECURSOR	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYcoprotein GP220]
2845	8089	13263	4.39	3.0E-16 P03200	SWISSPROT		
3906	8042	14202	0.68	3.0E-16 T08169.1	EST_HUMAN	EST	6060 Infant Brain, Berto Socaris Homo sapiens cDNA clone HIBBA13 5' end
973	B120		1.52	2.0E-16 AL183279.2	NT	NT	Homo sapiens chromosome 21 segment HS21C078
2650	7748		1.74	2.0E-16 JG3061.1	NT	NT	Human SSA-related endogenous retroviral LTR-like element
4149	9276	14412	1.23	2.0E-16 X69211.1	NT	NT	H. sapiens DNA for endogenous retroviral like element
1869	5374	10513	2.74	1.0E-16 AE200719.1	NT	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
380	6869		21.64	1.0E-16 AA628592.1	EST_HUMAN	EST	af38g1.61 Soares_total_fetus_Nb2hIF8_Bw Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR12 ORF repetitive element;
1973	7090	12319	2.07	1.0E-16 BI527874.2	EST_HUMAN	EST	QVD5010148-07070-028-410 BN0148 Homo sapiens cDNA CMV-NNT003
3720	8658	14011	2.64	9.0E-17 AV900048.1	EST_HUMAN	EST	CMT-NNT003-200300-153-501 NN1003 Homo sapiens cDNA QVD-OT0032-4803010-165-301 OT0032 Homo sapiens cDNA
1019	6160		2.04	8.0E-17 AW880701.1	EST_HUMAN	EST	QVD-OT0032-4803010-165-301 OT0032 Homo sapiens cDNA
3869	8005		0.83	8.0E-17 AL163280.2	NT	NT	Homo sapiens chromosome 21 segment HS21C080
1470	6897		2.64	7.0E-17 6753097	NT	NT	Mus musculus apolipoprotein B editing complex 2 (Apobec2), mRNA
200	5395	10539	6.48	6.0E-17 AW983800.1	EST_HUMAN	EST	RCI-HN0003-2205010-021-504 HN0003 Homo sapiens cDNA NC05503.1
420	5207	10319	2.67	5.0E-17 TB4110.1	EST_HUMAN	EST	Y053703.1 Streptococcus lung (#837210) Homo sapiens cDNA clone IMAGE:78839 5'
1504	6831		1.25	3.0E-17 D14547.1	NT	NT	Human DNA, SINE repetitive element
2089	7204	12449	1.08	3.0E-17 AW111912.1	EST_HUMAN	EST	xd88e0084.x1 ScareasNFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2604784 3'
3177	8328		1.28	3.0E-17 P05410	SWISSPROT	Z-M-RELATED G PROTEIN-COUPLED RECEPTOR MRG	
3620	8759	13915	1.18	3.0E-17 BE328522.1	EST_HUMAN	EST	Iw05504.x1 NCI CGAP_L124 Homo sapiens cDNA clone IMAGE:3161899 3'
3620	8759	13916	1.18	3.0E-17 BE328522.1	EST_HUMAN	EST	Iw05604.x1 NCI CGAP_L124 Homo sapiens cDNA clone IMAGE:3161898 3'
350	5633	10672	2.53	2.0E-17 AI270080.1	EST_HUMAN	EST	q83se08x1 NCI CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1859922 3' similar to contains Atu repetitive element
351	5633	10672	2.82	2.0E-17 AI270080.1	EST_HUMAN	EST	q83se08x1 NCI CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1859922 3' similar to contains Atu repetitive element
889	6136		1.24	2.0E-17 AA722632.1	EST_HUMAN	EST	zg8id04.x1 Scareas fetal heart_NbHH8W Homo sapiens cDNA clone IMAGE:389751 3'
2424	7529	12781	1.33	2.0E-17 Q28983	SWISSPROT	ZONADHESIN PRECURSOR	
2424	7529	12782	1.33	2.0E-17 Q28983	SWISSPROT	ZONADHESIN PRECURSOR	

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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2895	8049	13216	6.11	2.0E-17	P12038	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDa NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
748	5805	11061	2.89	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1723	6850		0.88	1.0E-17	AJ271738.1	NT	Hom sapiens XbaI pseudodelta-like region, segment 2/2
1778	6804	12112	2.75	1.0E-17	AL163207.2	NT	Hom sapiens chromosome 21 segment HS21C07
2105	7220	12484	1.28	1.0E-17	P02481	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2317	7425	12879	1.44	1.0E-17	U78410.1	NT	Hom sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3554	8695		0.89	1.0E-17	AF2246869.1	NT	Hom sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4108	9238		7.68	1.0E-17	R08842.1	EST_HUMAN	Y30607.1! Soares fetal liver spleen 1NFLS Homo sapiens cDNA 5' end similar to retrovirus-related pol
5185	10282		1.16	1.0E-17	AA288037.1	EST_HUMAN	EST11488 Uterus Homo sapiens cDNA 5' end similar to substrate 1 (PTPN15) mRNA
3765	8902	140546	1.61	8.0E-18	4758977	NT	Hom sapiens protein Myostatin non-receptor type substrate 1 (PTPN15) mRNA
348	6529	10686	40.25	7.0E-18	AW316976.1	EST_HUMAN	xx10644.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb120888 80S RIBOSOMAL PROTEIN L4 (HUMAN);
346	6529	10687	40.25	7.0E-18	AW316976.1	EST_HUMAN	xx10644.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb120888 80S RIBOSOMAL PROTEIN L4 (HUMAN);
3277	8428	13587	1.08	6.0E-18	X71781.2	NT	Rattus norvegicus partial GdnPh-1 gene for gdnf-derived neuropeptide nekn1, enhancer region
4712	9828		3.18	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-SULFANYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
1149	6285	11450	12.11	5.0E-18	AI280214.1	EST_HUMAN	qm65g11.x1 Soares_8toweeks_8toweeks_2NbHPB&W Homo sapiens cDNA clone IMAGE:18386683 3' similar to contains Alu repetitive element
120	6320	10463	1.1	4.0E-18	BE044078.1	EST_HUMAN	hg36h04.x1 NCI CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29_b3
120	6320	10484	1.1	4.0E-18	BE044078.1	EST_HUMAN	hg36h04.x1 NCI CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29_b3
1731	6858	12082	30.81	4.0E-18	AA621814.1	EST_HUMAN	hg36h04.x1 NCI CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gbM26326
850	6001	11173	15.02	3.0E-18	AA614198.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETON 18 (HUMAN);
831	6079	11247	2.19	3.0E-18	BE088634.1	EST_HUMAN	P46782 40S RIBOSOMAL PROTEIN S5.; CM05-BT0560-210304-268-Q07 BT0560 Homo sapiens cDNA
3923	9069	14218	0.88	3.0E-18	AL163247.2	NT	Hom sapiens chromosome 21 segment HS21C047
248	5439	10579	3.23	2.0E-18	AW386820.1	EST_HUMAN	QY1-L70036-160200-070-07 LT0036 Homo sapiens cDNA
1154	6280	19834	2.0E-18	BE250097.1	EST_HUMAN	601114352F NIH 3T3 cell line IMAGE:3356044 5'	
3100	8253	12403	1	2.0E-18	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM

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Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4393	8513		0.61	1.0E-18	T85406.1	EST_HUMAN	y03305.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1205639 5' similar to contains L1 repetitive element;
544	6710	10848	4.69	9.0E-19	AA281681.1	EST_HUMAN	zt11008.1 NCI_GAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER18.12 MER19 repetitive element;
545	6710	10849	2.47	9.0E-19	AA281681.1	EST_HUMAN	zt11008.1 NCI_GAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER18.12 MER19 repetitive element;
1050	6191		2.5	8.0E-19	AW974002.1	EST_HUMAN	EST337007 MAGE sequences, MAGN Homo sapiens cDNA
2226	7338	12592	2.68	7.0E-18	4758139	NT	Hom sapiens DEAD1H (Asp-Glu-Ala-Asp) His box polypeptide 6 (RNA helicase, 64kD) (DDX6) mRNA
3760	8897	1222	6.0E-19	AV852830.1	EST_HUMAN	PM0-C-0248-131089-001-801 CT0248 Homo sapiens cDNA	
4442	9561	14703	1.35	8.0E-19	P34986	SWISSPROT OLFACTORY RECEPTOR 6 (M50)	
4442	9561	14704	1.35	8.0E-19	P34986	SWISSPROT OLFACTORY RECEPTOR 6 (M50)	
4768	8881		1.48	8.0E-19	AJ271735.1	NT	Hom sapiens Xo pseudautosomal region; segment 1/2
6009	10112	16243	1.03	8.0E-19	AL120877.1	EST_HUMAN	DKFZp762F182_1 J762 (synonym: hra2) Homo sapiens cDNA clone DKFZp762F182_5
553	6718	10850	0.84	4.0E-19	AB007970.1	NT	Hom sapiens mRNA, chromosome 1 specific transcript KUA0501
2843	7741	12894	1.19	4.0E-18	BF697362.1	EST_HUMAN	60213810F1 NIH_MSC_56 Homo sapiens cDNA clone IMAGE:4287674_5'
6108	10206		0.88	4.0E-18	AL163268.2	NT	Hom sapiens chromosome 21 segment HS21C008
3831	8887	14120	1.04	3.0E-19	Q28897	SWISSPROT BETA-2 ADRENERGIC RECEPTOR	
3831	8887	14121	1.04	3.0E-19	Q28897	SWISSPROT BETA-2 ADRENERGIC RECEPTOR	
4260	8385	14521	0.89	3.0E-19	O43900	SWISSPROT LIM-ONLY PROTEIN 8 (TRIPLE LIM DOMAIN PROTEIN 6)	
4260	8385	14522	0.83	3.0E-19	O43900	SWISSPROT LIM-ONLY PROTEIN 8 (TRIPLE LIM DOMAIN PROTEIN 6)	
4423	9545	14683	1.07	3.0E-19	AY708138	EST_HUMAN	AV708138 ADC Homo sapiens cDNA clone ADCAMA11_6'
2629	7832	12880	33.68	2.0E-19	AL163201.2	NT	Hom sapiens chromosome 21 segment HS21C001
4424	8544		1.43	2.0E-19	AI311783.1	EST_HUMAN	q091e02_X1 NCI_GAP_Kids Homo sapiens cDNA clone IMAGE:19168888 3' similar to TR-Q68388 Q68388
481	5949		2.72	1.0E-18	EE409811.1	EST_HUMAN	POLEIN GENE;
2148	7280	12507	1.19	1.0E-18	I-807895.1	EST_HUMAN	y078907.1 Scores adult brain N2B4HB5Y Homo sapiens cDNA clone IMAGE:1841688 5' similar to contains MER10 repetitive element;
2678	7778		1.37	1.0E-18	D28044.1	NT	Human gene for Ah-receptor, exon 7-9
2810	7988		5.49	1.0E-18	4758077	NT	Hom sapiens protein lysine phosphatase, non-receptor type substrate 1 (PTPN51) mRNA
3382	8526	13688	1.23	1.0E-19	AA834967.1	EST_HUMAN	g46512.e1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:138863 3' similar to contains MER37.12 MER37 repetitive element;
3269	8408	13571	0.89	7.0E-20	BF322455.1	EST_HUMAN	FMA-4AND038-0508010-003-e04 AND038 Homo sapiens cDNA
3542	8883	13849	3.35	6.0E-20	PR9188	SWISSPROT ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY	

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4246 8371	14504		2.83	6.0E-20	BE022434.1	EST_HUMAN	60144231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4568 8888			1.46	5.0E-20	AV729123.1	EST_HUMAN	AV729123 NIH_Human cDNA clone IMAGE:3916231 5'
1632 6761	11857		1.38	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C037
4182 9308	14445		1.39	3.0E-20	P28279	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 14
4594 97112	14849		0.83	3.0E-20	AA037816.1	EST_HUMAN	ZIG3b12.81 Scores treatment_virus_NbHPV Human cDNA clone IMAGE:484695 3' similar to controls L1 & L1 repetitive element;
831 6983			20.39	2.0E-20	AW303868.1	EST_HUMAN	x24e10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW:RS5_MOUSE_P07461 40S RIBOSOMAL PROTEIN S5.;
1112 6260	11413		2.98	2.0E-20	AA616835.1	EST_HUMAN	ng6309.31 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224068
1112 6250	11414		2.96	2.0E-20	AA516335.1	EST_HUMAN	ng6309.31 NCI_CGAP_Lip2 FUNCTION UNKNOWN.;
2778 6983			12.84	2.0E-20	AV903868.1	EST_HUMAN	ng6309.31 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224068.
4923 10033	16174		3.73	2.0E-20	Q28883	SWISSPROT	G1224068_ORE2: FUNCTION UNKNOWN.;
4923 10033	15176		3.78	2.0E-20	Q28883	SWISSPROT	ZONADHESIN PRECURSOR
6124 10225			1.16	2.0E-20	6174838 NT	EST_HUMAN	Homo sapiens malate dehydrogenase 1, NAD (aldehyde) MDH1 mRNA_x21d061.r1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:7128115 similar to SW:RS5_MOUSE_P07461 40S RIBOSOMAL PROTEIN S5.;
2010 7874	12384		1.83	1.0E-20	AA281681.1	EST_HUMAN	MEER19 repetitive element;
4418 8538	14876		0.94	1.0E-20	BF115168.1	EST_HUMAN	hr34108.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135165 3' similar to controls L1,L2,L1 repetitive element;
2878 8032			0.97	8.0E-21	AA003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Human cDNA clone MIP12-8.21
2081 7177	12416		2.98	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
2081 7177	12416		2.86	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
3678 8818	13976		0.9	7.0E-21	AL168300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4221 8959			0.25	7.0E-21	AA046502.1	EST_HUMAN	z467ea06.r1 Scores_digenet_diseases_NbHPV Human cDNA clone IMAGE:4872859 5'
4079 82039	14348		0.6	6.0E-21	BE408811.1	EST_HUMAN	601504125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:38388310 5'
9225 6073	11241		0.69	5.0E-21	6902031 NT	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4341 8463	14680		2.97	5.0E-21	BE0988839.1	EST_HUMAN	601649811F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3833880 5'
4770 9883	15030		7.42	5.0E-21	4885474 NT	EST_HUMAN	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
1747 6873	12073		1.2	4.0E-21	AA970713.1	EST_HUMAN	oc88e06.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16630 Q16630
2253 7363	12619		1.05	3.0E-21	AL168201.2	NT	PMS2 mRNA ;contains Off+H OFF repetitive element;
9052 8205	13360		3.39	3.0E-21	AJ007973.1	NT	Homo sapiens chromosome 21 segment HS21C001
							LGMD2B gene

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Table 4

Single Exon Probes Expressed In BT474 Cells

Probe seq ID	Exon seq ID No:	ORF seq ID No:	Expression Signal	Most Similar BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
141	6388	11249		18.37	2.0E-21 BE163247.1	EST_HUMAN	QV3-HT0468-17020-080-012-HT0468 Homo sapiens cDNA
836	6084	11250	0.95	2.0E-21 AB007857.2	NT	Homo sapiens mRNA for KIAA0391 protein, partial cds	
838	6084	11250	0.96	2.0E-21 AB007857.2	NT	Homo sapiens mRNA for KIAA0391 protein, partial cds	
1217	6349			2.35	2.0E-21 BE064410.1	EST_HUMAN	RC4-HT0311-141199-001-H08-BT0311 Homo sapiens cDNA
2001	7701	12859		1.72	2.0E-21 Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2601	7701	12857		1.72	2.0E-21 Q28983	SWISSPROT	ZONADHESIN PRECURSOR
1259	6388	11565	1.63	1.0E-21 AA557657.1	EST_HUMAN	n48004..61 NCI_CGAP_P74 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER28_b2	
1410	6337		2.71	1.0E-21 AI601284.1	EST_HUMAN	arg88d12x1 Barbed endonuclease HPIRB7 Homo sapiens cDNA clone IMAGE:2162343 3'	
4388	8508	14850		2.25	9.0E-22 AI702438.1	EST_HUMAN	1294663..x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2286204 3' similar to TR:Q15408
950	6098			5.92	8.0E-22 BE144748.1	EST_HUMAN	CMP-HT0178-281089-078-H05 HT0178 Homo sapiens cDNA
684	6324	10982	4.97	7.0E-22 AL163248.2	NT	Homo sapiens chromosome 21 segment HS21_C048	
4257	8882	14515	1.94	7.0E-22 Q61638	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)	
5020	10122	18254	1.08	7.0E-22 AB008681.1	NT	Homo sapiens gene for actin receptor type IB, complete cds	
4035	9168	14303	1.01	8.0E-22 AA405040.1	EST_HUMAN	z085c10..1r Scores testis_NHT Homo sapiens cDNA clone IMAGE:742857 5'	
3614	8763		1.28	4.0E-22 AJ271736.1	NT	Homo sapiens Xq11 pseudoadhesin region; segment 1/2	
980	8108		0.83	3.0E-22 AI468678.1	EST_HUMAN	hn14p10..x1 Scores cDNA clone IMAGE:2156811 3' similar to gbl18563 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN) contains L1..L1 repetitive element;	
2535	7698	12886	2.31	3.0E-22 AI659036.1	EST_HUMAN	w885b0..x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428839 3' similar to SW:RL21_HUMAN	
3650	8769		1.46	3.0E-22 D14718.1	NT	P46778 60S RIBOSOMAL PROTEIN L21.1	
4769	9882	16029	2.88	3.0E-22 AI090125.1	EST_HUMAN	Human chromosomal protein HM31 related gene qb28c07..x1 Scores_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to	
1657	7074		1.38	2.0E-22 N24942.1	EST_HUMAN	comt1..x1 Scores_melanocyte_2N1H M Homo sapiens cDNA clone IMAGE:237338..3	
2495	7559	12847	1.32	2.0E-22 P24910	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR	
3401	8545	13704	3.77	2.0E-22 8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKACG3), mRNA	
4203	8928	14460		1.73	2.0E-22 AW817794.1	EST_HUMAN	PM4-SNB020-01040-008-H02 SNB020 Homo sapiens cDNA
1889	7009	12229	1.11	1.0E-22 AW885317.1	EST_HUMAN	PM4-SNB020-01040-008-H02 SNB020 Homo sapiens cDNA	
3392	8536	13897	1.42	1.0E-22 D14547.1	NT	Human DNA, SINE repetitive element	
3657	8858	13858	0.6	8.0E-23 AF088349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	
3282	8498		2.2	7.0E-23 AV647246.1	EST_HUMAN	AV647246 GLC Homo sapiens cDNA clone GLCAW C07..3	
3415	8558		1.77	8.0E-23 AF188333.1	NT	Rattus norvegicus RM1B (Rm1B) mRNA, complete cds	
4242	8357	14500	1.08	8.0E-23 AL163249.2	NT	Homo sapiens chromosome 21 segment HS21_C048	

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**Table 4**  
**Single Exon Probes Expressed in BT474 Cells**

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
665	5825	10963	3.85	2.0E-23	AJ288880.1	NT	Human sapiens KIAA0851 gene (partB). X73 gene and LZTF1 gene
1144	7868		3.08	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2756	7850	13105	1.39	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2759	7850	13108	1.39	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3353	8498		0.91	2.0E-23	AJ201468.1	EST_HUMAN	q87311_M_ NCL CGAP_P728 Homo sapiens cDNA clone IMAGE:1943767 3' similar to TR:Q13537 Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE;
3688	8834		3.7	2.0E-23	BE165980.1	EST_HUMAN	MR3-H10487-180201-15-001 HT0487 Homo sapiens cDNA clone IMAGE:205418 6
3949	9084	14237	2.51	2.0E-23	H569831.1	EST_HUMAN	Y16802.11 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208418 6
3949	9084	14238	2.61	2.0E-23	H569831.1	EST_HUMAN	Y16802.11 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208418 6
4503	8822	14764	1.68	1.0E-23	AL163232.2	NT	Human sapiens chromosome 21 segment HS21C052
4731	8844		5.27	1.0E-23	AL163210.2	NT	Human sapiens chromosome 21 segment HS21C010 ab75a08..s1 Stretagene fetal retina 0372022 Homo sapiens cDNA clone IMAGE:882758 3' similar to
551	5716		3.88	9.0E-24	AA663213.1	EST_HUMAN	TRE18822_E18822 CA PROTEIN;
4817	9735	14872	1.03	8.0E-24	P23269	SWISSPROT	OLFACTOORY RECEPTOR-LIKE PROTEIN 13
4817	9735	14873	1.03	8.0E-24	P23269	SWISSPROT	OLFACTOORY RECEPTOR-LIKE PROTEIN 13
3860	8868		1.12	7.0E-24	AW837864.1	EST_HUMAN	Q9D047-1720201-122-608 DT0047 Homo sapiens cDNA Macaca fasciata mRNA for Testis-Specific Protein 7 (TSPY), complete cds
704	8881		2.18	6.0E-24	AB001421.1	NT	Human sapiens chromosome 21 segment HS21C049
8339	5891	11169	14.22	6.0E-24	AL163249.2	NT	Human sapiens chromosome 21 segment AML1 and CBR1 on chromosome 21q22, segment 3/3
3943	9079	14232	7.47	5.0E-24	AJ228043.1	NT	Human sapiens cDNA clone Y594 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
6076	10179	16310	1.53	3.0E-24	FD0837.1	EST_HUMAN	HSCZR0081 normalized infant brain cDNA Homo sapiens cDNA clone IMAGE:809161 6'
2326	7434	12687	1.07	2.0E-24	AA167159.1	EST_HUMAN	ZP11080.1 Strategene fetal retina 8072022 Homo sapiens cDNA clone IMAGE:809161 6'
3176	8913		0.88	2.0E-24	AW888189.1	EST_HUMAN	RC3-HN0088-Q08540-0021-h09 NN0088 Homo sapiens cDNA
1709	68337	12058	3.49	1.0E-24	77038340	NT	Human sapiens CG1-127 probin (LOC561646), mRNA
2634	7732		1	1.0E-24	AW820184.1	EST_HUMAN	Q90-570284-100400-188-c10 S10284 Homo sapiens cDNA
2992	8147	13307	0.65	1.0E-24	DB9423.1	NT	Mus musculus mRNA for HGT ketothi, partial cds
4244	8369		1.97	1.0E-24	AF148315.1	EST_HUMAN	Human sapiens PTEN (PTEN) gene, exon 2
5182	10278	16417	1.03	9.0E-25	AW857138.1	EST_HUMAN	RC1-CT0302-040400-017-002 CT0302 Homo sapiens cDNA
4982	10090	15223	3.25	7.0E-25	AA4483044.1	EST_HUMAN	ne82e10.61 MER1 repetitive element;
1664	6782		1.32	5.0E-25	AW850271.1	EST_HUMAN	IL3-CT0216-161189-03-D04 CT0219 Homo sapiens cDNA
1459	6888	11774	1.45	4.0E-25	T38107.1	EST_HUMAN	Y556H04.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA IMAGE:121763 5'
3383	8527		3.48	4.0E-25	AW887671.1	EST_HUMAN	PM3-OT0083-280200-001-607 O10083 Homo sapiens cDNA
4294	9416		3.86	4.0E-25	BE170957.1	EST_HUMAN	QV3-H10643-14040-149-611 HT0643 Homo sapiens cDNA
3301	8448	13610	2.96	3.0E-25	8923321	NT	Human sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA

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**Table 4**  
**Single Exon Probes Expressed In BT474 Cells**

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
3301	8448	13814	2.88	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA	
1354	6483	11663	3.09	2.0E-25	5632158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA	
2285	7984	12845	4.17	2.0E-25	BEE88016.1	EST_HUMAN	801611530F1 NIH_3T3 clone cDNA clone IMAGE:3913087 5'	
2792	7617	12869	8.6	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16	
4151	9287	14422	1.6	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16	
4161	9287	14423	1.6	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16	
362	6542	10884	0.98	1.0E-25	AL040229.1	EST_HUMAN	DKFZp434H0313_7'34 (synonym: Hes3). Homo sapiens cDNA clone DKFZp434H0313 6'	
1262	6382	12768	1.98	1.0E-25	8835487	NT	Human endogenous retrovirus, complete genome	
2412	7518	12768	2.79	1.0E-25	Q08056	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)		
4828	8940	15082	2.68	1.0E-25	BE162737.1	EST_HUMAN	PM1-HTO464-080100-002-h09 HT054 Homo sapiens cDNA	
2458	7360	12812	1.98	9.0E-28	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C013	
1600	6719	116908	1.3	7.0E-28	AF003628.1	NT	Homo sapiens X-linked epidermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	
3853	8038	14242	1.18	7.0E-28	X89211.1	NT	Homo sapiens DNA for endogenous retroviral like element	
4131	8269	14398	1.87	7.0E-28	AW340153.1	EST_HUMAN	h02a02X1 Scores_NIR_T_GBC_S11 Homo sapiens cDNA clone IMAGE:280583683 3	
2207	7318	12570	2.88	8.0E-28	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypanogen gene families ZF22h04.1 Strategene neuregulin (ZG37231) Homo sapiens cDNA clone IMAGE:945271 6'	
3328	8474	13687	1	8.0E-28	AA208131.1	EST_HUMAN	ZS8h08X1 Barstead et al. HPLB86 Homo sapiens cDNA clone IMAGE:ZS18610 3' similar to WPF49C12.1 CE03571	
1179	6314	11462	1.72	5.0E-28	AI708235.1	EST_HUMAN	GS38h05X1 Barstead et al. HPLB86 Homo sapiens cDNA clone IMAGE:ZS18610 3' similar to WPF49C12.1 CE03571	
1178	6314	11463	1.72	6.0E-28	AI708235.1	EST_HUMAN	WPF49C12.1 CE03571	
1658	6687	12102	1.21	4.0E-28	AA328548.1	EST_HUMAN	EST33448 Embryo_12 week_II Homo sapiens cDNA clone 5' end	
1770	6898	12357	0.86	3.0E-28	D14647.1	NT	Human DNA, SINE repetitive element	
2004	7121			1.15	AL045855.2	EST_HUMAN	DKFZp434I068_1'434 (synonym: neuroepithelium NT2RAM/837234 Homo sapiens cDNA clone IMAGE:5483943 6'	
2026	7143			2.18	3.0E-28	AA115895.1	EST_HUMAN	ZT30d08.1 Strategene K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); similar to abM4338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); ZS30f010.1 Strategene clone (ZG37204) Homo sapiens cDNA clone IMAGE:ZS8427 6' similar to TR-G889337
3759	8898	14046	1.25	3.0E-28	AA152464.1	EST_HUMAN	G685312.4 THYROID RECEPTOR INTERACTOR	
3759	8898	14047	1.25	3.0E-28	AA152464.1	EST_HUMAN	ZG37201 Strategene clone (ZG37204) Homo sapiens cDNA clone IMAGE:ZS8427 5' similar to TR-G889337	
680	6838	10978	5.51	2.0E-28	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082	
1879	6869			1.73	2.0E-28	AL038699.2	EST_HUMAN	DKFZp434L171_s1568 (synonym: Hifd2) Homo sapiens cDNA clone IMAGE:ZS8427 3'
3216	8367	12351	5.31	2.0E-28	X88894.1	NT	M.musculus mRNA for astrotcytic phosphoprotein, PEA-15	

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**Table 4**  
**Single Exon Probes Expressed In BT474 Cells**

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
132	6330	104761	40.29	1.0E-28	BE170371.1	EST_HUMAN	QV44HT0538-020300-123-602 HT0538 Homo sapiens cDNA MR2-BN0114-240500-030-907 BN0114 Homo sapiens cDNA
2532	7635	12883	0.85	1.0E-28	BE514995.1	EST_HUMAN	MR2-BN0114-240500-030-907 BN0114 Homo sapiens cDNA
2648	7746		25.15	1.0E-28	AF281085.1	NT	Homo sapiens dihydrofolate dehydrogenase (GADPH) mRNA, complete cds w/460-4,x1 NC1_CGAP_Lur8 Homo sapiens cDNA clone IMAGE:2408160 3' similar to contains THR.R2
10	5221	10333	3.08	8.0E-27	AI831462.1	EST_HUMAN	THR repetitive element:
558	6721		4.14	8.0E-27	AI163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1424	6551	11732	72.92	8.0E-27	AW162737.1	EST_HUMAN	av87n8_x1 Schneider fetal brain 0004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to gbkK00658
1424	6551	11733	72.92	8.0E-27	AW162737.1	EST_HUMAN	TUBUJIN ALPHA-1 CHAIN (HUMAN); av87n8_x1 Schneider fetal brain 0004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to gbkK00658
2149	7232	12510	1.98	8.0E-27	AW849776.1	EST_HUMAN	PM2-SNOOT8-220300-002-607 SN0018 Homo sapiens cDNA
3468	8317	13479	2.34	8.0E-27	P12238	SWISSPROT	ADP-ATP CARRIER PROTEIN LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3)(ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
682	6840		2.02	7.0E-27	Z70884.1	NT	Human endogenous retroviral element HC2
6074	10176		2.28	7.0E-27	AW626172.1	EST_HUMAN	h51h12_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2876879 3' similar to TR-O76040
2362	7469	12724	2.17	4.0E-27	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
2033	7163	12353	2.58	3.0E-27	X60658.1	NT	R_rattus RY48 mRNA for a potential ligand-binding protein
4245	6370	14503	1.31	3.0E-27	BE071624.1	EST_HUMAN	PM0-BT0527-050100-001-411 BT0527 Homo sapiens cDNA
40	6251	10387	28.93	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1802	7021		45.43	2.0E-27	AA566345.1	EST_HUMAN	h51h12_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:10006590 similar to gbkM17886 60S rRNA
3085	8238		10.82	2.0E-27	AW629172.1	EST_HUMAN	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); h51h12_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2876878 3' similar to TR-O76040
3209	8860	13521	2.17	2.0E-27	AF11167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; and unknown gene
3209	8860	13522	2.17	2.0E-27	AF11167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
435	5504		1.48	1.0E-27	AL163246.2	NT	Homo sapiens chromosomes 21 segment HS21C046
897	6143	11311	1.58	1.0E-27	AB028698.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
1711	6839	12040	0.87	1.0E-27	4827059	NT	Homo sapiens xylosidase (H. influenzae) homolog (XYLB) mRNA
4058	9188		0.83	1.0E-27	BE350127.1	EST_HUMAN	h08g01_x1 NC1_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146266 3' similar to contains MER22_b5
							MER22 repetitive element:

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Table 4

Single Exon Probes Expressed In BT474 Cells

Probe seq ID No:	Exon seq ID No:	ORF seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
137	5333			1.83	9.0E-28	BE548389.1	EST_HUMAN Iw17c11.x1 NCI CGAP_Lu24 Human sepiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
308	6495	10836		2.49	9.0E-28	AU128260.1	EST_HUMAN SECREDIT NEUREXIN III-ALPHA-C PRECURSOR OR_31 TR:307280 TR:Q07313;
5144	10244	16381		1.53	9.0E-28	AI58011B.1	EST_HUMAN tx12b99.x1 NCI CGAP_U12 Human sepiens cDNA clone IMAGE:2178809 3' similar to contains OFR.H OFR repetitive element;
5144	10244	16382		1.53	9.0E-28	AI58011B.1	EST_HUMAN repetitive element;
1183	6318	11489		12.82	7.0E-28	AU142750.1	EST_HUMAN AU142750 Y79AA1 Human sepiens cDNA clone Y79AA1000824 5'
318	65502			2.47	5.0E-28	AI621003.1	EST_HUMAN w018c07.x1 NCI CGAP_Pan1 Human sepiens cDNA clone IMAGE:24855892 3' similar to contains THFR.b1 THR repetitive element;
3884	9118	142863		1.27	6.0E-28	RT76782.1	EST_HUMAN Y88H10.1 Scarce plecenta Nbz2+P Human sepiens cDNA clone IMAGE:1468443 3'
2550	76391	12848		1.79	4.0E-28	AW185086.1	EST_HUMAN x08398.x1 NCI CGAP_Kb11 Human sepiens cDNA clone IMAGE:28955504 3' similar to SW.GG85_HUMAN Q08398 GOLGIN-48.;
2948	8100	13284		1.43	4.0E-28	4505216	NT Human sepiens myosin phosphatases, target subunit 1 (MYPFT1), mRNA
3084	62237	13387		2.63	4.0E-28	BE40901.1	EST_HUMAN 6013030703F1 NIH_MGC_21 Human sepiens cDNA clone IMAGE:383853015 5'
1287	6416			1.61	3.0E-28	AF165582.1	NT Human sepiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
6100	102200			0.82	3.0E-28	AF008680.1	NT Human sepiens T cell receptor beta locus, TCRBV7/S3A2 to TCRBV12S2 region
84	52283	10433		9.61	2.0E-28	BE062167.1	EST_HUMAN RC1-BT0254-22030D-019-c05 BT0254 Human sepiens cDNA
1167	63022	11468		7.61	2.0E-28	Y11107.3	NT Human sepiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2450	7554	12800		2.09	2.0E-28	AI346854.1	EST_HUMAN q035b06.x1 NCI CGAP_Lu6 Human sepiens cDNA clone IMAGE:1610468 3' similar to contains L1.b2.L1 repetitive element;
3343	8489	13665		0.62	2.0E-28	AI163209.2	NT Human sepiens chromosome 21 segment HS21C009
1488	6616	11803		2.07	1.0E-28	D38044.1	NT Human gene for Ah-receptor, exon 7-9
2202	7314	12566		1.03	1.0E-28	BF533236.1	EST_HUMAN QV1-BT0821-1-20900-350-b03 BT0821 Homo sapiens cDNA
4541	9859			0.83	1.0E-28	I09410.1	NT Human zinc finger protein ZNF131 mRNA, partial cds
1616	6744	11839		1.25	7.0E-28	AW1865447.1	EST_HUMAN EST378521 MAGE sequences, MAG1 Human sepiens cDNA
658	5755	10889		8.3	8.0E-28	AI869748.1	EST_HUMAN WP68001.x1 NCI CGAP_Bm26 Human sepiens cDNA clone IMAGE:24868935 3' similar to TR-015475 O15475 UNNAMED HERV-H PROTEIN ;contains LTR7.b1 LTR7 repetitive element;
4984	10092			1.32	5.0E-28	AL163203.2	NT Human sepiens chromosome 21 segment HS21C003
3217	8868			2.16	4.0E-28	AI762387.1	EST_HUMAN cm16c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH-TBC_cm16c02 random
4392	96112	14654		1.32	3.0E-28	AB0542297.1	NT Human sepiens PTFs gene for 6-pyruvoyltryptophylserine synthase, complete cds
4701	98117	14985		1.03	3.0E-28	BF333238.1	EST_HUMAN QV1-BT0821-1-20900-350-b03 BT0821 Homo sapiens cDNA

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
492	5659	10784	2.02	2.0E-29	AF084869.1	NT	Homo sapiens enviro protein RC-8 (env) gene, complete cds
492	5659	10785	2.02	2.0E-29	AF084869.1	NT	Homo sapiens enviro protein RC-8 (env) gene, complete cds
1547	6876	11860	6.63	2.0E-29	AB083604.1	EST_HUMAN	Wf05c10_x1 NCI CGAP_Ut Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR_O16548 O16548
1547	6875	11861	5.63	2.0E-29	AB083604.1	EST_HUMAN	Wf05c10_x1 NCI CGAP_Ut Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR_O16548 O16548
4253	8878	14509	2.04	2.0E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C038
1530	6857		2.08	7.0E-30	BE091133.1	EST_HUMAN	PM4-B10724-160400-0004-d11 BT0724 Homo sapiens cDNA
1783	68098	12117	1.11	8.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3173	8824	13485	3.1	8.0E-30	BE080283.1	EST_HUMAN	QV08D147-28040-0-214-f12 BN0147 Homo sapiens cDNA
4724	8824	13485	0.94	8.0E-30	BE080283.1	EST_HUMAN	QV08D147-28040-0-214-f12 BN0147 Homo sapiens cDNA
38883	91222	14265	30.82	5.0E-30	A1389892.1	EST_HUMAN	168220x5_x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Atu repetitive element
2128	7242	12484	1.89	4.0E-30	AV693747.1	EST_HUMAN	QV24-D70042-09020-0-050-008 DT0043 Homo sapiens cDNA
2128	7242	12485	1.89	4.0E-30	AV693747.1	EST_HUMAN	QV24-D70042-09020-0-050-008 DT0043 Homo sapiens cDNA
1153	68289		2.88	3.0E-30	A1389894.1	EST_HUMAN	qq83c05_x1 Scores: tel_fus_N121-HPa_9w Homo sapiens cDNA clone IMAGE:16938920 3' similar to contains MER29_l2 MER29 repetitive element;
3738	8876	14027	0.83	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
674	58392	10972	1.27	2.0E-30	AW887315.1	EST_HUMAN	GMD-C70307-31010-168-H03 CT0307 Homo sapiens cDNA
1085	6224		1.82	2.0E-30	F08888.1	EST_HUMAN	HSC23F5-1 normalized infant brain cDNA Homo sapiens cDNA clone o-23105
1489	6816	11804	3.7	2.0E-30	BE75877.1	EST_HUMAN	RC54-H70582-11040-0-013-H08 HT0582 Homo sapiens cDNA
2879	7773	13024	4.7	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-118-E04 NT0101 Homo sapiens cDNA
2885	8039	13204	7	2.0E-30	AF114158.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3768	88016	140163	2.23	2.0E-30	AW26581.1	EST_HUMAN	U4-H-B1-460-12-0-U1.1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4745	8858	15008	3.09	2.0E-30	BE288845.1	EST_HUMAN	6011168850F1 NIH MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4745	8858	16007	3.09	2.0E-30	BE288845.1	EST_HUMAN	6011168850F1 NIH MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
284	6873	10816	14.45	1.0E-30	C18839.1	EST_HUMAN	C18838 Human placenta cDNA (TFUwara) Homo sapiens cDNA clone IMAGE:2810901 5'
536	5702	10835	7.24	1.0E-30	AW488897.1	EST_HUMAN	hs30044_x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810901 5' similar to contains MER1.3 MER1 repetitive element;
714	5871	11018	3.43	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C03
2184	7006	12858	2.77	1.0E-30	AA844977.1	EST_HUMAN	ae7708.6 Strategene linc (#37720) Homo sapiens cDNA clone IMAGE:888560 3'
2439	7642	12785	1.44	1.0E-30	BT47728.1	EST_HUMAN	6022022660F1 NCI CGAP Bm87 Homo sapiens cDNA clone IMAGE:4167891 5'
2874	81228	13291	1.24	1.0E-30	S803081	NT	Homo sapiens methionine aminopeptidase, eIF-2-associated p67 (MNPEP), mRNA
3028	8180	13339	0.87	1.0E-30	AA1315045.1	EST_HUMAN	EST188868 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3748	8884	14034	0.8	9.0E-31	T73025.1	EST_HUMAN	ycg65608.1 Strategene liver (#837224) Homo sapiens cDNA clone IMAGE:855705'
3748	8884	14035	0.8	9.0E-31	T73026.1	EST_HUMAN	ycg65608.1 Strategene liver (#837224) Homo sapiens cDNA clone IMAGE:855706'
1078	6218	11383	6.59	8.0E-31	8923389.NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA	
2389	7490		8.10	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C018
4895	10006	15150	0.98	8.0E-31	P23275	SWISSPROT	OLFACTOORY RECEPTOR 15 (OR3)
4895	10006	15151	0.98	8.0E-31	P23276	SWISSPROT	OLFACTOORY RECEPTOR 15 (OR3)
709	5666		1.37	7.0E-31	AA372837.1	EST_HUMAN	EST8455 Colorectal carcinoma IV Homo sapiens cDNA 5' end
2629	7727	12882	2.1	7.0E-31	BE326517.1	EST_HUMAN	Iw005611.X1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:31820123'
2629	7727	12883	2.1	7.0E-31	BE326517.1	EST_HUMAN	Iw005611.X1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:31820123'
3856	8785		2.31	8.0E-31	AF2223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-9, end partial cds, alternatively spliced
189	5384	10526	2.84	5.0E-31	MG06894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
189	5384	10527	2.84	6.0E-31	MG06894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
694	5768		3.28	4.0E-31	AJ271735.1	NT	Homo sapiens Xq pseudosomal region; segment 1/2
							POLYPEPTIDE N ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP-A CETYLGALACTOSAMINYL TRANSFERASE) (GALNAC-POLYPEPTIDE_N)
1624	6752	11845	1.08	4.0E-31	Q10473	SWISSPROT	
1829	6852		1.27	4.0E-31	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2750	7644		1.67	4.0E-31	5730338.NT	NT	Homo sapiens SET domain and matrix transposase fusion gene (SETMAR) mRNA
2553	7650	12813	2.37	3.0E-31	6005871.NT	NT	Homo sapiens SEC03, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC03L), mRNA
1920	7039	12260	1.98	2.0E-31	AW838171.1	EST_HUMAN	QV24L0051-2a030-111-03 L70651 Homo sapiens cDNA
2188	7509	12553	1.54	2.0E-31	AI939398.1	EST_HUMAN	Ig44g5.X1 Scores_1.NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:21113723'
2321	7429	12682	0.98	2.0E-31	AL119245.1	EST_HUMAN	DKFZp761G1613_r761 (synonym: hnrn2) Homo sapiens cDNA clone DKFZp761G1613
2418	7523	12776	3.48	2.0E-31	AA4488824.1	EST_HUMAN	aa88f11.81 Strategene fetal retina B37/202 Homo sapiens cDNA clone IMAGE:338413 3' similar to contains
16	5226	10339	5.7	1.0E-31	U83163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1678	8805	12000	7.67	1.0E-31	O93371	SWISSPROT	OLFACTOORY RECEPTOR 2C1
1678	8805	12001	7.67	1.0E-31	O93371	SWISSPROT	OLFACTOORY RECEPTOR 2C1
1678	8805	12002	7.67	1.0E-31	O93371	SWISSPROT	DKFZp547B235_r1 s47 (synonym: hnrn1) Homo sapiens cDNA clone DKFZp547B235
4605	9723	14857	1.1	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_r1 s47 (synonym: hnrn1) Homo sapiens cDNA clone DKFZp547B235
4605	9723	14868	1.1	1.0E-31	AL134376.1	EST_HUMAN	Human familial Alzheimer's disease (STM12) gene, complete cds
2828	7983		1.08	9.0E-32	U56987.1	NT	

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2089	7185	12423	6.64	8.0E-32	A1056770.1	EST_HUMAN	ox15a09.x1 Scores fetal_liver_spleen_cDNA clone IMAGE:16753843'
4829	8641	15039	0.94	7.0E-32	PC2651	SWISSPROT KD (P445)	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121
1036	8177	11342	48.23	5.0E-32	AF110027.1	NT Homo sapiens PRO1181 mRNA, complete cds	
832	5080		1.85	4.0E-32	AL163246.2	NT Homo sapiens chromosome 21 segment HS21C048	
465	5623	10763	3.08	3.0E-32	Y17283.1	NT Homo sapiens FL-1 gene, partial	
1467	6594	11783	16.89	3.0E-32	A1V73160.1	EST_HUMAN	AV73160 HTF Homo sapiens cDNA clone HTFKCOT 6
2873	8027	13194	0.84	3.0E-32	5174574	NT Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLL14) mRNA	
2873	8027	13185	0.84	3.0E-32	5174574	NT Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLL14) mRNA	
2838	7738		1.93	1.0E-32	DB4450.1	NT Homo sapiens mRNA for phenylalanine tRNA synthetase, complete cds	
3067	8220		1.47	1.0E-32	B07432289.1	EST_HUMAN	6015733207Fl NIH_3T3 mRNA clone IMAGE:3831433 5'
3462	8604		5.35	9.0E-33	BE327112.1	EST_HUMAN	Iw07c05.x1 NCI_CGAP_LU24 Homo sapiens cDNA clone IMAGE:31892216 3' similar to TR:O88538 O88538
60	5271	10403	6.57	7.0E-33	5031738	NT Homo sapiens WW DOMAIN BINDING PROTEIN 11.;	
60	5271	10404	6.57	7.0E-33	5031738	NT Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA	
2143	7257	12503	1.13	7.0E-33	A1590115.1	EST_HUMAN	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2810	7709		5.84	7.0E-33	AV730058.1	EST_HUMAN	1012609.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to domain OFR.H1 OFR repetitive element;
3226	8376		13.21	7.0E-33	AV971307.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE08 6'
3718	8856		1.03	8.0E-33	AL163285.2	NT Homo sapiens chromosome 21 segment HS21C036	
1787	6613		1.49	5.0E-33	BF373515.1	EST_HUMAN	Q7V-F10169-100700-271-e02 FT0169 Homo sapiens cDNA
1805	7024	12243	2.08	6.0E-33	4507208	NT Homo sapiens spermidine synthase (SRM) mRNA	
1805	7024	12244	2.08	5.0E-33	4507208	NT Homo sapiens spermidine synthase (SRM) mRNA	
2261	7361		1.73	6.0E-33	AL163285.2	NT Homo sapiens chromosome 21 segment HS21C036	
4032	9163	14305	0.88	5.0E-33	AB014539.1	NT Homo sapiens mRNA for KIAA0688 protein, partial cds	
1129	6268		1.69	4.0E-33	AL163207.2	NT Homo sapiens chromosome 21 segment HS21C007	
2117	72232	12474	3.01	4.0E-33	4768887	NT Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA	
2397	7603		2.47	4.0E-33	A1A626921.1	EST_HUMAN	ab51b11.11 Strategene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844317 6' similar to
2516	7620	12863	1.28	4.0E-33	AL163210.2	NT Homo sapiens chromosome 21 segment HS21C010	control Abu repetitive element containing MER28.12 MER28 repetitive element;
4462	8881	14719	1.67	4.0E-33	AW283349.1	EST_HUMAN	UH4B12-eh1c-03-U1.1 NC_GAP_Sub4 Homo sapiens cDNA clone IMAGE:2272149 3'

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1090 6229			4.74	3.0E-39	BE350127.1	EST_HUMAN	ht08g01_x1 NC1_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contents MER29_b3 MER29 repetitive element;
1091 6229			4.22	3.0E-39	BE350127.1	EST_HUMAN	ht08g01_x1 NC1_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contents MER29_b3 MER29 repetitive element;
2426 7840			1.24	3.0E-39	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone Gl.CB.CF08 3'
18 6227			1.23	2.0E-39	AI160189.1	EST_HUMAN	q8z7g03_x1 Scores_fetal_heart_NbHH18W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFRH_OFR repetitive element;
101 6227			1.88	2.0E-39	AI160189.1	EST_HUMAN	q8z7g03_x1 Scores_fetal_heart_NbHH18W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFRH_OFR repetitive element;
4397 9517			3.67	2.0E-39	BE156039.1	EST_HUMAN	MRO-H1046-160300-202-018 HT0406 Homo sapiens cDNA ab51g11.1 Stratego lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X010734 cds1 TUBULIN BETA-5 CHAIN (HUMAN);
4970 10078	16216		15.38	2.0E-39	AA626983.1	EST_HUMAN	Homo sapiens hypothetical protein SIRP-32 (SIRP-B2), mRNA
6078 10179	16314		1.37	2.0E-38	11421332	NT	Homo sapiens hypothetical protein SIRP-32 (SIRP-B2), mRNA
6078 10179	16316		1.37	2.0E-38	11421332	NT	Homo sapiens hypothetical protein SIRP-32 (SIRP-B2), mRNA
8 6219			1.37	1.0E-38	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2151 7264	12612		1.17	8.0E-34	3822761	NT	Homo sapiens hypothetical protein FLJ10800 (FLJ10800), mRNA
4475 9594	14733		0.81	8.0E-34	BE062570.1	EST_HUMAN	QV2-E528-07-288-019-807 BT0258 Homo sapiens cDNA yf1865_x1 Scores_fetal_liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
1456 6583	11771		1.63	7.0E-34	T08346.1	EST_HUMAN	Human G2 protein mRNA, partial cds
470 6637	10773		1.44	6.0E-34	U10681.1	NT	Human G2 protein mRNA, partial cds
470 6637	10779		1.44	6.0E-34	U10681.1	NT	Human G2 protein mRNA, partial cds
1880 7010			2.57	5.0E-34	770363D	NT	Human splicing factor Numb-binding protein NumbBP (LOC61729), mRNA
5044 101448	15275		4.3	5.0E-34	U30883.1	NT	Human splicing factor SRp55-1 (SRP-55) mRNA, complete cds
6127 10227			1.06	6.0E-34	N88282.1	EST_HUMAN	2827g11.11 Scores_fetal_liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:283828 6'
1689 7118	12352		1.33	4.0E-34	AI804687.1	EST_HUMAN	hs94-08.1 NC1_CQAP_P-28 Homo sapiens cDNA clone IMAGE:2249184 3'
2881 7778	13028		1.69	4.0E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10889 (FLJ10889), mRNA
3162 8303	13469		1.02	4.0E-34	5803168	NT	Homo sapiens splicing factor 3e, subunit 3, 60kD (SF3A3), mRNA
1520 8647	11834		18.47	1.0E-34	P12236	SWISSPROT	ADP ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADPATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3631 8760	13944		1.42	1.0E-34	AF003629.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4045 9176	14317		0.75	1.0E-34	AY008897.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4045 9176	14318		0.75	1.0E-34	AY008897.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4469 9878			2.13	1.0E-34	BE071414.1	EST_HUMAN	R22-BT0508-240400-016-h08 BT0508 Homo sapiens cDNA

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe seq ID No:	Exon seq ID No:	ORF seq ID NO:	Expression Signal	Most Similar (Top) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4909	10019	15163	1.45	1.0E-34	BF509718.1	EST_HUMAN	U+H+H4_esp-h-04-0-UJ_s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:30868839 3'
4909	10019	15164	1.49	1.0E-34	BF509718.1	EST_HUMAN	U+H+H4_esp-h-04-0-UJ_s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:30868839 3'
3623	8762	12918	1.31	9.0E-35	AW683302.1	EST_HUMAN	H177906.1 NCI_CGAP_G14 Homo sapiens cDNA clone IMAGE:28687875
223	5416		39.92	8.0E-35	6031160	NT	Homo sapiens prohibitin (PHB) mRNA
1749	8675	12080	2.13	8.0E-35	BF568937.1	EST_HUMAN	ras53ab8.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:32588134 3' similar to TR:078912
1749	8675	12081	2.13	8.0E-35	BF568937.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA;
4836	8848	16092	2.74	8.0E-35	BF168105.1	EST_HUMAN	601688588F NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
1420	6547	11728	0.98	6.0E-35	A476715.1	EST_HUMAN	656203.61 Soares testis_NHT Homo sapiens cDNA clone 1368397 3'
1970	7087	12314	5.54	8.0E-35	6003975	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
4927	8158	14301	0.63	8.0E-35	AV297181.1	EST_HUMAN	UH+BWD-gld-d-CS-h-0-UJ_s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2731433 3'
1724	6851	12055	1.38	5.0E-35	X833392.1	NT	H.sapiens immunoglobulin kappa light chain variable region L14
2745	7839	13094	1.34	6.0E-35	AB007868.2	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
2830	8135	13289	1.38	6.0E-35	6812639	NT	Homo sapiens Ring1 end YY1 binding protein (RYYBP), mRNA
4387	8507	14849	1.91	6.0E-35	AF023268.1	NT	Homo sapiens cdk2 kinase (CLK2), propin1, cate1, glucocerebrosidase (GBA), and metadlin genes, complete cds; metadlin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
1444	6572	11769	28.28	4.0E-35	BE257607.1	EST_HUMAN	601109718F NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1830	6553	12174	8.38	4.0E-35	H9183.1	EST_HUMAN	yu68a07..1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:241238 5' similar to contig10
1592	6171	11911	40.59	3.0E-35	BF2268182.1	EST_HUMAN	PTR5 repetitive element;
2312	7421		1.77	3.0E-35	AF224492.1	NT	Homo sapiens phosphatidyl scramblase 1 gene, complete cds
104	7883	10450	1.29	2.0E-35	N8895.1	EST_HUMAN	K6932f_HUMAN REPEITIVE ELEMENT
1100	6524	11492	1.28	2.0E-35	T1909.1	EST_HUMAN	A971f_Human Homo sapiens cDNA clone A971
2200	7312	12584	2.32	2.0E-35	AB018413.1	NT	Homo sapiens mRNA for Gab2, complete cds
2845	7743	12898	1.9	2.0E-35	AW686505.1	EST_HUMAN	hu68a12x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878166 3' similar to SW:TR12_HUMAN Q14689 THYROID RECEPTOR INTERACTING PROTEIN 12;
3293	8440	13601	0.62	2.0E-35	6012459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3293	8440	13602	0.62	2.0E-35	6012459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3643	8884		1.04	2.0E-35	AB020702.1	NT	TCBAP2E328 Pediatric acute lymphoblastic leukemia Baydar-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3887	9023	14180	0.77	2.0E-35	BE247676.1	EST_HUMAN	

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Score	Top Hit Descriptor
3887	8123	14181	0.77	2.0E-35 BE247578.1	EST_HUMAN	TCBAP2E432B Pediatric pre-B cell acute lymphoblastic leukemia Bay/for-HGSC project=TCBAP432B
4840	9758		2.94	2.0E-35 H49229.1	EST_HUMAN	Y18g12.11 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:214079 5'
45	6257	10378	4.38	1.0E-35 AA681648.1	EST_HUMAN	Imf16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
45	6257	10378	4.38	1.0E-35 AA681949.1	EST_HUMAN	Imf16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
751	6997	11082	16.62	1.0E-35 AW385473.1	EST_HUMAN	IL2-ST0162-131089-008-d12-ST0162 Homo sapiens cDNA
761	6807	11083	16.62	1.0E-35 AW385473.1	EST_HUMAN	IL2-ST0162-131089-008-d12-ST0162 Homo sapiens cDNA clone IMAGE:115762 5' similar to y893ad11.11 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:115762 5' similar to SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN;
910	6030		1.48	1.0E-35 T87947.1	EST_HUMAN	Homo sapiens hypothetical protein (LOC51233), mRNA
2513	7816	12885	3.28	1.0E-35	7706894 NT	Homo sapiens CGAP_Kd13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29 DS
2728	7824	13070	1.24	1.0E-35 BE350127.1	EST_HUMAN	MER29 repetitive element;
2728	7824	13080	1.24	1.0E-35 BE350127.1	EST_HUMAN	h08g11.1x NCI_CGAP_Kd13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29 DS
9121	8273	13428	1.25	1.0E-35	6008030 NT	MER29 repetitive element;
3142	8283	13450	3.15	1.0E-35 AV650422.1	EST_HUMAN	Home sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
3142	8283	13451	3.15	1.0E-35 AV650422.1	EST_HUMAN	AV650422 GLC Home sapiens cDNA clone GLCCEF063'
4400	9520	14680	3.82	1.0E-35	7656908 NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
4400	9520	14681	3.82	1.0E-35	7656905 NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
3960	8185	14247	0.86	9.0E-36	AW821707.1	RC3-S10315-180200-01-f12 ST10315 Homo sapiens cDNA
2898	8050	13217	1.52	7.0E-36	AW857679.1	CAT-C70315-091289-009-d07 CTC8316 Homo sapiens cDNA
3094	8247		4.75	7.0E-36	4557498 NT	Home sapiens C-terminal binding protein 2 (CTBP2) mRNA
2005	7122	12353	1.48	6.0E-36	7706822 NT	Home sapiens niflun 2 (NIFL2), mRNA
2393	7501		4	6.0E-36 AB035346.1	NT	Home sapiens TBL8 gene, exon 12
3817	8168	13812	0.81	6.0E-36 BF515101.1	EST_HUMAN	U+HBW1-env-c-12q-0-U1-er NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3068642 3'
4943	10053	15191	1.28	6.0E-38 ABP30501.1	NT	Ratius norvegicus mRNA for Dlg8 gamma, complete cds
133	6331	10476	11.17	5.0E-38 AI277735.1	NT	Home sapiens Xq pseudautosomal region; segment 1/2
2714	76018	13063	62.37	5.0E-38 BE388438.1	EST_HUMAN	60128567F1 NIH_3T3 MGIC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
3580	6755	13897	1.8	5.0E-36 AL163209.2	NT	Home sapiens chromosome 21 segment HS21C009
4755	68688	15017	1.85	6.0E-38	5728720 NT	Home sapiens API6-like 1 (API6L1), mRNA
4755	68688	15018	1.85	6.0E-38	5728720 NT	Home sapiens API6-like 1 (API6L1), mRNA
1227	63359	11629	2.69	4.0E-38 BE010038.1	EST_HUMAN	PM3-BN0176-100400-01-04 BN0176 Homo sapiens cDNA RETROVIRUS-RELATED POLYPROTEIN [CONTAINS REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1452	6380	11768	1.83	4.0E-38 P10268	SWISSPROT	

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1657 6786	11970		1.72	4.0E-38	BE582574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3828398 5'	EST_HUMAN	
2204 7316			5.27	4.0E-38	BE247772.1	EST_HUMAN	282020 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:28202020 5'
3335 8481	13947		1.86	4.0E-38	BE582289.1	EST_HUMAN	60122268F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804168 6'
3335 8481	13948		1.88	4.0E-38	BE582289.1	EST_HUMAN	60122268F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804168 6'
4710 9833	14977	0.63	4.0E-38	AL182042.2	NT	Homo sapiens chromosome 21 segment HS21 C014	
5110 10211	18348		0.74	4.0E-38	AA805361.1	EST_HUMAN	ck05511.1 nt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1506869 3' similar to SW.D3H1_RAT P28286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
694 5651	10893		2.64	3.0E-38	AF068610.1	NT	Homo sapiens neuretin III-alpha gene, partial cds
1512 68339	11828		1.43	3.0E-38	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1612 66339	11827		1.43	3.0E-38	AF110239.1	NT	Homo sapiens calcitonin/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
2273 72631	12631		1.23	3.0E-38	7682401	NT	Homo sapiens KIAA0962 protein (KIAA0962), mRNA
4479 8389	14738		7.19	3.0E-38	10181139	NT	Mus musculus junctophilin 1 (Jip1-pending), mRNA
3149 8340	13480		5.87	2.0E-38	BE265208T.1	EST_HUMAN	6011086343F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3342708 5'
4839 10049	15187		8.68	2.0E-38	AW880376.1	EST_HUMAN	Q10701030-240300-174-H04 OT0030 Homo sapiens cDNA
8886 60336	11207		1.67	1.0E-38	BE108310.1	EST_HUMAN	6013008386F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2129 7243	12483		1.08	1.0E-38	BE146223.1	EST_HUMAN	RC1-HT0217-131198-021-H07 HT0217 Homo sapiens cDNA
2129 7243	12487		1.08	1.0E-38	BE146223.1	EST_HUMAN	RC1-HT0217-131198-021-H07 HT0217 Homo sapiens cDNA
2185 72898	12546		1.32	1.0E-38	BF073761.1	EST_HUMAN	6021384831F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272888 5'
3328 8473			1.34	1.0E-38	AF165982.1	NT	Homo sapiens human endogenous retrovirus W prov-CB-18 protease (pro) gene, partial cds
1288 6417			3.18	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_T1_434 (synonym: hts3) Homo sapiens cDNA clones DKFZp434E0422 5'
1756 68882	12083		0.85	7.0E-37	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
1766 68882	12089		0.95	7.0E-37	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
2401 72507	12753		2.6	4.0E-37	AA702779.1	EST_HUMAN	2850504 nt Soares_fetal_liver_spleen_1NF1S_S1 Homo sapiens cDNA clone IMAGE:448015 3'
2012 7129	12368		1.98	3.0E-37	AL048858.1	EST_HUMAN	DKFZp434_2418_T1_434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434_2418
2012 7129	12367		1.86	3.0E-37	AL048858.1	EST_HUMAN	DKFZp434_2418_T1_434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434_2418
2483 7987			4.6	3.0E-37	AW961150.1	EST_HUMAN	EST373222 IMAGE sequences, MAGF Homo sapiens cDNA
2834 8088			3.61	3.0E-37	AW861150.1	EST_HUMAN	EST373222 IMAGE sequences, MAGF Homo sapiens cDNA
379 51588	10733		1.65	2.0E-37	D89780.1	NT	Homo sapiens mRNA for ANL1, complete cds
379 51588	10734		1.65	2.0E-37	D89780.1	NT	Homo sapiens mRNA for ANL1, complete cds
1082 62221	11387		2.12	2.0E-37	AU31202 NT2RP3	Homo sapiens cDNA clone NT2RP3002168 5'	AU31202 NT2RP3 Homo sapiens cDNA clone NT2RP3002168 5'

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Probe seq ID NO:	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar (T <sub>cop</sub> ) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1082	8221	11383	2.12	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP30021861 6'
3870	8006	14162	5.62	2.0E-37	480210 NT	Homo sapiens cytochrome P450, subfamily 27A1 (CYP27A1b) mRNA, poly(A)-tail, (CYP27A1b) mRNA	
4224	8349	14482	0.68	2.0E-37	482685 NT	Homo sapiens DEATH (Asp-Glu-Ala-Asp(His)) box polypeptide 1 (DDX1) mRNA	
2081	7197	12442	3.65	1.0E-37	AL163281.2	NT	
3180	8331			1.18	1.0E-37	AW882032.1	Homo sapiens chromosome 21 segment HS21C081
3834	8070	14226	0.78	1.0E-37	AF188011.1	NT	RC3-C70347-21040-016-H03 CT0347 Homo sapiens cDNA
4918	10028	15170	2.24	1.0E-37	BF377179.1	EST_HUMAN	Homo sapiens ribonuclease III (RNase) mRNA, complete cds
1224	6558	11626	1.79	8.0E-38	11486955 NT	QVO-FN10180-28D070-318-c010 FN10180 Homo sapiens cDNA	
2469	7573	12826	1.23	8.0E-38	BF3-46222.1	EST_HUMAN	Grb2-associated binder 2 (KIAA0571), mRNA
2165	7278	12823	3.61	7.0E-38	AW972825.1	EST_HUMAN	C3AP_Biner Homo sapiens cDNA clone IMAGE:4163892 6'
3073	8226	13377	1.1	7.0E-38	AW884259.1	EST_HUMAN	Est3-920684-08040-144-409 OT0564 Homo sapiens cDNA
4200	8226	14466	0.82	7.0E-38	HI16092.1	EST_HUMAN	Y15f107.71 Scores adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:711973 6'
3014	8168	15923	1.89	6.0E-38	BF033033.1	EST_HUMAN	601485722F1 NIH_3T3C_68 Homo sapiens cDNA clone IMAGE:3859348 6'
725	5881	11029	1.5	5.0E-38	AW97181.1	EST_HUMAN	EST3-83303 IMAGE sequences, MAGL_Homo sapiens cDNA
2430	7634	12787	3.2	5.0E-38	A1237740.1	NT	RIBIII gene (partial), exon 8
1115	5317	10458	3.02	4.0E-38	225468.1	NT	B_tauri mitochondrial epsilont arabinose tRNA, complete CDS
1116	5317	10459	3.02	4.0E-38	ZB6488.1	NT	B_tauri mitochondrial epsilont arabinose tRNA, complete CDS
1159	6295	11460	0.68	3.0E-39	11435947 NT	Homosapiens chromosome 12 open reading frame 3 (C12orf3), mRNA	
2091	72016		2.18	3.0E-38	AF003530.1	NT	Homeobox protein CDXA (CDXA) gene, complete cds and flanking repeat regions
3673	83112		1.78	3.0E-38	7349507 NT	Homosapiens HIRA interacting protein 4 (Hirip4), mRNA	
3834	8910	14123	1.48	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3834	8970	14123	1.48	3.0E-38	P53539	SWISSPROT	SSU72 PROTEIN
49	5261	10383	1.61	2.0E-38	AL163248.2	NT	Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA
1380	65118	11683	0.25	2.0E-38	5302097 NT	2W300117 Scores ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:710785 6' similar to SW-M12_RABIT P46701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;	
1658	6786	11980	1.88	2.0E-38	AA43753.1	EST_HUMAN	2W3000117 Scores ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:710785 6' similar to SW-M12_RABBIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
3520	8891		1.04	2.0E-39	AF070870.1	NT	Homosapiens protein phosphatase 2C alpha 2 mRNA, complete cds
4554	8972	14814	14.68	2.0E-38	4557987 NT	Homosapiens keratin 18 (KRT18), mRNA	
1094	6232		1.83	1.0E-38	AA401670.1	EST_HUMAN	ZU620211 Scores testis, N-TT Homo sapiens cDNA clone IMAGE:742539 6' similar to contains element MER19 repetitive element;
2000	7117	12953	1.95	1.0E-38	4885289 NT	Homosapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA	

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Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2016	7132	12369	1.02	1.0E-38	7661869	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2468	7570	12824	3.73	1.0E-38	AF270591.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4127	8235	14394	1.03	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4201	9423	14556	1.44	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4201	9423	14557	1.44	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4670	8888	14826	1.07	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10800 (FLJ10800), mRNA
53	5285	10392	3.67	8.0E-39	4502312	NT	Homo sapiens ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1401	6528	11708	1.7	8.0E-39	4758228	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA wtSS�0.1x NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TRF87850 P87850
1843	6884			1.95	8.0E-39	AI823404.1	EST_HUMAN
2085	7201	12445	3.54	7.0E-39	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1008	6152	11319	2.47	5.0E-39	AF003508.1	NT	Homo sapiens X-linked arthrobioctetameric dyphosphate protein gene (EDA), exon 2 and flanking repeat regions
2854	8108	13272	0.8	5.0E-39	AI750154.1	EST_HUMAN	AI36804.1x Banstead cDNA HPLR7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR-Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT :contains LTR; m1 LTR? repetitive element;
6449	6714	10848	28.8	4.0E-39	AB015610.1	NT	Chlorobacillus antibiotic mRNA for ribosomal protein S1X, complete cds
3669	8700	13860	0.71	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
46	6258	10360	12.67	3.0E-39	AA631949.1	EST_HUMAN	fmf1fe Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
46	5288	10381	12.67	3.0E-39	AA631949.1	EST_HUMAN	fmf1fe Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	5288	10382	12.67	3.0E-39	AA631949.1	EST_HUMAN	fmf1fe Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
898	6048		7.83	2.0E-39	BE469203.1	EST_HUMAN	6013016077-1 NIH MfGC_21 Homo sapiens cDNA clone IMAGE:3535289 5'
913	6063		11.41	2.0E-39	AI526119.1	EST_HUMAN	promtma7_D01.1 brainrat Homo sapiens cDNA 5'
1033	6174		3.5	2.0E-39	AF00573.1	NT	Homo sapiens homogenate 1,2-dihydrogenase gene, complete cds
1644	6972		60.74	2.0E-39	AV372318.1	EST_HUMAN	PM0-BT0340-211289-003-d02 BT0340 Homo sapiens cDNA
1976	7092	12322	1.67	2.0E-39	AA720574.1	EST_HUMAN	rw21p2.61 NCI CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.3 THR repetitive element;
2504	7868	12849	1.06	2.0E-39	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4382	8013	14846	1.68	2.0E-39	BF370207.1	EST_HUMAN	RC4-HN0037-28070-011-a10 F1037 Homo sapiens cDNA
1528	6555	11842	2.69	1.0E-39	AJ0058345.1	NT	Homo sapiens KVI_QT1 gene
1528	6555	11843	2.69	1.0E-39	AJ0058345.1	NT	Homo sapiens DKFZp434P211, mRNA
1645	6873	11857	3.43	1.0E-39	7657020	NT	EST384065 MAGE sequences, MAGB Homo sapiens cDNA
4830	9748	14883	12.37	1.0E-39	AW0651985.1	EST_HUMAN	EST384065 MAGE sequences, MAGB Homo sapiens cDNA
4830	9748	14894	12.37	1.0E-39	AW0651985.1	EST_HUMAN	

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 Table 4  
 Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4671	9787	14832	7.78	1.0E-39	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211) mRNA
654	5719	10851	1.73	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2) mRNA
1238	6368	11640	8.31	9.0E-40	4765145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1239	6368	11641	8.31	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1462	8589	11773	1.72	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby/fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3764	8901	14053	0.79	9.0E-40	4503184	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
3946	10307	14233	3.9	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
3013	8197	13325	0.97	8.0E-40	AA078165.1	EST HUMAN	TH15A04 Chromosome 7 HeLa cDNA library Homo sapiens cDNA clone TH15A04
3897	9033		4.43	8.0E-40	B539868F1 NIH_3T3	EST HUMAN	G0128868F1 NIH_3T3 cDNA clone MAGE3619168 5'
2689	7786	13036	7.39	6.0E-40	AA4381275.1	EST HUMAN	EST700527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2689	7786	13036	7.39	6.0E-40	AA361275.1	EST HUMAN	EST700527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2569	7670	12926	1.21	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C025
1887	7007	12227	1.7	4.0E-40	AI688005.1	EST HUMAN	ts1801_x1 NCI CGAP_Pz28 Homo sapiens cDNA clone IMAGE2248873 3' similar to TR:Q73505 O73505 POL PROTEIN; X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2059	7214		2.31	4.0E-40	AF0036528.1	NT	Homo sapiens KIAA0433 protein (KIAA0433) mRNA
4367	8488	14632	8.7	4.0E-40	7682117	NT	Homo sapiens wh1207_x1 NCI CGAP_Kd11 Homo sapiens cDNA clone IMAGE2380548 3'
4103	9232	14369	0.9	3.0E-40	AI620949.1	EST HUMAN	XP_521008_x1 Scarcosin testis_NHT Homo sapiens cDNA clone IMAGE1838647 3'
323	6508		5.16	2.0E-40	AI223038.1	EST HUMAN	XP_24610_x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE2761098 3' similar to SWRS5_MOUSE
795	5649		20.8	2.0E-40	AW303868.1	EST HUMAN	P97461 40S RIBOSOMAL PROTEIN S5;
1838	6559		1.06	2.0E-40	AV731601.1	EST HUMAN	AV731601 HTF-Homo sapiens cDNA clone HTFAZE06 5'
1838	7067	12278	4.87	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type 7 (PSMA7) mRNA, and translated products
1838	7057	12279	4.87	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type 7 (PSMA7) mRNA, and translated products
2150	7263	12511	1.89	2.0E-40	5453592	NT	Homo sapiens aryl/Myb cyclase-associated protein 2 (CCAP2) mRNA
2651	7749		1.69	2.0E-40	BB276932.1	EST HUMAN	601121567F1 NIH_3T3 mRNA clone IMAGE3346784 5'
3103	8256	13407	4.43	2.0E-40	9453392	NT	Homo sapiens aryl/Myb cyclase-associated protein 2 (CCAP2) mRNA
4874	8885	16132	1.41	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C025
4874	8885	15133	1.41	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C025

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**Table 4**  
**Single Exon Probes Expressed in BT474 Cells**

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
884	6034			28.04	1.0E-40 AA225889.1	EST_HUMAN	nc0969.1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:1007608
2583	7587	12842	5.11	1.0E-40 BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3863803 5'	
2647	7748			1.35	1.0E-40 BE018348.1	EST_HUMAN	bb78a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TRQ8Z76 Q8Z168
2659	7785	13045	1.07	1.0E-40 BF641030.1	EST_HUMAN	SYNTAXIN 17 :	
2699	7786	13046	1.07	1.0E-40 BF641030.1	EST_HUMAN	602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067738 5'	
3289	8429			1.29	1.0E-40	4507142 NT	Homo sapiens sorting neprin 3 (SNX3) mRNA
4582	8700	14838	6.49	1.0E-40	4508012 NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products	
3782	8919	14070	0.6	9.0E-41 W01586.1	EST_HUMAN	za38a02.h1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:2946502 5'	
829	7922	11148	1.72	7.0E-41 A1924384.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463898 3'	
829	7922	11149	1.72	7.0E-41 A1924384.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'	
4627	9745	14889	1.16	7.0E-41 BE39592.1	EST_HUMAN	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3803965 5'	
4627	9745	14890	1.16	7.0E-41 BE39592.1	EST_HUMAN	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3803966 5'	
278	5487	10610	2.24	6.0E-41 AB037163.1	NT	Homo sapiens Down syndrome candidate region 1(DSCR1), mRNA	
2101	7216	12463	1.5	6.0E-41	7857042 NT	yc03e10.s1 Strategic lung (#837210) Homo sapiens cDNA clone IMAGE:786226 3'	
1814	8937	12139	1.12	5.0E-41 TG2628.1	EST_HUMAN	Homo sapiens target of myb 1 (chicken) homolog (TOM1), mRNA	
4083	9212	1077	5.0E-41	48858361 NT			
399	5659	1.74	4.0E-41 BE195318.1	EST_HUMAN	QV0-LTT0367-150200-114-009 HT0367 Homo sapiens cDNA		
1089	6237	11400	1.23	4.0E-41 AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005683 5'	EST_HUMAN	AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005683 5'	
1447	6544	11723	8.1	4.0E-41 A1027117.1	EST_HUMAN	ow4960.51 Soares_pariathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1049784 3' similar to TR:000537 O00537 CYTOCHROME C-LIKE POLYPEPTIDE. ;contains LTR5.b1 LTR5 repetitive element;	
1417	6544	11724	8.1	4.0E-41 A1027117.1	EST_HUMAN	ow4560.6.1 Soares_pariathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1049784 3' similar to TR:000537 O00537 CYTOCHROME C-LIKE POLYPEPTIDE. ;contains LTR5.b1 LTR5 repetitive element;	
1432	8559	11742	1.48	4.0E-41 AB006881.1	NT	Im86c04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to OFR.b1	
1648	8774	11963	4.24	4.0E-41 A1500408.1	EST_HUMAN	OFR repetitive element;	
2855	8010	13171	3.4	4.0E-41 A1228041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3	
2855	8010	13172	3.4	4.0E-41 A1228041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3	
4115	9243	14979	1.67	4.0E-41 X072835.1	NT	H. sapiens DNase I hypersensitive site (HSS-3) enhancer element	
848	8696	11284	1.63	3.0E-41 AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidearginine deiminase type II, complete cds	
4311	9453	14658	2.53	3.0E-41 AB026889.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)	

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5090 10190			1.14	3.0E-41	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1837 6704	11894		30.23	2.0E-41	AA3701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1862 7079	12363		1.48	2.0E-41	AA331840.1	EST_HUMAN	EST35318 Embryo, 8 week Homo sapiens cDNA 5' end
2201 7913	12565	2.66	2.0E-41	D8892.1	NT	Human mRNA for KIAA0207 gene, complete cds	
2248 7958	12615	6.13	2.0E-41	X89531.1	NT	Gorilla DNA for ZNF580 gene homolog	
2788 .6704	11884		12.68	2.0E-41	AA3701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3816 88552	14100	0.81	2.0E-41	6032108	NT	Homo sapiens son of sevenless (Drosophila) homolog 1 (SOS1) mRNA	
4691 8709	14847	1.07	2.0E-41	AL163287.2	NT	Homo sapiens dihydrotansine 21 segment HS21 C037	
4591 9709	14848	1.07	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21 C037	
3180 8341	13503	1.03	1.0E-41	BE869735.1	EST_HUMAN	6011445647 F1 NIH_3T3 cDNA clone IMAGE:3849803 5'	
3180 8341	13504	1.03	1.0E-41	BE869735.1	EST_HUMAN	6011445647 F1 NIH_3T3 cDNA clone IMAGE:3849803 5'	
4539 9857	14801	12.01	1.0E-41	6878168	NT	Mus musculus tubulin alpha 8 (Tub8), mRNA	
462 66320	10769	4.87	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDXA) gene, complete cds and flanking repeat regions	
5131 10231	15368	0.67	8.0E-42	6878031	NT	Mus musculus neural precursor cell expressed, developmentally down-regulated gene 1 (Nedd1), mRNA	
853 6081		2.26	7.0E-42	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21 C035	
1887 6887	12209	2.26	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p44K230) mRNA, complete cds	
1887 6887	12210	2.26	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p44K230) mRNA, complete cds	
2286 7376		1.62	6.0E-42	AW238656.1	EST_HUMAN	xp22f8.x1 NCI CGAP_HN10_Homo sapiens cDNA clone IMAGE:271789 3 similar to contains L1,M1,L1 repetitive element;	
4891 10097		1.61	6.0E-42	AI284770.1	EST_HUMAN	qu24n09.x1 NCI CGAP_Br12_Homo sapiens cDNA clone IMAGE:1885761 similar to contains ALu repetitive element;	
131 6229		5.3	5.0E-42	AI271735.1	NT	Homo sapiens Xq1 pseudautosomal region; segment 1/2	
497 66068	10760	1.3	6.0E-42	BE217813.1	EST_HUMAN	h31e11.x1 NCI CGAP_Lu24_Homo sapiens cDNA clone IMAGE:3175052 3'	
486 6654		4.28	5.0E-42	5730038	NT	Homo sapiens SET domain and matrix transposase fusion gene (SETMAR) mRNA	
487 6655		2.43	6.0E-42	6730039	NT	Homo sapiens SET domain and matrix transposase fusion gene (SETMAR) mRNA	
762 59008	11084	2.41	4.0E-42	AF055068.1	NT	Homo sapiens MHC class 1 region	
752 59008	11085	2.41	4.0E-42	AF055068.1	NT	Homo sapiens MHC class 1 region	
1087 - 6207	11370	2.48	4.0E-42	AF188011.1	NT	Homo sapiens ribonuclease III (RNase) mRNA, complete cds	
4168 9292	14430	1.58	4.0E-42	X69417.1	NT	H_sapiens PROB-27 mRNA	
4205 8830	14463	0.97	4.0E-42	AI2468219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	
4227 8852	14483	4.48	4.0E-42	4508498	NT	Homo sapiens regulatory factor X-4 (Influences HLA class II expression) (RFX4) mRNA	
4857 8876	14813	11.81	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA	
1483 8820	11810	1.94	2.0E-42	BF378834.1	EST_HUMAN	RCO-TN0078-110803-024-B07 TN0078 Homo sapiens cDNA	

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2389	7495		2.16	2.0E-42	AW898344.1	EST_HUMAN	RC3-ANN0070-2704000-011-h10 Homo sapiens cDNA 2819293 3'
2402	7608	12767	13.69	2.0E-42	AW260059.1	EST_HUMAN	RC3-ANN0070-2704000-011-h10 Homo sapiens cDNA clone IMAGE:2819293 3'
732	6887	11039	2.53	1.0E-42	X5147.1	NT	Human endogenous retrovirus pHE-1 (ERV)
1044	8185	11382	0.99	1.0E-42	AW288609.1	EST_HUMAN	U1-H-B11-est-04-04-U1-s1 NCI CGAP Sub Homo sapiens cDNA clone IMAGE:2721871 3'
1102	6240	11403	1.05	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1102	6240	11404	1.05	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1246	7812	11654	10.38	1.0E-42	AF087168.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGQG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1246	7812	11655	10.38	1.0E-42	AF087168.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGQG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1715	82045	12042	0.95	1.0E-42	11423219	NT	Homo sapiens reo (LOC51201), mRNA
2026	742	12982	1.17	1.0E-42	AF110298.1	NT	Homo sapiens PDNIP1 gene, exon 17
2816	7619	12987	1.01	1.0E-42	617468	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2833	80837	13254	5.88	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 6 (yeast homolog)-like (ORC6) mRNA, and translated products
3686	88265	13980	2.3	1.0E-42	76820277	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3772	8909	14082	0.83	1.0E-42	5031610	NT	Homo sapiens Gdgl vesicular membrane trafficking protein p18 (BET1) mRNA
3800	6038	14186	1.09	1.0E-42	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4225	9350	14483	1.57	1.0E-42	AL163289.2	NT	Homo sapiens chromosome 21 segment HS21C080
4560	8684	14823	0.98	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0187-161089-a03 ST0187 Homo sapiens cDNA
4711	8827	14970	2.01	1.0E-42	8803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4711	8827	14971	2.01	1.0E-42	8803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4748	9859	15008	4.99	1.0E-42	4508758	NT	Homo sapiens ryandine receptor 3 (RYR3) mRNA
4842	8854	16099	1.01	1.0E-42	AB083114.1	NT	Homo sapiens mRNA for KIAA1288 protein, partial cds
651	5812	10947	18.09	8.0E-43	AV738624.1	EST_HUMAN	AV738624 CB Homo sapiens cDNA clone CB1AH108 5'
651	6812	10948	18.09	8.0E-43	AV738624.1	EST_HUMAN	AV738624 CB Homo sapiens cDNA clone CB1AH108 5'
693	5855	11030	6.14	8.0E-43	8823276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
693	6855	11001	6.14	8.0E-43	8823276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
693	6855	11002	6.14	8.0E-43	8823276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
3619	8758	13914	6.92	7.0E-43	AW246442.1	EST_HUMAN	2822251 5prime NIH NCC 7 Homo sapiens cDNA clone IMAGE:2822251 5'
1349	6478		32.87	6.0E-43	AA481890.1	EST_HUMAN	res72d06_s1 NCI CGAP_Ew1 Homo sapiens cDNA similar to gbr:050686 60S
2554	7857		2.04	8.0E-43	AV708201.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN);
138	6358		1.73	6.0E-43	AL163213.2	NT	AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'
							Homo sapiens chromosome 21 segment HS21C013

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
502	5669	10803	2.63	5.0E-43	AA362780.1	EST_HUMAN	ESTB6033 Testis   Homo sapiens cDNA clone HITFANCO85'
2809	7886	13126	1.81	6.0E-43	AV732578.1	EST_HUMAN	Homo sapiens X-linked arthritochalcin dysplasia protein gene (EDA), exon 2 and flanking repeat regions
974	7887	11280	12.54	4.0E-43	AF003528.1	NT	Homo sapiens calcium channel epsilon1E subunit (CACNA1E) gene, exons 7-9, and partial cds, alternatively spliced
1218	6348		3.61	3.0E-43	AF222391.1	NT	Homo sapiens genes encoding La autoantigen
1708	6236	12037	4.39	3.0E-43	AB7889.1	NT	ANL1-EV1-4AML1-EV1 fusion protein [rearranged translocation] [human, leukemic cell line SK-1, mRNA Mutant, 6398 nt]
3558	8699	19859	1.14	3.0E-43	SE8902.1	EST_HUMAN	mk65d08.1  NCI_C3AP_P7 Homo sapiens cDNA clone IMAGE:1017418 q61tca9.x1 Soares...testis_NIH_Homo sapiens cDNA clone IMAGE:1733568 3 similar to contains PTR7.13
4258	8391	14529	0.77	3.0E-43	AA348154.1	EST_HUMAN	PTR7 PTR7 repetitive element; Homo sapiens Rat-like GTP-binding protein (RAB27A) gene, exons 1b and 2
179	5373		9.84	2.0E-43	AI190764.1	EST_HUMAN	Homo sapiens Rat-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1682	6780	11886	2.89	1.0E-43	AF154838.1	EST_HUMAN	Homo sapiens Rat-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1682	6780	11889	2.63	1.0E-43	AF154836.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
1720	6847	12051	1.05	1.0E-43	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2638	7783	13031	6.01	1.0E-43	BFS4B2B3.1	EST_HUMAN	602022313F1  NCI_C3AP_Bm67 Homo sapiens cDNA clone IMAGE:4167686 5'
891	6041	11212	4.32	8.0E-44	AI222855.1	EST_HUMAN	qh238p01x1 Soares cDNA clone IMAGE:1B45532 3'
891	6041	11213	4.32	8.0E-44	AI222855.1	EST_HUMAN	qh238p01x1 Soares cDNA clone IMAGE:1B45532 3'
4849	8656	16100	1.08	8.0E-44	AW373185.1	EST_HUMAN	RCE-BT0503-081/289-011-912 BT0503 Homo sapiens cDNA RCE-BT0503-081/289-011-912 BT0503 Homo sapiens cDNA
4849	8655	15101	1.03	8.0E-44	AW373185.1	EST_HUMAN	yes6e01x1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:124920 5'
6583	5219		1.87	7.0E-44	RD0035.1	EST_HUMAN	yes6e01x1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:124920 5'
2215	7327	12579	1.12	7.0E-44	5031988	NT	Homo sapiens LIM domain-containing protein 6 translocation partner in lipoma (LPP) mRNA
2835	8089	13255	2.28	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2835	8089	13256	2.28	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3841	8977	14132	2.47	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4220	8846	14476	0.89	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
5107	10208	15345	0.81	7.0E-44	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
301	5489		3.01	6.0E-44	AF288880.1	NT	Homo sapiens KIAA0085.1 gene (partial), X73 gene and LZTF1 gene
330	5513		2.52	5.0E-44	AF288880.1	NT	Homo sapiens KIAA0085.1 gene (partial), X73 gene and LZTF1 gene
3396	8540	13689	3.05	4.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
5002	10107		1.11	4.0E-44	AF45225.1	EST_HUMAN	tt11d02/x1 NCI_C3AP_Pani Homo sapiens cDNA clone IMAGE:2130147 3'
1788	6821		1.25	3.0E-44	6912477	NT	Homo sapiens kerophterin alpha 6 (imprinting alpha 7) (KPN48), mRNA
2503	7606	12856	2.91	3.0E-44	BE880028.1	EST_HUMAN	6011461629F1 NIH_M/GC_69 Homo sapiens cDNA clone IMAGE:3833839 5'

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Table 4

Single Exon Probes Expressed In BT474 Cells

Probe seq ID No.	Exon seq ID No.	ORF seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3071	8224	13375	5.79	3.0E-44	AA168851.1	EST_HUMAN	2p18q5.11 Strategene fetal retina cDNA clone IMAGE:309777 6'
3857	9003	14161	1.29	3.0E-44	AA337234.1	EST_HUMAN	EST42299 Endometrial tumor Homo sapiens cDNA 5' end similar to alpha-1-mitotrophin F
1051	8182	11359	2.89	2.0E-44	4826685 NT	Homo sapiens DEAH(H(Acp-Glu-Ala-Asp)H) box polypeptide 1 (DDX1) mRNA	
1051	6192	11357	2.89	2.0E-44	4826685 NT	Homo sapiens DEAH(H(Acp-Glu-Ala-Asp)H) box polypeptide 1 (DDX1) mRNA	
1210	6342	11512	5.87	2.0E-44	5803200 NT	Homo sapiens transmembrane trafficking protein (TMF21), mRNA	
1210	6342	11513	5.87	2.0E-44	5803200 NT	Homo sapiens transmembrane trafficking protein (TMF21), mRNA	
1316	6445	11624	4.08	2.0E-44	AF133588.1	NT	Homo sapiens RAB36 (RAB36) mRNA, complete cds
1378	6608	11687	1.42	2.0E-44	BE465325.1	EST_HUMAN	Iwai4006.xt NCI_OCAF_Lu24 Homo sapiens cDNA clone IMAGE:3182838 3' similar to SW.OXYB_HUMAN
2138	7250	12498	4.42	2.0E-44	AF070851.1	NT	P22039 OXYSTEROL-BINDING PROTEIN :
2574	7674	7792	5.82	2.0E-44	5801833 NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (GLAPS4), mRNA	
3452	8594	13758	1.69	2.0E-44	DS7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4542	9610	14803	1.43	2.0E-44	AW684378.1	EST_HUMAN	PM-510018-12000-003-004 SNU0016 Homo sapiens cDNA
61	6263	10389	8.43	1.0E-44	7657334 NT	Homo sapiens Missheaven/NIK-related kinase (MINK), mRNA	
51	5263	10390	8.43	1.0E-44	7657334 NT	Homo sapiens Missheaven/NIK-related kinase (MINK), mRNA	
678	5741	10869	2.85	1.0E-44	AV853132.1	EST_HUMAN	RC1-0249-Q30340-026-H12 C70249 Homo sapiens cDNA
1200	6333		1.5	1.0E-44	AW684803.1	EST_HUMAN	RC1-510039-110300-012-001 BN0039 Homo sapiens cDNA
16386	6716		6.07	1.0E-44	AL168303.2	NT	Homo sapiens chromosome 21 centromere HS21C103
2208	7318	12588	2.63	1.0E-44	AA434544.1	EST_HUMAN	2w53c02.1 Scores total fetus Nb2HF8_Bw Homo sapiens cDNA clone IMAGE:773763 5' similar to contains TLR.13 TLR repetitive element ;
2208	7318	12589	2.63	1.0E-44	AA434545.1	EST_HUMAN	2w53c02.1 Scores total fetus Nb2HF8_Bw Homo sapiens cDNA clone IMAGE:773763 5' similar to contains TLR.13 TLR repetitive element ;
2722	7917	13073	1.32	1.0E-44	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM5 protein, JM5 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha 2$
3706	8844		4.68	1.0E-44	AA465869.1	EST_HUMAN	est009_81 Scores NIHMPU_S1 Homo sapiens cDNA clone IMAGE:811684 3'
8085	10186	18333	0.9	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5085	10185	18334	0.9	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
4551	8669	14811	1.98	9.0E-45	8822391 NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA	
4651	8669	14812	1.68	8.0E-45	8822391 NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA	
2489	7000	12848	6.38	8.0E-45	5174718 NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA	
5069	10168	15302	7.57	8.0E-45	5174718 NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA	
2925	8079		1.04	7.0E-45	AL160131.1	NT	Novel human gene mapping to chromosome 22

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3951	9086		6.84	6.0E-45	AW157570.1	EST_HUMAN	eu8307.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782309 3' similar to SW:R13A_HUMAN P40428 60S RIBOSOMAL PROTEIN L13A;
893	6043		2.58	5.0E-45	AL1682265.2	NT	Homo sapiens chromosome 21 segment HS21_C013
2005	7120	12356	2.29	6.0E-45	BF335827.1	EST_HUMAN	CMA-CND044-18020-615-01 CND044 Homo sapiens cDNA clone IMAGE:2116463 3' similar to SW:PAK1_MOUSE
3184	8345	13509	2.30	6.0E-45	AI523766.1	EST_HUMAN	tg8407.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116463 3' similar to SW:PAK1_MOUSE
1146	6281	11446	8.31	4.0E-45	X05826.1	NT	P0384 PAIRED BOX PROTEIN PA-X-1.; H.sapiens ART4 gene
2228	7978	126227	3.65	4.0E-45	BF2856922.1	EST_HUMAN	601169440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3638426 5'
3312	8469		1.03	3.0E-45	T71480.1	EST_HUMAN	y33507.x1 Soares fetal liver spleen 1NF13 Homo sapiens cDNA clone IMAGE:110245 6'
4084	8459		1.3	3.0E-45	T71480.1	EST_HUMAN	yd3567.x1 Soares fetal liver spleen 1NF13 Homo sapiens cDNA clone IMAGE:110245 6'
2472	7576		1.49	2.0E-45	AL168218.2	NT	Homo sapiens chromosome 21 segment HS21_C018
3004	8158	13315	1.89	2.0E-45	A1249213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
119	5578		1.71	1.0E-45	BF388855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608168 5'
408	6576		2.78	1.0E-45	BF388855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608168 5'
472	5639	10781	1.14	1.0E-45	45084112	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1176	6311	11479	1.44	1.0E-45	7657280	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3078	8232	13383	6.31	1.0E-45	U32168.1	NT	Human pro-α2 chain of collagen type XI (COL11A2) gene, complete cds
3473	8816	13782	0.87	1.0E-45	BB59558	NT	Human pro-α2 chain of collagen type XI (COL11A2) gene, complete cds
3560	8701	13861	0.72	1.0E-45	A504681.1	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
4453	8875	14714	4.73	1.0E-45	BE368833.1	EST_HUMAN	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3811803 5'
2419	7024	12778	25.33	8.0E-48	AI433261.1	EST_HUMAN	62308.x1 NCI_CGAP_Cat4 Homo sapiens cDNA clone IMAGE:2132169 3' similar to gb:J00314_mc2
2419	7624	12777	25.33	8.0E-48	AI433261.1	EST_HUMAN	t3208.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132169 3' similar to gb:J00314_mc2
2220	7392	12585	1.91	7.0E-46	U46007.1	NT	Radius nonretinal epithelial mRNA, complete cds
4553	8971		6.61	7.0E-46	BF3388165.1	EST_HUMAN	601227282F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3818119 5'
4775	8688		1.48	7.0E-46	BF084386.1	EST_HUMAN	RC4-BT0310-11030-016-410 BT0310 Homo sapiens cDNA clone IMAGE:2437876 3' similar to contains MER19.12
2718	7913	13063	3.3	6.0E-46	AI884381.1	EST_HUMAN	WT3108.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437576 3' similar to contains MER19.12
2718	7813	13069	3.3	6.0E-46	AI884381.1	EST_HUMAN	MER19 repetitive element;
201	5586		5.07	5.0E-46	AL168210.2	NT	Homo sapiens chromosome 21 segment HS21_C010
3515	8656	13822	1.28	5.0E-46	BE877194.1	EST_HUMAN	7681901.x1 Lupekl_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:32779408 3'
3516	8656	13823	1.28	6.0E-46	BE877194.1	EST_HUMAN	7681901.x1 Lupekl_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:32779408 3'

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe seq ID	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
640	5801		1.91	4.0E-43	AA601143.1	EST_HUMAN	nc04608_s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104620 3' similar to gb:X53741_ma1 FIBULIN-1, ISOFORM PRECURSOR (HUMAN);
1719	6840	12049	8.22	4.0E-45	AW770544.1	EST_HUMAN	hb8c03_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008838 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN) contains element MER7 repetitive element;
1719	6846	12050	8.22	4.0E-46	AW770544.1	EST_HUMAN	hb8c03_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008838 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN) contains element MER7 repetitive element;
2702	7788	13049	1.41	4.0E-48	M18048.1	NT	Human endogenous retrovirus RTVL-H2
5126	10226	16361	0.65	4.0E-48	BE04260.1	EST_HUMAN	hs42e07_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:304020_3'
5126	12226	16362	0.65	4.0E-48	BE04260.1	EST_HUMAN	hs42e07_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:304020_3'
2141	7255	12501	2.28	3.0E-46	54533620	NT	Homo sapiens solute carrier family 35 (GMP, static acid transporter), member 1 (SLC35A1), mRNA
2262	7372	12823	1.87	3.0E-48	7657263	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU1552), mRNA
2408	7512	12762	7.52	3.0E-46	AF160212.1	NT	Homo sapiens VAMP-associated 33 kDa protein mRNA, complete cds
4371	9492	14633	0.81	3.0E-46	4606378	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4742	8686	16002	1.38	3.0E-48	Z73630.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; V_lambda
4742	8685	15003	1.38	3.0E-46	Z73630.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; V_lambda
838	5580	11153	0.59	2.0E-46	AA408646.1	EST_HUMAN	nc04608_s1 NCI_CGAP_Qc3 Homo sapiens cDNA clone IMAGE:380408 3' similar to contains THR_b2 THR repetitive element;
1577	6106		1.15	2.0E-46	AA672246.1	EST_HUMAN	Z27a11.91 Soares_fetal_liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:421880_3'
1652	8780	11872	2.98	2.0E-48	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-selectosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
4959	10087	15204	1.07	2.0E-46	AA439228B.1	EST_HUMAN	z589e02_z1 Soares_jefts_NHT Homo sapiens cDNA clone IMAGE:7268650 5' similar to SW:RSP_MOUSE_Q01730_RSP-1 PROTEIN;
1236	6868	11639	4.98	1.0E-48	4502684	NT	Hom sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2258	7988	12824	2.78	1.0E-48	AW978516.1	EST_HUMAN	EST380825 MAGE sequences, MAGE Hom sapiens cDNA
2377	7483	12737	2.33	1.0E-46	H97330.1	EST_HUMAN	EST480865 WATM1 Homo sapiens cDNA clone AB20805
3232	8882	18642	1.72	1.0E-46	AA631812.1	EST_HUMAN	np78e02_s1 NCI_CGAP_Pc2 Homo sapiens cDNA clone IMAGE:1132386 similar to gb:X76717 H. sapiens MT-11 mRNA, (HUMAN);
4844	8986		3.11	1.0E-48	AB023197.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
788	5920		3.32	9.0E-47	AJ27735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4810	10220	16185	3.19	8.0E-47	AW770828.1	EST_HUMAN	HG3004_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:30008534 3' similar to TR:076703 O75703
1820	6943	12161	11.91	8.0E-47	Y16538.1	NT	Homo sapiens HLA-C gene; exon 5; Individual 18323
1820	6943	12162	11.91	8.0E-47	Y16538.1	NT	Homo sapiens HLA-C gene; exon 5; Individual 18323
2678	7775	13028	1.41	8.0E-47	6433855_NT	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B68), epsilon isoform (PPP2R5E) mRNA
2896	8161	13312	1.6	8.0E-47	AJ223043.1	NT	Homo sapiens 959 kb config between AML1 and CBF1 on chromosome 21q22, segment 3/3
3806	8745	13890	0.76	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
3806	8745	13891	0.75	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
2619	7623	12889	1.27	8.0E-47	AL163246.2	NT	Homo sapiens chromosomes 21 segment HS21C048
1407	6334	11713	3.52	4.0E-47	EF575596_NT	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
643	5709	10844	8.98	3.0E-47	BE007634.1	EST_HUMAN	601497630F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3886721 5'
643	5709	10845	8.99	3.0E-47	BE007634.1	EST_HUMAN	601497630F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3886721 6'
8119	5972	11134	3.04	3.0E-47	N57483.1	EST_HUMAN	yyf4804.61 Scores: multiple, scattered. 2N6HMSP Homo sapiens cDNA clone IMAGE:277327 3'
845	6898	11261	7.87	3.0E-47	AL163284.2	NT	Homo sapiens chromosomes 21 segment HS21C034
2023	7140	12380	4.73	3.0E-47	AB007689.1	NT	Homo sapiens KIAA0439 mRNA, partial cds
3285	8434	13586	0.76	3.0E-47	4504116_NT	NT	Homo sapiens glutamate receptor, ionotropic, Kainate 1 (GRIK1) mRNA
3839	8076	478	4.78	3.0E-47	UB3181.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
4240	9462	14589	1.92	3.0E-47	MT12559.1	NT	Human T-cell receptor active alpha-chain mRNA from J4 cell line, complete cds
143	5940	10484	1.27	2.0E-47	45045318_NT	NT	Homo sapiens myosin phosphatase, targeted subunit 2 (MYPFT2) mRNA
869	6116	11284	2.44	2.0E-47	AL163209.2	NT	Homo sapiens chromosomes 21 segment HS21C009
969	6116	11285	2.44	2.0E-47	AL163209.2	NT	Homo sapiens chromosomes 21 segment HS21C009
1608	6734	11927	3.51	2.0E-47	7682109_NT	NT	Homo sapiens KIAA0428 gene product (KIAA0428) mRNA
1891	6820	12019	3.36	2.0E-47	AA524514.1	EST_HUMAN	ng43h12_s1 NCI_CGAP_Ce3 Homo sapiens cDNA clone IMAGE:837607 3'
4324	8448	14578	1.79	2.0E-47	4504888_NT	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8) mRNA
4363	9485	14826	1.94	2.0E-47	AA568592.1	EST_HUMAN	nt23g07_s1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:914852
4363	9485	14827	1.64	2.0E-47	AA568592.1	EST_HUMAN	nt23g07_s1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:914852
4483	8602	14741	1.72	2.0E-47	5174848_NT	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4781	8684	15040	1.14	2.0E-47	AW868166.1	EST_HUMAN	EST377239 MAGE sequences, MAGI Homo sapiens cDNA
6181	10278	15416	1.01	2.0E-47	8055289_NT	NT	Homo sapiens low density lipoprotein receptor related protein-detected in tumor (LRPDT1) mRNA
1413	6540	11717	4.29	1.0E-47	AJ33429.1	EST_HUMAN	np89103_x1 Scores: fetal_lung_NbHL18W Homo sapiens cDNA clone IMAGE:1831168 3'
3800	8897	14083	0.98	1.0E-47	BE280477.1	EST_HUMAN	601165321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3800	8897	14084	0.98	1.0E-47	BE280477.1	EST_HUMAN	601165321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
6059	10161	15294	2.53	1.0E-47	AW813806.1	EST_HUMAN	RC3-ST0187-130-400-01-402-310/97 Homo sapiens cDNA

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar [Top] Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1625 6753	11943		2.36	9.0E-48	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
1254 6384			1.3	8.0E-49	4501900	NT	Homo sapiens amine oxidase 1 (ACY1), mRNA
1286 6384			1.17	8.0E-49	4501900	NT	Homo sapiens amine oxidase 1 (ACY1), mRNA
3113 8265	13421		3.72	8.0E-48	AW788477.1	EST_HUMAN	In6tbs_x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:30011133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN); In6tbs_x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:30011133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
3113 8268	13422		3.72	8.0E-48	AW788477.1	EST_HUMAN	In6tbs_x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:30011133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
490 5658			1.47	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA208 protein, partial cds
491 5658			12.54	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA208 protein, partial cds
1511 6838	11825		1.42	7.0E-48	6912719	NT	Homo sapiens tau-like kinase 1 (TLK1), mRNA
1848 9770	11983		6.89	7.0E-48	5730038	NT	Homo sapiens SET domain and matrix transposase fusion gene (SETMAR) mRNA
3534 8725	13883	0.93	6.0E-48	AI781111.1	EST_HUMAN	webtbs_x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2388613 3'	
3291 10305	13600	1.62	6.0E-48	4828891	NT	Homo sapiens phosphodiesterases 1A, calmodulin-dependent (PDE1A) mRNA	
1878 7095	12326		35.4	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXorf6) mRNA
1878 7095	12326		35.4	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXorf6) mRNA
3611 8750	13907	0.7	3.0E-48	AW684531.1	EST_HUMAN	In14612_x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2372265 3' similar to SW10CRE_HUMAN P68565 DOWN SYNDROME CRITICAL REGION PROTEIN B.;	
44 5256	10377	2.62	2.0E-48	AA631940.1	EST_HUMAN	fmitb7 Regional genomic DNA specific cDNA library/Homo sapiens cDNA clone CR17-28	
4506 8625	14768	1.11	2.0E-48	BEC246066.1	EST_HUMAN	TCBAP1D38:42 Pediatric pre-B cell acute lymphoblastic leukemia Bay/Ho-HGSC project-TCBAP1D38:42	
5188 10298	15433	0.87	2.0E-48	NE57147.1	NT	Homo sapiens endogenous retrovirus pHE-1 (ERV9)	
65 6268	10394	11.65	1.0E-48	7708534	NT	Homo sapiens chaperlin resistance-associated overexpressed protein (LOC51747), mRNA	
874 6025	11163	8.27	1.0E-48	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-1, Alzheimer disease) (APP), mRNA	
1077 6217	11381	2.49	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA	
1077 6217	11382	2.48	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA	
1300 6430	11604	4.11	1.0E-48	6032032	NT	Homo sapiens RNA binding motif protein 8 (RBM8) mRNA	
1821 7040	12261	39.39	1.0E-48	AL1683302_2	NT	Homo sapiens chromosome 21 segment HS21C102	
3469 8811	13777	0.91	1.0E-48	AL1683246_2	NT	Homo sapiens chromosome 21 segment HS21C048	
6113 10214	18351	1.22	1.0E-48	M10678.1	NT	Human endogenous retroviral DNA (4-1) complete retroviral segment	
2207 7124	12360	1.23	8.0E-49	AB26497.1	NT	Mus musculus MyoD2 mRNA for myostatin containing PDZ domain, complete cds	
1335 5661	10704	2.55	7.0E-49	5728980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA	
1335 5661	10705	2.65	7.0E-49	5728980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA	

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Table 4

Single Exon Probes Expressed In BT474 Cells

Probe seq ID No:	Exon seq ID No:	ORF seq ID No:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
392	5581	10704	1.66	7.0E-49	5728890	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
392	5581	10705	1.58	7.0E-49	5728890	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
393	5581	10704	2.3	7.0E-49	5728890	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
393	5581	10705	2.3	7.0E-49	5728890	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1223	6355	11625	4.13	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C034
194	5389	10532	71.58	8.0E-49	AW781740.1	EST_HUMAN	RIBOSOMAL PROTEIN S4 (HUMAN); gpM20582 Mouse LRP2 protein mRNA from a repetitive element, complete (MOUSE);
1385	6494	11676	1.28	8.0E-49	BF038269.1	EST_HUMAN	6014587738F1 NIH_3T3
1385	6494	11678	1.26	8.0E-49	BF038269.1	EST_HUMAN	MAGE-3881272 5'
710	5897	11013	7.34	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
710	5897	11014	7.34	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1806	6830	12146	2.24	5.0E-49	AA172121.1	EST_HUMAN	#28e07.1 Strategene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610860 5' similar to complete LTR7.23 LTR7 repetitive element;
2713	7808	13062	7.74	5.0E-49	U17714.1	NT	TR:G233226 G233226 RTVL-H PROTEIN; contains LTR7.23 LTR7 repetitive element; Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
3258	8408	13567	8.38	5.0E-49	11438355	NT	Homo sapiens similar to ribosomal protein S27 (metallopanthenolipin 1) (H. sapiens) (LOC33362), mRNA
623	5689	10820	23.9	4.0E-49	AW189533.1	EST_HUMAN	x08b01.1x NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:28755983 3' similar to WP:BG0350_2B
559	5724	10855	3.83	3.0E-49	X688698.1	NT	H.sapiens mRNA for acetyl-CoA carboxylase zc31c03.1 Severe retina N2b-4fR Homo sapiens cDNA clone IMAGE:3605894 5' similar to contains L1.13 L1 repetitive element;
2609	7708		1.11	3.0E-49	AA016131.1	EST_HUMAN	Human type IV collagen (COL4A8) gene, exon 40
4888	10078	16214	2.28	3.0E-49	U46899.1	NT	EST_HUMAN
650	5821		1.55	2.0E-49	BE165980.1	EST_HUMAN	MIR3-T0487-15020-113-901 HT0487 Homo sapiens cDNA
3207	8358	13519	1.73	2.0E-49	N28448.1	EST_HUMAN	yc23d08.1 Severe melanocyte 2NbmH Homo sapiens cDNA clone IMAGE:262371 5'
3556	8897	13857	0.65	2.0E-49	Af028564.1	NT	Homo sapiens RNA binding protein II (RBMI) gene, complete cds
800	6050		9.92	1.0E-49	BF053327.1	EST_HUMAN	601488631F1 NIH_3T3
1568	6693	11883	30.88	1.0E-49	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1813	6538	12152	3.89	1.0E-49	BE256216.1	EST_HUMAN	6011115769F1 NIH_3T3
4989	10088		1.57	9.0E-50	AF01476.1	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
168	6361	10501	3.43	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
711	5874	11021	1.6	8.0E-50	X65097.2	NT	Homo sapiens mRNA for VIP receptor 2
711	6574	11022	1.6	8.0E-50	X65097.2	NT	Homo sapiens mRNA for VIP receptor 2

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 Table 4  
 Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1034	6175			1.65	8.0E-60	AF000573.1	NT
1774	6900	12108	3.91	8.0E-50	4501830	NT	Homo sapiens homogenate 1,2-dioxogenase gene, complete cds
2465	7669	12310	1.94	8.0E-50	7708334	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2455	75559	12811	1.91	8.0E-50	7708334	NT	Homo sapiens p47 (LOC51874) mRNA
2600	7750	13007	3.04	8.0E-50	4826858	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
616	6776	10907	2.59	7.0E-50	BE088591.1	EST_HUMAN	Q9G-BT0703-280400-211-608 BT0703 Homo sapiens cDNA OV1-BT0881-280400-181-902 BT0703 Homo sapiens cDNA
6191	10288	18424	0.62	7.0E-50	BE087807.1	EST_HUMAN	QV1-BT0881-280400-181-902 BT0703 Homo sapiens cDNA
8191	10288	15425	0.62	7.0E-50	BE087807.1	EST_HUMAN	QV1-BT0881-280400-181-902 BT0703 Homo sapiens cDNA
4320	8442		0.73	8.0E-60	BE794381.1	EST_HUMAN	601588563SF1 NIH IMGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
1805	6928	12143	1.98	8.0E-60	BF582889.1	EST_HUMAN	CM10-BT0792-300500-388-b056 BT0792 Homo sapiens cDNA
1805	6928	12144	1.98	8.0E-60	BF582889.1	EST_HUMAN	CM10-BT0792-300500-388-b056 BT0792 Homo sapiens cDNA
917	6068		2.42	4.0E-50	AA501143.1	EST_HUMAN	nc544608_s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_m1
3430	8572	13172	0.98	4.0E-50	AL163248.2	NT	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN); Homo sapiens chromosome 21 segment HS21-C048
1842	7031		2.01	3.0E-50	MI16048.1	NT	Human endogenous retrovirus RTNL-H2
2489	7693	12841	1.4	3.0E-50	BE259188.1	EST_HUMAN	6011605717F1 NIH IMGC_16 Homo sapiens cDNA clone IMAGE:3360309 5'
3281	8430	13692	0.83	3.0E-50	AA746142.1	EST_HUMAN	6003106_s1 NCI CGAP_X63 Homo sapiens cDNA clone IMAGE:1922627 3'
778	6932		5.43	2.0E-50	AF055088.1	NT	Homo sapiens MHC class I region
1081	6220	11388	5.34	2.0E-50	45637752	NT	Homo sapiens midline 1 (OphTB2B syndrome) (MID1) mRNA
1454	6881	11770	1.39	2.0E-50	AF138303.1	NT	Homo sapiens deoxyn D mRNA, complete cds, alternatively spliced
3271	8420	13581	1.06	2.0E-50	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II genes, complete cds; and unknown genes
4234	8358	14491	0.68	2.0E-50	D86424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
4849	9861	16105	1.18	2.0E-50	AW869169.1	EST_HUMAN	MR3-NSN0068-040500-008-f01 SNT0068 Homo sapiens cDNA
4849	8981	16108	1.18	2.0E-50	AW869169.1	EST_HUMAN	MR3-NSN0068-040500-008-f01 SNT0068 Homo sapiens cDNA
481	5628	10768	1.92	1.0E-50	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21-C009
2345	7452		4.95	1.0E-50	AJ271735.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 12
3266	8416	13577	1.42	7.0E-51	AW888218.1	EST_HUMAN	np:88869_s1 NCI CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12671_m1
4840	8638	14802	6.31	8.0E-61	AA810842.1	EST_HUMAN	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); XN3463.X1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2885564 3' similar to TR:Q8Z340
2988	8143	13305	0.7	7.0E-61	AW274720.1	EST_HUMAN	Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
							QV4-NT0928-200400-180-d08 NT0928 Homo sapiens cDNA
							XN3463.X1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2885564 3' similar to TR:Q8Z340
							Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
							DKFZp434B2229_J1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2229 5'

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## Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4138	62658	14406	1.01	7.0E-51	AL078828.1	EST_HUMAN	DKFZp634B2229 nt 434 (synonym: hhs3) Homo sapiens cDNA clone IMAGE:27288173'
4323	9450	14583	1.33	7.0E-51	AV295603.1	EST_HUMAN	U1+BW0-adj-b-0-U1.s1 NCI CGAP_Subs Hom sapiens cDNA clone IMAGE:27288173'
1542	68770	11856	1.02	6.0E-51	6878783	NT	Homo sapiens putative DNA binding protein (MBP), mRNA
1881	7098	12329	3.03	8.0E-51	7857286	NT	Homo sapiens KIAA0828 protein Max2 interacting nuclear target (MINT) homolog (KIAA0828), mRNA
3455	8897	13761	13.38	6.0E-51	7857286	NT	Homo sapiens KIAA0828 protein Max2 interacting nuclear target (MINT) homolog (KIAA0828), mRNA
782	6949	11109	6.83	6.0E-51	AL1632038.2	NT	Homo sapiens chromosome 21 segment HS21_0003
894	5957	11120	1.73	5.0E-51	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
892	7806	11307	1.03	5.0E-51	AL133204.1	NT	Newer human gene mapping to chromosome X
1621	6749	11943	2.16	5.0E-51	5031880	NT	Homo sapiens p285 proto-oncogene-associated paf1 homolog (POH1) mRNA
2555	7853	12898	5	5.0E-51	AL007556.1	NT	Homo sapiens mRNA for nucleophosmin 155
3916	9052	14211	1.63	6.0E-51	MS09898.1	NT	Human Ku (p70) mRNA, complete cds
3918	9052	14212	1.63	6.0E-51	MS09898.1	NT	Human Ku (p70) mRNA, complete cds
5054	10158	15287	1.44	5.0E-51	AB0317832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds tr81059_x1 NCI CGAP_Pari Homo sapiens cDNA clone IMAGE:2224720 3' similar to g:MM26328
130	5328	10474	57.38	3.0E-51	AL567348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN); tr81068_x1 NCI CGAP_Pari Homo sapiens cDNA clone IMAGE:2224720 3' similar to g:MM26328
1173	6313	11481	185.78	3.0E-51	AL567348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
4303	9425	14580	1.89	3.0E-51	AL159142.1	NT	Newer human gene mapping to chromosome 22
384	5844	10885	6.18	2.0E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
638	5844	10983	2.35	-2.0E-51	BE391063.1	EST_HUMAN	601285564F NIH MG-44 Homo sapiens cDNA clone IMAGE:3607463 5'
686	5844	10884	2.36	2.0E-51	BE391063.1	EST_HUMAN	601285564F NIH MG-44 Homo sapiens cDNA clone IMAGE:3607463 5'
1702	6830	12032	4.18	2.0E-51	AA233352.1	EST_HUMAN	zg30a05_r1 Strategene NT2 neuronal precursor 8317230 Homo sapiens cDNA clone IMAGE:684880 5' similar to TR_G233226_62333226 RTV-H PROTEIN, 3'ntars LTR?3 LTR? repetitive element;
3714	6852	14006	2.49	2.0E-51	AA492446.1	EST_HUMAN	U27603_x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
4469	6888	14727	0.67	2.0E-51	AV137826.1	EST_HUMAN	U1+B11-adj-d-02-U1.s1 NCI CGAP_Subs Hom sapiens cDNA clone IMAGE:2716891 3'
110	5314	10453	27.83	1.0E-51	4803528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1509	6833	49.99	1.0E-51	AV742248.1	EST_HUMAN	AV742248_C8 Homo sapiens cDNA clone CBFBCC12.6'	
3168	6819	13481	1.41	1.0E-51	AF009894.1	NT	Homo sapiens ubiquitous TPR motif, Y isoform (UTY) mRNA, alternative transcript 3, complete cds
147	5344	10487	8.69	8.0E-52	AA1720574.1	EST_HUMAN	trw21602_s1 NCI CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.3
1510	6837	11824	1.7	8.0E-52	X84900.1	NT	H. sapiens mRNA for laminin-6, ephab3 chain

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1637	6785	11890	1.87	8.0E-52	11889028 NT		Homo sapiens hypothetical protein FLJ13558 similar to N-myc downstream regulated 3 (FLJ13558), mRNA
1867	6785	11891	1.87	8.0E-52	11889028 NT		Homo sapiens hypothetical protein FLJ13558 similar to N-myc downstream regulated 3 (FLJ13558), mRNA
3869	6785	11890	6.18	8.0E-52	11889028 NT		Homo sapiens hypothetical protein FLJ13558 similar to N-myc downstream regulated 3 (FLJ13558), mRNA
3969	6785	11891	8.18	8.0E-52	11889028 NT		Homo sapiens hypothetical protein FLJ13558 similar to N-myc downstream regulated 3 (FLJ13558), mRNA
1189	6323		1.38	8.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-27128s-049-d07 BT0537 Homo sapiens cDNA
1707	6835	12038	2.13	8.0E-52	AF109867.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4418	9538	14879	1.7	5.0E-52	Z78588.1	NT	H.sapiens flow-sorted chromosome 0 HindIII fragment. SC8pA18H7
1675	6804	11909	1.24	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1788	6923	12133	1.17	4.0E-52	47658843 NT		Homo sapiens nucleophosmin 155kD (NUP155), mRNA
3901	9037	14198	0.77	4.0E-52	4507500 NT		Homo sapiens T-cell lymphoma invasion and metastasis 1 (TAMM) mRNA
4068	9188		10.26	3.0E-52	11437042 NT		Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
681	6728	10856	3.35	2.0E-52	M10978.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
561	5723	10857	3.35	2.0E-52	M10978.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1768	6894	12101	1.78	2.0E-52	AB057898.1	NT	Homo sapiens KIAA0459 mRNA, partial cds
2470	7674	12827	4.79	2.0E-52	BE207575.1	EST_HUMAN	b686107_y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE3030421 5' similar to gBX16493 M.musculus mRNA for Zpf-1 zinc finger protein (MOUSE);
2698	7784		13.92	2.0E-52	BF077892.1	EST_HUMAN	602084710F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE4248891 5'
4082	10070	16208	4.19	2.0E-52	AL157198.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5000	10105	15235	1.13	2.0E-52	AI141802.1	EST_HUMAN	q86e05_s1 Searce_NIHMPU_S1 Homo sapiens cDNA clone IMAGE16801843
6000	10103	16238	1.13	2.0E-52	AI141802.1	EST_HUMAN	q86e05_s1 Searce_NIHMPU_S1 Homo sapiens cDNA clone IMAGE16807843
651	5697	10830	1.3	1.0E-52	AA634445.1	EST_HUMAN	ZU757b12_s1 Searce_festis_NHT Homo sapiens cDNA clone IMAGE7438783
1380	65098	11689	12.29	1.0E-52	4504028 NT		Homo sapiens glutamato-ammonium ligase (glutamine synthetase) (GLUL) mRNA
2508	7611		1.78	1.0E-52	4502238 NT		Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA
3031	8185	13340	1.68	1.0E-52	S81070.1	NT	pd=reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element] RTVL-Hp1. Gammic, 650 nt]
4370	9491	14635	0.83	9.0E-53	AF001446.1	NT	Homo sapiens core Binding Factor subunit (CBFA1) gene, exon 3
5178	10276	15413	1.59	9.0E-53	AB040937.1	NT	Homo sapiens mRNA for KIAA1564 protein, partial cds
4074	9204	14340	7.43	5.0E-53	4758543 NT		Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/22) (HNRPC) mRNA
48	6280	10384	1.49	4.0E-53	AL1683285.2	NT	Homo sapiens chromosome 21 segment HS21C088

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
48	5260	10385		1.49	4.0E-63	AL163285.2	NT
4789	8692	16043		1.29	4.0E-53	7705414	NT
2821	7720	12874		1.42	3.0E-53	AB026898.1	NT
3712	8650	14004		0.89	3.0E-53	AW050806.1	Human sepiens DNA, DLECT to ORCTL4 gene region, section 1/2 (DLECT1, ORCTL3, ORCTL4 genes, complete cds)
4553	9681	14820		1.22	3.0E-53	AW805563.1	EST_HUMAN
467	5625			3.25	2.0E-53	AA366556.1	EST_HUMAN
2303	7417	126617		16.62	2.0E-53	U78027.1	NT
2509	7612			4.83	2.0E-53	4602816	NT
2688	7785	13033		1.12	2.0E-53	4757915	NT
2888	7785	13034		1.12	2.0E-53	4757916	NT
4033	9164	14303		3.37	2.0E-53	MB1673.1	NT
5163	10290	15427		1.4	2.0E-53	7682083	NT
1453	68585	11773		2.62	1.0E-53	A1271736.1	NT
3301	8635	13698		1.24	1.0E-53	AB026898.1	NT
4946	10054	16162		1.07	1.0E-53	BE2963388.1	EST_HUMAN
204	5389	10541		4.55	8.0E-54	BE366785.1	EST_HUMAN
1849	6970	12191		1.84	8.0E-54	4504610	NT
382	6591	10733		1.12	7.0E-54	AA8126337.1	EST_HUMAN
1844	6865	12183		1.14	7.0E-54	Y16845.1	NT
2188	7300	12549		2.51	7.0E-54	N21177.1	EST_HUMAN
23	5234	10349		1.12	6.0E-54	AB003618.1	NT
383	5392	10737		1.03	6.0E-54	8927148	NT
383	5392	10738		1.03	6.0E-54	8927148	NT
3267	8416	13578		0.9	6.0E-54	8927148	NT
3979	9113	14261		1.15	6.0E-54	4602872	NT
4441	8660	14702		1.05	6.0E-54	AV754746.1	EST_HUMAN
						AV754746 TP Human sepiens cDNA clone TPGAAC10 5'	
						YW88012.61 Scores 1 placenta, 8t6weeks_2ntHPB685W Human sepiens cDNA clone MAGE257388 3'	
						similar to contains LTR7.13 LTR7 repetitive element;	
						Human sepiens DNA for MLCB, exon 4, and partial cds	
						Human sepiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA	
						Human sepiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA	
						Human sepiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA	
						Human sepiens chloride channel 6 (CLCN6) mRNA	
						Human sepiens chloride channel 6 (CLCN6) mRNA	

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4812	8924	15065	2.14	8.0E-54	4505808	NT	Human sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4845	8987		1.47	8.0E-54	Y08461.1	NT	Human sapiens stc pseudogene, p68 isoform
4983	8987		2.7	8.0E-54	Y08461.1	NT	Human sapiens stc pseudogene, p68 isoform
2135	7249	12495	7.98	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 64 (ZINC FINGER PROTEIN HPF2)
178	5372		281.14	4.0E-54	AF110103.1	NT	Tupai beilongeri beta-actin mRNA, partial cds
857	6105	11274	223.4	4.0E-54	AA308784.1	EST_HUMAN	EST177698 Jurkat T-cells VI Human sapiens cDNA 5' end similar to glyceradehyde-3-phosphate dehydrogenase
1817	6940	12167	2.28	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1817	6940	12168	2.25	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3187	8538		1.52	4.0E-54	AI853886.1	EST_HUMAN	WD28d11.x1 Scores NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2328269 3' similar to TR:002711 PRO-POL-DUTYPASE POLYPROTEIN
89	5298	10437	11.81	3.0E-54	AA313487.1	EST_HUMAN	EST185371 Celox (HCC) cell line Homo sapiens cDNA 5' end
2589	7630		1.02	3.0E-54	AI908767.1	EST_HUMAN	LB-T150-160309-007 BT150 Homo sapiens cDNA
841	5802	10835	4.73	2.0E-54	6031600	NT	Human sapiens killer cell lectin-like receptor subfamily Q, member 1 (KLRL1), mRNA
1374	6952	11684	1.16	2.0E-54	4507164	NT	Human sapiens nuclear antigen Sp100 (SP100) mRNA
1582	6891	11877	1.14	2.0E-54	AA655008.1	EST_HUMAN	NT8305.61 NCI CGAP_Pt3 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element;
2511	7614	12864	2.48	2.0E-54	AW169175.1	EST_HUMAN	ASB2q3.y1 Schneider fetal brain 00040 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW:CUL1_HUMAN Q13818 CUL1IN HOMOLOG 1;
2584	7685	12820	1.03	2.0E-54	AL163210.2	NT	Human sapiens chromosome 21 segment HS21C010
2861	8016	13182	1.16	2.0E-54	AW057524.1	EST_HUMAN	TRQ202084 Q82084 PHOSPHOLIPASE C NEIGHBORING;
3535	8977		8.84	2.0E-54	AA532825.1	EST_HUMAN	NT45g08.51 NCI CGAP_Pt3 Homo sapiens cDNA clone IMAGE:905468 similar to gb:J53777 60S RIBOSOMAL PROTEIN L23 (HUMAN);
3827	8963	14113	0.72	2.0E-54	4506378	NT	Human sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
3827	8963	14114	0.72	2.0E-54	4506379	NT	Human sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4177	8903		3.18	2.0E-54	4502842	NT	Human sapiens chaperonin containing T-complex subunit 8 (CCT8) mRNA
4419	8539		0.85	2.0E-54	AF208161.1	NT	Human sapiens synctylin precursor, mRNA, complete cds
4850	8982	15107	1.18	2.0E-54	7706448	NT	Human sapiens peptidylarginine deiminase type III (LOCS1702), mRNA
4444	9163		1.41	1.0E-54	BF315418.1	EST_HUMAN	6018602020F1 NIH_3T3_Home sapiens cDNA clone IMAGE:4128535 5'
1320	8449		0.72	8.0E-55	Y07828.2	NT	Human sapiens RFB30 gene for RING finger protein
1323	8452		2.12	8.0E-55	Y07828.2	NT	Human sapiens RFB30 gene for RING finger protein
1780	6908	12113	1.38	6.0E-55	AA704871.1	EST_HUMAN	AB8509.51 Scores_fetal_liver_spleen cDNA clone IMAGE:462617 3'
1780	6908	12114	1.39	6.0E-55	AA704871.1	EST_HUMAN	AB8509.51 Scores_fetal_liver_spleen cDNA clone IMAGE:462617 3'

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit BLAST E	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4737 8850	14897	14897	1.57	8.0E-55	AW208021.1	EST_HUMAN	UH-B1-afg-09-04-U1.1 NT	cDNA clone IMAGE:2723538 3'
54 7892	10393	3.01	4.0E-55	AW857894.1	EST_HUMAN	EST310844	MAGE_Homo sapiens cDNA	
671 6890	10770	34.27	4.0E-55	4826973 NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RSYAY1A1) mRNA			
1451 6579	11768	1.84	4.0E-55	7881713 NT	Homo sapiens predicted celebiplas protein (GS3786), mRNA			
1451 6579	11767	1.84	4.0E-55	7881713 NT	Homo sapiens predicted celebiplas protein (GS3786), mRNA			
15220 8368		1.83	4.0E-55	BF061411.1	EST_HUMAN	752210.x1 Scarses_NSF_F8_9W_0T_PA_P_S1_Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.13 L1 repetitive element.		
2018 7135	12373	4.48	4.0E-55	4506150 NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSM42) mRNA			
2018 7135	12374	4.48	4.0E-55	4606150 NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSM42) mRNA			
2078 7194	12497	3.73	4.0E-55	4503314 NT	Homo sapiens diacylglycerol kinase, gamma (60kD) (DGKG) mRNA			
2078 7194	12498	3.73	4.0E-55	4503314 NT	Homo sapiens diacylglycerol kinase, gamma (60kD) (DGKG) mRNA			
2287 7338	12468	7.71	4.0E-55	4507726 NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA			
3283 8412	13574	1.07	4.0E-55	AL183300.2 NT	Homo sapiens chromosome 21 segment HS21C100			
376 6553	10687	2.88	2.0E-55	X57147.1 NT	Human endogenous retrovirus pRE7 (ERV9)			
550 5715		1.74	2.0E-55	M10876.1 NT	Human endogenous retroviral DNA (4-1) complete retroviral segment			
648 5809	10844	3.88	2.0E-55	4507286 NT	Homo sapiens synaptosomal-binding protein 1 (STXBP1) mRNA, and translated products			
2826 8030	13248	2.08	2.0E-55	4507798 NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Argentman syndrome) (UBRE3A) mRNA			
4741 8854	15001	2.82	2.0E-55	BE719888.1 NT	CM1-H1T0876-1508100-357-q03 HT0876 Homo sapiens cDNA			
92 6301	10440	1.85	1.0E-55	4605050 NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA			
180 5381	10822	78.12	1.0E-55	UD08823.1 NT	Oncogenes cinkulus New Zealand white elongation factor 1 alpha (RefSeq) mRNA, complete cds			
1151 6287	11452	3.88	1.0E-55	AB020710.1 NT	Homo sapiens mRNA for KIAA0503 protein, partial cds			
1855 7072	12288	47.44	1.0E-55	BE277881.1 NT	601120116F1 NIH MGCG_20_Homo sapiens cDNA clone IMAGE:2887027 5'			
1855 7072	12287	47.44	1.0E-55	BE277881.1 NT	601120116F1 NIH MGCG_20_Homo sapiens cDNA clone IMAGE:2887027 5'			
2305 7444		4.47	1.0E-55	6803174 NT	Homo sapiens SMA3 (SMA3) mRNA			
2488 7692	12840	9.84	1.0E-55	X13111.1 NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)			
2524 7627	12873	2.04	1.0E-55	AB007886.2 NT	Homo sapiens mRNA for KIAA0406 protein, partial cds			
2524 7627	12874	2.04	1.0E-55	AB007886.2 NT	Homo sapiens mRNA for KIAA0406 protein, partial cds			
25715 7675	12029	3.13	1.0E-55	L54057.1 NT	Homo sapiens C1P mRNA, partial cds			
3380 8634	13886	0.97	1.0E-55	W28198.1 EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA			
3864 9098	14248	3.8	1.0E-55	AL163267.2 NT	Homo sapiens chromosome 21 segment HS21C087			
4270 9304	14833	1.18	1.0E-55	AL163210.2 NT	Homo sapiens chromosome 21 segment HS21C010			
46598 9815		1.15	1.0E-55	N77281.1 EST_HUMAN	W44903 nt Scarses fetal liver spleen NFLS Homo sapiens cDNA clone IMAGE:245620 5'			

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4786	8809	16049	4.45	1.0E-55	AB037163.1	NT	Homo sapiens DSCKREb mRNA, complete cds
4788	8808	15050	4.45	1.0E-55	AB037163.1	NT	Homo sapiens DSCKREb mRNA, complete cds
5112	10213	16350	1.07	1.0E-55	892325	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA ylocg03.11 Scores adult brain N2bt5HB55Y Homo sapiens cDNA clone IMAGE:175044 5' similar to contains
2695	7792	13042	3.22	7.0E-56	H18954.1	EST_HUMAN	THR repetitive element
1708	6884	12035	1.43	5.0E-58	AW897712.1	EST_HUMAN	RC3-BN0053-17/20-011-101 BN0053 Homo sapiens cDNA
28	5237	10351	28.3	4.0E-58	AF41349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
26	5237	10362	28.3	4.0E-58	AF41349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2155	7268		1.1	4.0E-58	BP2075B8.1	EST_HUMAN	601862059F1 NIH MGIC_63 Homo sapiens cDNA clone IMAGE:40816551 5'
2870	7768	13017	6.1	4.0E-58	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2870	7768	13018	6.1	4.0E-58	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2773	5650	10822	5.49	4.0E-58	AF003528.1	NT	Homo sapiens X-linked arachidonic acid esterolytic dyphosphatase protein gene (EDA), exon 2 and flanking repeat regions
2783	7679	12833	1.16	4.0E-58	AL632488.1	EST_HUMAN	W009108X1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2305101 3' similar to SW:DCOR_MUSPA
2783	7679	12833	1.16	4.0E-58	AL632488.1	EST_HUMAN	P27119 ORNITHINE DECARBOXYLASE ;
2783	7678	12834	1.16	4.0E-58	AL632488.1	EST_HUMAN	W009108X1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2305101 3' similar to SW:DCOR_MUSPA
1341	6476	11653	4.09	3.0E-58	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
1776	6001	12109	4.35	3.0E-58	6912743	NT	Homo sapiens 5'-3' exonuclease 2 (XRN2), mRNA
2134	7248	12464	1.14	3.0E-59	6912697	NT	Homo sapiens oncogene TC21 (TC21), mRNA
3102	8255	13405	1.85	3.0E-59	AJ325828.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3102	8255	13403	1.85	3.0E-59	AJ325828.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3812	8849		2.77	3.0E-58	AF055068.1	NT	Homo sapiens MHC class I region
3892	8028	14187	0.78	3.0E-58	BE383512.1	EST_HUMAN	601310203F1 NIH MGIC_44 Homo sapiens cDNA clone IMAGE:3631848 6'
4402	9222	14683	4	3.0E-58	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C88
4545	9653	14803	2.31	3.0E-58	5920295	NT	Homo sapiens superkiller relativity 2 (S. cerevisiae homolog), mRNA
622	6688		2.42	2.0E-58	AA1188918.1	EST_HUMAN	2462208.61 Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:8462083
731	7889	11037	2.24	2.0E-58	BE0645B6.1	EST_HUMAN	RCA4-B10310-11030-016-F10 B10310 Homo sapiens cDNA
731	7889	11038	2.24	2.0E-58	BE0645B6.1	EST_HUMAN	RCA4-B10310-11030-015-F10 B10310 Homo sapiens cDNA
2957	8111	13274	1.4	2.0E-58	AB037835.1	NT	Homo sapiens mRNA for RIA1414 protein, partial cds
3287	8444		1.88	2.0E-58	AB0106881.1	NT	Homo sapiens gene for activin receptor type IB, complete cds
3521	8082	13829	1.11	2.0E-58	AY703184.1	EST_HUMAN	AY703184 ADB Homo sapiens cDNA clone AD802310 5'
881	6127		3.6	1.0E-58	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PTPL-1) mRNA, complete cds

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1638	61683	11849	5.72	1.0E-58	AA283038.1	EST_HUMAN	254b09.1 Scores over tumor NH10T Homo sapiens cDNA clone IMAGE:7281137 5' similar to gb:U04854
3852	81791	13946	1.81	1.0E-58	AW689853.1	EST_HUMAN	INTERLEUKIN ENHANCER-BINDING FACTOR (HUMAN); hg23c11.x1 NCI_CGAP_GCA
3952	81791	13949	1.81	1.0E-58	AW689853.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_GCA Homo sapiens cDNA clone IMAGE:2948462 3'
5015	10118	15251	1.04	1.0E-58	AB05162.1	EST_HUMAN	QV-BT077-130189-279 BT077 Homo sapiens cDNA
624	5784			9.0E-57	AW880885.1	EST_HUMAN	QD-O10038-0703010-1524033 OT10033 Homo sapiens cDNA
285	5483	10825	2.62	8.0E-57	AW816405.1	EST_HUMAN	QV4-S10234-181199-037-406 S10234 Homo sapiens cDNA
885	6035	11208	7.78	8.0E-57	AW284589.1	EST_HUMAN	AT06410.x1 NCI_CGAP_Bm63 Homo sapiens cDNA clone IMAGE:2769261 3' similar to gb:U05875
1828	60981	12173	1.48	8.0E-57	AA486109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN); zv61b12.1 Scores_ests_NHT Homo sapiens cDNA clone IMAGE:767161 6'
2593	7698	12852	8.47	7.0E-57	7857582	NT	Homo sapiens GDS-ASSOCIATED PROTEIN (SWAP), mRNA
3233	8883	13843	1.28	7.0E-57	7857582	NT	Homo sapiens NME7 (NME7), mRNA
3233	8883	13844	1.28	7.0E-57	7242168	NT	Homo sapiens NME7 (NME7), mRNA
3254	8404	13563	0.78	7.0E-57	6005979	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3855	8081	14147	1.61	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PI4K230) mRNA, complete cds
3855	8081	14148	1.61	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PI4K230) mRNA, complete cds
3734	8972	14024	2.03	4.0E-57	AB026989.1	NT	Homo sapiens DNA_DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
4880	10086	15227	1.06	4.0E-57	BE783849.1	EST_HUMAN	601471228F1 NH_MGC_67 Homo sapiens cDNA clone IMAGE:3874135 6'
805	5058	11121	2.34	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1338	6164		51.92	3.0E-57	AA230278.1	EST_HUMAN	nc1307.51 NCI_CGAP_Pri Homo sapiens cDNA clone IMAGE:10038037 similar to SWRS10_HUMAN
2368	7474	12723	1.39	3.0E-57	AA346835.1	EST_HUMAN	P48783_40S RIBOSOMAL PROTEIN S10.1;
2684	7760	13011	1.49	3.0E-57	BEE766822.1	EST_HUMAN	EST64770 Hippocampus II Homo sapiens cDNA 5' end
2684	7760	13012	1.49	3.0E-57	BEE766822.1	EST_HUMAN	7638b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:32288443 3' similar to WP-Y47H8C2
3674	9143		80.77	3.0E-57	AW853984.1	EST_HUMAN	CE20283;
4037	9168	14509	5.42	3.0E-57	PO8547	SWISSPROT	RC3-CT0254-110301-027-410 CT0254 Homo sapiens cDNA LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1443	6571	11768	1.17	2.0E-57	AI478804.1	EST_HUMAN	Im25c10.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA repetitive element, contains Aliu
1515	6842	11823	1.8	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds

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Single Exon Probes Expressed in BT474 Cells

Probe seq ID NO:	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar (Top) BLAST: E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1515	8842	11829	1.8	2.0E-57	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
2378	7884	12738	0.97	2.0E-57	BE172528.1	EST_HUMAN	MFD-HT0569-01040-009-010 HT0569 Homo sapiens cDNA at02802.61 Soares, parathyroid, tumor, NBHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to
2891	7788	13038	2.49	2.0E-57	AA848419.1	EST_HUMAN	contains Alu repetitive element; contains element MER22, repetitive element;
3420	85852		1.38	2.0E-57	AL168204.2	NT	Homo sapiens chromosome 21 segment HS21C014
3638	8880	13842	0.7	2.0E-57	R07702.1	EST_HUMAN	ye8801.71 Soares fetal liver spleen INFSL Homo sapiens cDNA clone IMAGE:128809 5'
3638	8880	13843	0.7	2.0E-57	R07702.1	EST_HUMAN	ye8801.71 Soares fetal liver spleen INFSL Homo sapiens cDNA clone IMAGE:128809 5'
3894	8040	14230	1.15	2.0E-57	BE073284.1	EST_HUMAN	MFD-BT0665-060300-103-503 BT0665 Homo sapiens cDNA
4485	8604	14742	6.05	2.0E-57	AL168283.2	NT	Homo sapiens chromosome 21 segment HS21C033
2213	7325	12575	1.07	1.0E-57	AW503208.1	EST_HUMAN	UHF-BND-eR-9-07-U-LTR NIH MSC_50 Homo sapiens cDNA clone IMAGE:3078348 6'
687	5749		15.12	8.0E-58	BE88715.1	EST_HUMAN	801445848F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3880211 5'
683	6814	10950	4.07	8.0E-58	AI798376.1	EST_HUMAN	K24507.21 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220191 3' similar to TRCO6475 O15475
683	5814	10951	4.07	8.0E-58	AI798376.1	EST_HUMAN	UNNAMED HERV+PROTEIN; TS4407.21 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220161 3' similar to TR-O18475 O18475
1888	6888	12211	1.61	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1888	6888	12212	1.61	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2844	8088		2.62	8.0E-58	7706132	NT	Homo sapiens DHFC1 protein (LOC51304), mRNA
4900	10011	15158	1.53	7.0E-58	BE208503.1	EST_HUMAN	b405g04.11 NIH_MCC_7Homo sapiens cDNA clone IMAGE:2823510 5' similar to TR-Q861489 Q861489 DHM1 PROTEIN.
2234	7346	12601	1.02	6.0E-58	BS395061.1	EST_HUMAN	601308465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3831000 5'
2355	7882	12713	8	6.0E-58	AU130689.1	EST_HUMAN	AU130689.1 NT2RP3 Homo sapiens cDNA clone NT2RP300 288 5'
2868	8020	13188	0.88	6.0E-58	BE242160.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Bayf or-HGSC project=TCAA_Homo sapiens cDNA clone TCAAP-1219
2868	8020	13187	0.86	6.0E-58	BE242160.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Bayf or-HGSC project=TCAA_Homo sapiens cDNA clone TCAAP-1219
2868	54886	10827	3.03	5.0E-59	4507534	NT	Homo sapiens synaptosomal 1 (SYN1), mRNA
703	58855	11012	5.2	6.0E-58	BE163584.1	EST_HUMAN	RC4-NT0057-1-16050-016-005 NT0057 Homo sapiens cDNA
1197	6831	11499	3.29	6.0E-58	AW787948.1	EST_HUMAN	CW3-UW0043-240300-127-007 UM0043 Homo sapiens cDNA
1197	6831	11500	3.29	5.0E-58	AW787948.1	EST_HUMAN	CW3-UW0043-240300-127-007 UM0043 Homo sapiens cDNA
1188	6831	11499	2.28	5.0E-58	AW787948.1	EST_HUMAN	CW3-UW0043-240300-127-007 UM0043 Homo sapiens cDNA
1188	6831	11600	2.28	6.0E-58	AW787948.1	EST_HUMAN	CW3-UW0043-240300-127-007 UM0043 Homo sapiens cDNA
3304	8451	13813	3.85	6.0E-58	AA888183.1	EST_HUMAN	ar88007.51 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1603808 3'

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Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4232	8357	14489	0.67	6.0E-58	AI036745.1	EST_HUMAN	ts88007_x1 NC1 CGAP_GC8 Homo sapiens cDNA clone IMAGE:2238468 3' similar to SW_PPR02_ACACA_P18984 PROFILIN II;
371	5551	10694	5.7	4.0E-58	4502302 NT	Homo sapiens ATP synthase, H4 transporting mitochondrial F1 complex, O subunit (dihydropyridine sensitivity conferring protein) (ATP5C) mRNA	
787	53651	11111	1.23	4.0E-58	4504634 NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA	
1480	66307	11783	0.98	4.0E-58	4503848 NT	Homo sapiens coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B) (F9) mRNA	
2541	7844	12894	1.03	4.0E-58	AF265955.1	NT	Homo sapiens ubiquitin-conjugating B1R-domain enzyme APOLION mRNA, complete cds
2598	7697	12850	2.03	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3308	84553	13615	1	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3721	88559	14012	1.02	4.0E-58	5031660 NT	Homo sapiens EGFl-like repeats and discoidin-like domains 3 (EDIL3), mRNA	
333	55116	2.93	3.0E-58	R17879.1	EST_HUMAN	Y010e02.1 Scores infant brain (NIB) Homo sapiens cDNA clone IMAGE:31693_5'	
1396	65224	11703	1.81	3.0E-58	4768381 NT	Homo sapiens peptide YY (PYY) mRNA	
3158	83019	13483	3.32	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308943_5'
3158	83019	13489	3.32	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4308943_5'
940	6088	11258	8.84	2.0E-58	AF068824.1	NT	Homo sapiens 5'-aminolevulinate synthase 2 (ALAS2) gene, complete cds
1294	64223		39.27	2.0E-58	BE208632.1	EST_HUMAN	ba08007_y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 6 similar to gb:X88331 60S RIBOSOMAL PROTEIN L8 (HUMAN); gb:X081987 Mus musculus mRNA for TAX responsive element binding protein (MOUSE);
729	8377	11024	0.65	1.0E-58	M68134.1	NT	Human complement component C5 mRNA, 3' end
1089	8209	11372	6.86	1.0E-58	6274549 NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (NDUFB8), mRNA	
1332	6461	11640	3.63	1.0E-58	AW857182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1332	6481	11641	3.63	1.0E-58	AW857182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1877	88018	12003	1.29	1.0E-58	BE468132.1	EST_HUMAN	hy10688_x1 NC1 CGAP_GC8 Homo sapiens cDNA clone IMAGE:316935_3'
2763	70557	13113	2.83	1.0E-58	4759169 NT	Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2), mRNA	
2781	71226	12361	1.49	1.0E-58	6174444 NT	Homo sapiens G protein-coupled receptor 6A (GPR88A) mRNA	
3700	88338	13892	0.77	1.0E-58	4507628 NT	Homo sapiens transition protein 1 (during histone to prokaryotic replacement) (TNP1) mRNA	
4855	10063	15202	4.97	1.0E-58	AI141053.1	EST_HUMAN	cc43h01_x1 Scores_NihMfu_S1_Homo sapiens cDNA clone IMAGE:1678129_3'
2211	7323	12573	48.86	8.0E-59	4507378 NT	Homo sapiens TATA box binding protein (TBP) mRNA	
173	7984		2.08	6.0E-59	BF035327.1	EST_HUMAN	601483831F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3882088_5'
1765	6891	12097	0.98	5.0E-59	AIW157281.1	EST_HUMAN	TR-O76786_O75768 GANGLOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;

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Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1785	8891	12083	0.98	5.0E-59 AIV197281.1	EST_HUMAN	EST_0105_X1_Schneider fetal brain clone IMAGE:2783865 3' similar to TR:075788_015786_DANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.	
3104	8257	13408	6.48	5.0E-59 AIB07484.1	EST_HUMAN	W44C11.1 Socaris NCI_GCB_S1 Homo sapiens cDNA clone IMAGE:2588867 3'	
4828	9748	14891	7.69	5.0E-59 X83457.1	NT	H_sapiens DNA for ZNF80-linked ERV6 long terminal repeat	
794	5948	11109	2.42	4.0E-59 DB00065.1	NT	Human mRNA for KIAA0184 gene, partial cds	
1241	8371	11545	5.89	4.0E-59	4505818 NT	Human sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products	
1241	8371	11548	5.89	4.0E-59	4505818 NT	Human sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products	
5164	10282	16401	1.74	4.0E-59 AIB00847.1	EST_HUMAN	WS22612.X1_NCI_GCB_GCG_Homo sapiens cDNA clone IMAGE:24988928 3'	
9	6220		4.88	3.0E-59 AW065524.1	EST_HUMAN	EST377582_NAGE sequences, MAGI Homo sapiens cDNA	
224	54117	10554	3.68	3.0E-59	7692247 NT	Human sapiens KIAA0880 gene product (KIAA0880), mRNA	
1725	8852	12098	6.78	3.0E-59	4505860 NT	Human sapiens plasmalogen activator, tissue (PLA1a) mRNA	
1725	8852	12057	6.78	3.0E-59	4505860 NT	Human sapiens plasmalogen activator, tissue (PLA1a) mRNA	
2120	7236	12477	4.6	3.0E-59 AB028035.1	NT	Human sapiens mRNA for KIAA1112 protein, partial cds	
2120	7236	12478	4.8	3.0E-59 AB028035.1	NT	Human sapiens mRNA for KIAA1112 protein, partial cds	
2792	7850	13082	1.01	3.0E-59 AF232289.1	NT	Human sapiens NF-2 pseudogenes, exon 17	
3108	9259	13412	3.82	3.0E-59	4502014 NT	Human sapiens AKAP1 (AKAP1), mRNA	
3108	8259	13413	3.82	3.0E-59	4502014 NT	Human sapiens AKAP1 (AKAP1), mRNA	
3804	8841	14089	1.71	3.0E-59	4508044 NT	Human sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA	
4689	9776	14921	1.35	3.0E-59 AL168284.2	NT	Human sapiens chymotrypsin 21 segment HS21C384	
4809	8821	15063	1.62	3.0E-59	74275722 NT	Human sapiens protein tyrosine phosphatase, receptor type T (PTPRT), mRNA	
158	5355		15.3	1.0E-59 BE280411.1	EST_HUMAN	6011776757F_NIH_MGC_17_Homo sapiens cDNA clone IMAGE:35311827 6'	
2582	7683		1.63	1.0E-59 AA1748468.1	EST_HUMAN	EST38849_MAGE sequences, MAGO_Homo sapiens cDNA	
783	69118	11076	2.32	8.0E-60 AW0778465.1	EST_HUMAN	0168n1.61_NCI_GCAP_GCG1 Homo sapiens cDNA clone IMAGE:1308029 3' similar to TR:Q13537	
1483	8810	11788	3.19	8.0E-60	4759159 NT	Human sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRNP20) mRNA	
2162	7285	12513	6.26	8.0E-60	6174856 NT	Human sapiens different induction-related gene 1 (induced-specific induction protein) (RTP) mRNA	
2162	7285	12514	5.25	8.0E-60	6174856 NT	Human sapiens different induction-related gene 1 (induced-specific induction protein) (RTP) mRNA	
753	58019	11066	4.23	7.0E-60 AF055068.1	NT	Human sapiens MHC class 1 region	
754	68019	11068	13.42	7.0E-60 AF055068.1	NT	Human sapiens MHC class 1 region	
816	58639	11130	1.08	7.0E-60	4504634 NT	Human sapiens integrin 10 receptor, beta (IL10RB), mRNA	
2119	7234	12476	2.96	7.0E-60 AF077188.1	NT	Human sapiens cullin 4A (CUL4A) mRNA, complete cds	
2746	7840	13085	1.02	7.0E-60 AB011153.1	NT	Human sapiens mRNA for KIAA0581 (protein, partial cds)	

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe seq ID No:	Exon seq ID No:	ORF seq ID No:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4150	8276	14413	2.53	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODDC1) mRNA
4543	8858	14808	0.84	7.0E-60	AF284760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2169	12620		1.47	6.0E-60	BEE68761R1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:386069 3'	EST_HUMAN	
80	5289	10429	1.9	5.0E-60	AB07917.1	EST_HUMAN	wf52-07-k1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23592123'
80	5289	10429	1.9	5.0E-60	AB07917.1	EST_HUMAN	wf52-07-k1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23592123'
2218	7328	12580	1.14	4.0E-60	AW603208.1	EST_HUMAN	U1-H-BN0-akr-q-07-q-U1T NIH_MfGC_50 Homo sapiens cDNA clone IMAGE:3078348 6'
2218	7328	12581	1.14	4.0E-60	AW509208.1	EST_HUMAN	U1-H-BN0-akr-q-07-q-U1T NIH_MfGC_50 Homo sapiens cDNA clone IMAGE:3078348 6'
2842	8098		1.68	4.0E-60	AA289637.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to retrovirus-related pol
1870	68890	12214	3.4	3.0E-60	BEE826811.1	EST_HUMAN	6011386446F1 NIH_MfGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1870	68890	12215	3.4	3.0E-60	BEE826811.1	EST_HUMAN	6011386446F1 NIH_MfGC_44 Homo sapiens cDNA clone IMAGE:3690395 6'
1880	7000		22.16	3.0E-60	6031190	NT	Homo sapiens proline-rich (PRB) mRNA
4438	8555	14697	1.9	3.0E-60	A1274735.1	NT	Homo sapiens Xq13 pseudoeukaryosomal region; segment 1/2
29	6240	10356	1.44	2.0E-60	AY008285.1	NT	Homo sapiens adult carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1433	6560	11743	6.02	2.0E-60	Z11694.1	NT	H.sapiens 41kDa protein kinase related to at ERK2
1736	8882	12064	1.24	2.0E-60	M24603.1	NT	Human ber protein mRNA, 5' end
1748	8970	12074	1.14	2.0E-60	AY008285.1	NT	Homo sapiens adult carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
2571	7767	13019	1.01	2.0E-60	AW978005.1	EST_HUMAN	EST380114 MAGE sequences, MAGO_Homo sapiens cDNA
3568	8707	13868	0.68	2.0E-60	4737867	NT	Homo sapiens viral oncogene homolog B1 (BRAF) mRNA
3889	9025	14183	0.88	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
520	6888	10813	2.73	1.0E-60	BE78888.1	EST_HUMAN	PMS-H17888-27/20/2001-068 HT0805 Homo sapiens cDNA
3879	9016	14172	0.92	1.0E-60	AU1443389_Y79AA1	EST_HUMAN	AU1443389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
4936	10046	16186	1.21	1.0E-60	AL1652285.2	NT	Homo sapiens chromosome 21 segment HS21C088
1100	6238	11401	1.27	9.0E-61	AU118344	EST_HUMAN	AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 6'
2831	7729	12885	1.01	8.0E-61	AW008478.1	EST_HUMAN	W0050101 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:25085566 3'
2817	8071		2.67	8.0E-61	AW006478.1	EST_HUMAN	Human endogenous retrovirus PHE-1 (ERV6)
123	5322	10483	0.68	7.0E-61	X67147.1	NT	Human endogenous retrovirus PHE-1 (ERV6)
123	5322	10487	0.68	7.0E-61	776670	NT	Human endogenous retrovirus PXR2b protein (PXR2b), mRNA
283	5453	10691	2.73	6.0E-61	BE405910.1	EST_HUMAN	Hom sapiens PXR2b protein (PXR2b), mRNA
812	5385	11127	1.88	6.0E-61	BE405910.1	EST_HUMAN	6013050388F1 NIH_MfGC_21 Homo sapiens cDNA clone IMAGE:3685480 6'
1326	6465	11633	11.89	6.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1840	8768	11982	1.17	6.0E-61	BE267400.1	EST_HUMAN	601108228F1 NIH_MfGC_18 Homo sapiens cDNA clone IMAGE:3380148 6'

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1650	6788	11983	3.34	6.0E-81	AA596033.1	EST_HUMAN	nm06808_s1_NCI CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
3298	8437	13688	8.69	6.0E-81	AU130889.1	EST_HUMAN	AU130889 NT2RP3 Homo sapiens cDNA clone NT2RP3001283 5'
357	5838	10678	0.65	6.0E-81	4507600 NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIA1) mRNA	
1692	9821	12020	3.02	5.0E-81	4508008 NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PP1R10) mRNA	
3008	8162	13319	2.26	5.0E-81	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3161	8932	13495	1.48	5.0E-81	4502168 NT	Homo sapiens amyloid beta (A4) precursor protein (protease neutral-II, Alzheimer disease) (APP) mRNA	
3914	9089		1.69	8.0E-81	AJ229041.1	NT	Homo sapiens 659 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4988	5538	10679	0.65	5.0E-81	4507500 NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIA1) mRNA	
4198	8312	14447	1.29	3.0E-81	BE38278.1	EST_HUMAN	6015087865 NIH MG-44 Homo sapiens cDNA clone IMAGE:3681220 6'
498	6665	10800	1.57	2.0E-81	8922828 NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028) mRNA	
1245	6347	11517	3.89	2.0E-81	BE168410.1	EST_HUMAN	Q934HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1216	6247	11618	3.89	2.0E-81	BE168410.1	EST_HUMAN	Q934HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1678	6808	12008	1.52	2.0E-81	N53039.1	EST_HUMAN	Y83d11.s1 Scores fetal liver spleen 1NFL3 Homo sapiens cDNA clone IMAGE:248453 3' similar to qb-L28444 80S RIBOSOMAL PROTEIN L5A (LUMAN).
2804	7703		1.41	2.0E-81	NA3697.1	EST_HUMAN	Y03f11.1 Homo sapiens cDNA clone IMAGE:2701189 5'
494	6603		0.83	1.0E-81	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C033
773	6927	11088	1.22	1.0E-81	6453829 NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2) mRNA	
1405	6533	11711	1.19	1.0E-81	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C033
1869	6989	12213	3.94	1.0E-81	6015989 NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A) mRNA	
							xm11b05_Y1 NCI CGAP_L15 Homo sapiens cDNA clone IMAGE:2890339 5' similar to contains element M581 repetitive element;
2180	7283	12540	2.28	1.0E-81	AW827281.1	EST_HUMAN	
2768	7953	13119	1.57	1.0E-81	BE3985383.1	EST_HUMAN	6012735135 NIH MG-20 Homo sapiens cDNA clone IMAGE:3814687 6'
3367	8502	13670	0.88	1.0E-81	7662318 NT	Homo sapiens KIAA0808 gene product (KIAA0808) mRNA	
3713	8851	14005	1.52	1.0E-81	BE174455.1	EST_HUMAN	QV24110577-140300-077-d08 HT0577 Homo sapiens cDNA
4417	9537	14677	0.88	1.0E-81	4763249 NT	Homo sapiens TRAF family member -associated NFkB activator (TANK) mRNA	
4417	9537	14678	0.88	1.0E-81	4756249 NT	Homo sapiens TRAF family member -associated NFkB activator (TANK) mRNA	
4826	89338	15078	9.22	1.0E-81	AW288181.1	EST_HUMAN	U+H-BW04-01b-08-0-U1st NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4826	89338	16080	9.22	1.0E-81	AW288181.1	EST_HUMAN	U+H-BW04-01b-08-0-U1st NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4524	8642	14790	1.64	8.0E-82	AA6390420.1	EST_HUMAN	oed611.s1 NCI CGAP_QCB1 Homo sapiens cDNA clone IMAGE:1364725 3' similar to SW7POL_MLVRK F31785 POL POLYPROTEIN;
1108	6248	11409	1.12	7.0E-82	AV7114334.1	EST_HUMAN	AV7114334 DCB Homo sapiens cDNA clone DCEAMA08 5'
3490	8631	13798	0.7	7.0E-82	P17480	SWISSPROT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-80)

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2868	8122		1.44	6.0E-62	U08410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
3363	8310		4.59	6.0E-62	1141825N	NT	Human sapiens CG-486 protein (CG-486), mRNA
415	5563	10731	5.02	5.0E-62	A1950526.1	EST_HUMAN	wk6102_X1_NCI_C04P_Lu29 Homo sapiens cDNA clone IMAGE:2847204 3' similar to SW:3096_HUMAN
2383	7489	12742	2.82	5.0E-62	A1271735.1	NT	Human sapiens Xq pseudautosomal region; segment 1/2
2383	7489	12743	2.82	5.0E-62	A1271735.1	NT	Human sapiens Xq pseudautosomal region; segment 1/2
2562	7686	12805	1.11	6.0E-62	U384987.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
2552	7685	12806	1.11	5.0E-62	U384987.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
3400	8544	13703	2.69	5.0E-62	4506788	NT	Human sapiens ryandine receptor 3 (RYR3) mRNA
4304	8426	14561	1.76	5.0E-62	AA431093.1	EST_HUMAN	zw78a08_61 Scores: bestis_NHt Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
4532	8650		0.98	5.0E-62	A1W80589.1	EST_HUMAN	P4725_NARDILYSN; RCE5NN1089-10C500-021-HG3 NN1089 Homo sapiens cDNA
841	6693	11161	2.12	4.0E-62	AW161478.1	EST_HUMAN	au7103_Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:NM37104
841	5983	11162	2.12	4.0E-62	AW161478.1	EST_HUMAN	au7103_Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:NM37104
842	5983	11161	2.44	4.0E-62	AW161478.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); au7103_Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:NM37104
842	6693	11162	2.44	4.0E-62	AW161478.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); au7103_Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:NM37104
2435	7559	12782	4.32	4.0E-62	A1B27800.1	EST_HUMAN	wf1208_X1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23503359 3' similar to gb:X57138_maf HISTONE_H2B.2 (HUMAN);
2435	7639	12793	4.32	4.0E-62	A1B27800.1	EST_HUMAN	wf1208_X1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23503359 3' similar to gb:X57138_maf HISTONE_H2B.2 (HUMAN);
3380	8525		8.08	4.0E-62	4557987	NT	Human sapiens keratin 18 (KRT18) mRNA
73	5282	10420	0.7	3.0E-62	4857784	NT	Human sapiens neurofibromin 2 (bilateral acoustico-neuromatosis) (NF2) mRNA
3018	8172	13323	1.13	3.0E-62	AB040509.1	NT	Human sapiens mRNA for KIAA1478 protein, partial cds
3018	8172	13329	1.13	3.0E-62	AB040509.1	NT	Human sapiens mRNA for KIAA1478 protein, partial cds
3875	8314	13970	14.69	3.0E-62	X32858.1	NT	Human cyclotillin-related processed pseudogene
4948	10057	15195	228.4	3.0E-62	A1F229180.1	NT	Human sapiens alpha-enolase-activated semialdehyde synthase mRNA, complete cds
1234	8385	11538	2.82	2.0E-62	AI163284.2	NT	Human sapiens chitosome 21 segment HS2/Cd34
1046	8187	11354	1.22	1.0E-62	AI746540.1	NT	Human sapiens integrin 2 (SH3D1B) mRNA, complete cds
1559	8686	11875	10.74	1.0E-62	L78810.1	NT	Human sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds

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Table 4

Single Exon Probes Expressed In BT474 Cells

Probe seq ID No.	Exon seq ID No.	ORF seq ID No:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1811	8534	12149	1.89	1.0E-62	AAB25207.1	EST_HUMAN	af70e11.r1 Spores_NhIMPU_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WF:X01H12.1
2889	8534	12201	0.98	1.0E-62	AL036044.1	EST_HUMAN	DKEZp568F104_r1_568 (synonym: hikd2) Homo sapiens cDNA clone DKEZp568F104_5
3406	8548		0.97	1.0E-62	AB040911.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
4501	8620	14762	1.67	1.0E-62	-	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212). mRNA
330	5519	10853	2.1	9.0E-63	AW816405.1	EST_HUMAN	Q14-S10234-181189-037-008 S10234 Homo sapiens cDNA
4016	9148	14289	7.57	9.0E-63	AB022348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4015	9148	14280	7.57	9.0E-63	AB022348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
2354	7481	127117	18.68	8.0E-63	503_1810	NT	Homo sapiens IL-2-inducible T-cell kinase (ITK). mRNA
3443	8885	13748	2.77	8.0E-63	AF188348.1	NT	Gallus gallus Dach2 protein (Dach2). mRNA, complete cds
3443	8885	13747	3.27	8.0E-63	AF188349.1	NT	Gallus gallus Dach2 protein (Dach2). mRNA, complete cds
4239	8394	14497	4.21	8.0E-63	AI165268.2	NT	Homo sapiens chromosome 21 segment HS21C08B
830	6078		3.87	7.0E-63	AI872137.1	EST_HUMAN	Wnt5g11.x1 NCI_C3AP U12 Homo sapiens cDNA clone IMAGE:24396008 3'
3302	8449	13812	0.75	4.0E-63	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3788	8823	14072	1.19	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
3788	8823	14073	1.19	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
1939	7058	12280	2.85	3.0E-63	AB016260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2740	7834	13087	2.12	3.0E-63	J00310.1	NT	Human Me-RNA-4 gene 1
2781	6573	11649	10.08	3.0E-63	60056983	NT	Homo sapiens zinc finger protein 144 (ZNF144). mRNA
1883	5383	10625	1.65	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
195	5390	10533	1.29	2.0E-63	4885226	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EY2). mRNA
497	5684		1.72	2.0E-63	-	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamyltranspeptidase), catalytic (72.8kD) (GLCLC) mRNA
827	6880	11148	2.63	2.0E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1). mRNA
1581	6710	11901	1.49	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for RH blood CE group antigen polypeptide, complete cds
1581	6710	11902	1.49	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for RH blood CE group antigen polypeptide, complete cds
1777	6803	12111	2.88	2.0E-63	BE410739.1	EST_HUMAN	6015301827F1 NIH MGCC_21 Homo sapiens cDNA clone IMAGE:3636103 5'
3135	8286	13443	1.74	2.0E-63	-	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-1). Alzheimer disease (APP). mRNA
3260	8418	13580	2.28	2.0E-63	AF089718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3882	8018	14175	3	2.0E-63	388891.1	NT	Homo sapiens polymeric kidney disease-associated protein (PKD1) gene, complete cds
4835	8647	15091	1.35	2.0E-63	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
1527	6654	11840	1.29	1.0E-63	F0B485.1	EST_HUMAN	HSC22VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-2nd11

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 Table 4  
 Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1627	8654	11841	1.29	1.0E-63	FO8485.1	EST HUMAN	HSC2VD111 normalized Infant brain cDNA Homo sapiens cDNA clone o-zadf11
4319	8441	14574	2.78	1.0E-63	FO8485.1	EST HUMAN	HSC2VD111 normalized Infant brain cDNA Homo sapiens cDNA clone o-zadf11
4319	8441	14575	2.78	1.0E-63	FO8485.1	EST HUMAN	HSC2VD111 normalized Infant brain cDNA Homo sapiens cDNA clone o-zadf11
1048	6189		13.88	8.0E-64	BE280798.1	EST HUMAN	601165222F1 NIH MGCC_21 Homo sapiens cDNA clone IMAGE:3138038 6'
3518	8657		0.68	7.0E-64	BE394321.1	EST HUMAN	60131485F1 NIH MGCC_44 Homo sapiens cDNA clone IMAGE:3683204 5'
4700	8816	14833	2.21	7.0E-64	45D7490	NT	Homo sapiens thymidylate kinase-like peptidase (THOP1) mRNA
4700	8816	14864	2.21	7.0E-64	45D7490	NT	Homo sapiens thymidylate kinase-like peptidase 1 (THOP1) mRNA
1738	68683	12065	2.71	6.0E-64	AI651882.1	EST HUMAN	Wb51607X1 NCI CGAP_QC8 Homo sapiens cDNA clone IMAGE:2308220 3' similar to gbm16182 BETA-
1736	68683	12066	2.71	6.0E-64	AI651882.1	EST HUMAN	Wb51607X1 NCI CGAP_QC8 Homo sapiens cDNA clone IMAGE:2308220 3' similar to gbm16182 BETA-
3098	8262	13401	4.4	6.0E-64	AV028445.1	EST HUMAN	Wb13083X1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528438 3'
3099	8262	13402	4.4	6.0E-64	AV028445.1	EST HUMAN	Wb13083X1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528438 3'
821	5874	11137	3.78	6.0E-64	AF231910.1	NT	Homo sapiens chromosome 21 unknown mRNA
821	5874	11138	3.78	5.0E-64	AF231910.1	NT	Homo sapiens chromosome 21 unknown mRNA
1343	6472	11652	1.14	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
1728	6853	12053	1.38	5.0E-64	U88358.1	NT	Human (3)rib1, hamster mRNA, complete cds
2789	68117	11803	5.44	6.0E-64	7682205	NT	Homo sapiens KIAA0818 gene product (KIAA0818), mRNA
2789	68117	11803	5.44	5.0E-64	7682205	NT	Homo sapiens KIAA0818 gene product (KIAA0818), mRNA
3930	8068	14222	7.67	6.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
4211	8598	14468	0.65	5.0E-64	AF016898.1	NT	Homo sapiens B-ATF gene, complete cds
4211	8536	14469	0.65	5.0E-64	AF016898.1	NT	Homo sapiens B-ATF gene, complete cds
5161	8338	14468	0.67	5.0E-64	AF016898.1	NT	Homo sapiens B-ATF gene, complete cds
5161	8338	14469	0.67	5.0E-64	AF016898.1	NT	Homo sapiens B-ATF gene, complete cds
2182	7285	12542	2.86	3.0E-64	C18886.1	EST HUMAN	C18886 Human placenta cDNA (Tritjiwara) Homo sapiens cDNA clone GEN:539E02 6'
3231	8897	12549	0.71	3.0E-64	BET94381.1	EST HUMAN	60116565F1 NIH MGCC_7 Homo sapiens cDNA clone IMAGE:3843577 5'
3424	8668	13724	1.31	3.0E-64	AV711714	EST HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 6'
3424	8668	13725	1.31	3.0E-64	AV711714	EST HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 6'
1089	6228	-11383	1.18	2.0E-64	AI6808940.1	EST HUMAN	af00d08_31 Scores tests_NFT Homo sapiens cDNA clone IMAGE:1031151 3'
1404	6532	11710	1.92	2.0E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (4EIP) mRNA
2487	7601		1.3	2.0E-64	AI827030.1	EST HUMAN	Wb870101X1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:24622B1 3' similar to contains element L1 repetitive element;
2502	7605	12854	4.87	2.0E-64	AL168246.2	NT	Homo sapiens chromosome 21 segment HS21C048
2502	7605	12855	4.87	2.0E-64	AL168246.2	NT	Homo sapiens chromosome 21 segment HS21C048

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3118	8270	13428	1.05	2.0E-64	4604688	NT	Homo sapiens glutamyl-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA EST1310215 MAGE resequences, IMAGE Homo sapiens cDNA EST1310215 MAGE resequences, IMAGE Homo sapiens cDNA
3766	8903	14055	0.65	2.0E-64	AW658145.1	EST HUMAN	Homo sapiens chromosome 21 unknown mRNA
3768	8903	14056	0.65	2.0E-64	AW658145.1	EST HUMAN	Homo sapiens chromosome 21 unknown mRNA
255	6446	10534	1.7	1.0E-64	AF231919.1	NT	eu8601_x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2510136 3' similar to gb:LC1686_cds1 PROTHYMOSIN ALPHA (HUMAN) contains element MSR1 repetitive element;
1789	8916	12122	68.19	1.0E-64	AI28419.1	EST HUMAN	Homo sapiens transcription factor ISHM enhancer 3, JM11 protein, JM15 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha 2$ partial cds
3486	8837	13804	4.48	1.0E-64	AF198779.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3572	8713	13873	1.18	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3572	9719	13874	1.19	1.0E-64	AF228527.1	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA
3977	9013	14170	0.86	1.0E-64	8922829	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA
1058	6189	11394	6.24	6.0E-65	AV721898.1	EST HUMAN	AY721898 HTB Homo sapiens cDNA clone HTBZC08 5'
1927	7048		40.59	6.0E-65	AA656926.1	EST HUMAN	RRBOSOMAL PROTEIN L32 (HUMAN);
630	5790	10923	5.77	5.0E-65	AF084604.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1360	6489	11689	1.61	5.0E-65	7661851	NT	Homo sapiens KIAA0168 gene product (KIAA0168), mRNA
1360	6489	11670	1.51	5.0E-65	7661851	NT	Homo sapiens KIAA0168 gene product (KIAA0168), mRNA
2138	7252	12498	0.89	5.0E-65	AB033768.1	NT	Homo sapiens hPAO-D-cadmy10 mRNA for peptidylarginine deiminase type I, complete cds
3238	8388	13550	1.89	6.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3238	8388	13551	1.89	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
180	5385	10538	2.69	4.0E-65	AL120419.1	EST HUMAN	DKFZ476I0108_T761 (synonym: hany2) Homo sapiens cDNA clone DKFZ476I0108 5'
744	5800	11033	1.12	4.0E-65	AI286468.1	EST HUMAN	qm48601_x1 Soares placenta_8t6weeks_2NbHPatsW Homo sapiens cDNA clone IMAGE:16891600 3'
744	5800	11054	1.12	4.0E-65	AI286468.1	EST HUMAN	qm48601_x1 Soares placenta_8t6weeks_2NbHPatsW Homo sapiens cDNA clone IMAGE:16891600 3'
1080	6219	11385	1.97	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1488	6823	11811	2.14	4.0E-65	4566836	NT	Homo sapiens ribosomal protein L34 (RPL34), mRNA
2318	7428	12677	2.41	4.0E-65	BE221468.1	EST HUMAN	hu25604_x1 NCI CGAP_Mel16 Homo sapiens cDNA clone IMAGE:3171102 3'
2318	7428	12678	2.41	4.0E-65	BE221468.1	EST HUMAN	hu25604_x1 NCI CGAP_Mel16 Homo sapiens cDNA clone IMAGE:3171102 3'
3922	9058	14217	0.98	4.0E-65	AW658185.1	EST HUMAN	RC22-BN0033-160200-013-e03 EN0033 Homo sapiens cDNA
6167	10265	15405	0.92	4.0E-65	9055269	NT	Homo sapiens low density lipoprotein receptor related protein deleted in tumor (LRP01), mRNA
6167	10265	15406	0.92	4.0E-65	9055269	NT	Homo sapiens low density lipoprotein receptor related protein deleted in tumor (LRP01), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
83 5903	10443	10443	1.88	3.0E-65	5031978	NT	Homo sapiens pre-B cell colony-enhancing factor (PBEF) mRNA
84 6303	10443	1.37	3.0E-65	5031978	NT	Homo sapiens pre-B cell colony-enhancing factor (PBEF) mRNA	
1236 7870	2741	X78832.1	3.0E-65	X78832.1	NT	H_sapiens_H2B mRNA or zinc finger protein	
1973 6701	11889	3.1	3.0E-65	4504820	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products	
1834 6857	12179	1.48	3.0E-65	A1000892.1	EST_HUMAN	ov2303_61_Searces_ests_NH7 Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element	
2059 8113	13275	1.49	3.0E-65	D87078.2	NT	MSR1 repetitive element;	
3260 8409	13572	0.8	3.0E-65	4504950	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds	
3701 8839	13883	1.47	3.0E-65	A1000892.1	EST_HUMAN	ov2303_61_Searces_ests_NH7 Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element	
4518 9178	14874	1.39	3.0E-65	6912385	NT	MSR1 repetitive element;	
3385 8529	13691	6.17	2.0E-65	BF880284.1	EST_HUMAN	Homo sapiens activating protein (GAP and centrosome-associated) (GAPCENA), mRNA	
88 6285	203	2.03	1.0E-65	BF126544.1	EST_HUMAN	602165082F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286886 6'	
637 5703	10836	2.68	1.0E-65	7657486	NT	601768488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:40268901 6'	
2034 7152	12382	1.65	1.0E-65	AB040946.1	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homolog (RABE5), mRNA	
3354 8489	13887	1.18	1.0E-65	BE468681.1	EST_HUMAN	Homo sapiens mRNA for KIAA1513 protein, partial cds	
3973 9107	14255	2.13	1.0E-65	4504982	NT	h224689_x1 NCI_CGAP_GC20 Homo sapiens cDNA clone IMAGE:3208888 3'	
3973 9107	14256	2.13	1.0E-65	4504982	NT	Homo sapiens Glypean 4 (GPR4) mRNA	
4179 8905	14440	2.1	1.0E-65	AW028340.1	EST_HUMAN	w02839_x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543162 3'	
4179 8905	14441	2.1	1.0E-65	AW028340.1	EST_HUMAN	w02839_x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543162 3'	
70 5280	10416	1.98	8.0E-66	AL16031.1	NT	Novel human gene mapping to chromosome 22	
70 5280	10417	1.98	9.0E-68	AL16031.1	NT	Novel human gene mapping to chromosome 22	
1381 6480	11671	2.88	9.0E-68	6031890	NT	Homo sapiens 26S proteasome-associated p41 homolog (POH1) mRNA	
1381 6480	11672	2.88	9.0E-68	5031880	NT	Homo sapiens 26S proteasome-associated p41 homolog (POH1) mRNA	
1494 6621		5.38	9.0E-68	M87289.1	NT	Human transposon-like element, partial	
4344 9468	14502	1.18	8.0E-68	A1824853.1	EST_HUMAN	wn5707_x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449897 3' similar to WP:F16G9.4A	
4344 9468	14503	1.18	6.0E-68	A1824853.1	EST_HUMAN	CE18595;	
4344 9468	14504	1.18	6.0E-68	A1824853.1	EST_HUMAN	wn5707_x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449897 3' similar to WP:F16G9.4A	
4344 9468	14505	1.18	6.0E-68	A1824853.1	EST_HUMAN	CE18595;	
4344 9468	14506	1.18	6.0E-68	A1824853.1	EST_HUMAN	CE18595;	
1378 6504	11688	1.64	5.0E-68	BE084410.1	EST_HUMAN	RC4-B10311-141109-01-11-008 BT0311 Homo sapiens cDNA	
5091 10191	15330	2.25	5.0E-68	BE8588BA4.1	EST_HUMAN	601681692F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3351781 5'	

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 Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6031	101B1	1531	2.25	5.0E-58	BE898844.1	EST_HUMAN	6011981692F1 NIH MCG_9 Homo sapiens cDNA clone IMAGE:3951791 5'
781	8943	11105	0.87	4.0E-58	6079816 NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA	
2257	7387	12823	1.81	4.0E-58	X89211.1	NT	H_sapiens DNA for endogenous retroviral like element
2449	7553		2.75	4.0E-58	AL1223384.1	NT	Homo sapiens genomic DNA upstream of Jkappa locus
4761	8884		4.83	4.0E-58	9838487 NT		Human endogenous retrovirus, complete genome
1436	6583	11747	28.39	3.0E-58	4502098 NT		Homo sapiens solute carrier family 28 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC22A5), nuclear gene encoding mitochondrial protein, mRNA
1438	6663	11748	26.39	3.0E-58	4502098 NT		Homo sapiens solute carrier family 28 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC22A5), nuclear gene encoding mitochondrial protein, mRNA
1984	7101	12332	1.1	3.0E-58	N65323.1	EST_HUMAN	Y2Z7812.1 Scores _multiple_scenarios_2NbHMSP_H2B_1/H2B_2 [2] PIR:BB6812;
1984	7101	12333	1.1	3.0E-58	N65323.1	EST_HUMAN	Y2Z7812.1 Scores _multiple_scenarios_2NbHMSP_HISTONE_H2B_1/H2B_2 [2] PIR:BB6812;
1984	7101	12334	1.1	3.0E-58	N65323.1	EST_HUMAN	Y2Z7812.1 Scores _multiple_scenarios_2NbHMSP_HISTONE_H2B_1/H2B_2 [2] PIR:BB6812;
2689	7763	13018	4.38	3.0E-58	11141780 NT		Homo sapiens TGF-beta-induced transcription factor 2 (TGF2), mRNA
3038	8248	13986	0.5	3.0E-58	7862223 NT		Homo sapiens KIAA0848 gene product (KIAA0848), mRNA
60	8262	10387	2	2.0E-58	7857334 NT		Homo sapiens Misshephen/NIK-related kinase (MINK), mRNA
60	8262	10388	2	2.0E-58	7857334 NT		Homo sapiens Misshephen/NIK-related kinase (MINK), mRNA
421	8208	10320	0.98	2.0E-58	4505624 NT		Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5) mRNA, and translated products
421	8208	10321	0.89	2.0E-58	4505624 NT		Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5) mRNA, and translated products
1839	6980	12193	2.4	2.0E-58	AL163301.2	NT	Hom sapiens chromosomal 21 segment HS21C101
3508	8847	13813	1.16	2.0E-58	89223280 NT		Hom sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3745	8883	14033	1.02	2.0E-58	AL117233.1	NT	Novel human gene mapping to chromosome 1
4826	9743	14898	6.12	2.0E-58	AL133287.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
4825	9743	14897	6.12	2.0E-58	AL133287.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
1697	8825		1.77	1.0E-58	BE887173.1	EST_HUMAN	601508376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:39088891 5'
2850	8016	13180	1.52	1.0E-58	AV717817.1	EST_HUMAN	AV717817 DGB Homo sapiens cDNA clone DCEADCO7 5'
2850	8016	13181	1.52	1.0E-58	AV717817.1	EST_HUMAN	AV717817 DGB Homo sapiens cDNA clone DCEADCO7 5'
4364	8015	13180	2.87	1.0E-58	AV717817.1	EST_HUMAN	AV717817 DGB Homo sapiens cDNA clone DCEADCO7 5'
4364	8015	13181	2.97	1.0E-58	AV717817.1	EST_HUMAN	AV717817 DGB Homo sapiens cDNA clone DCEADCO7 5'

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## Single Exon Probes Expressed In BT474 Cells

Probe seq ID NO:	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4891 10002			0.61	8.0E-67	MT8198_1	EST_HUMAN	EST01750 Subtracted Hippocampus, Stratagene (cat. #886205) Homo sapiens cDNA clone HHCNPn81 similar to L1 repetitive element
379 55987	10732		1.89	7.0E-67	AW162232_1	EST_HUMAN	EST075022_1 Schneider fetal brain cDNA clone IMAGE-2782083 3' similar to gbmAS7104
1392 6320	11700		2.28	7.0E-67	AA383416_1	EST_HUMAN	EST18812 Testis   Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid ZK353
1689 6897	11884		4.25	7.0E-67	W85947_1	EST_HUMAN	EST05603_1 Scares_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE-416049_5'
1569 6897	11885		4.25	7.0E-67	W85947_1	EST_HUMAN	Zh66805_1 Scares_fetal_liver_spleen_cDNA clone IMAGE-416049_6'
2027 7144	12383		2.29	7.0E-67	7857243	NT	Homo sapiens testis 1,3,4-triphosphate 5'/6' kinase (TPK1), mRNA
2027 7144	12384		2.29	7.0E-67	7857243	NT	Homo sapiens testis 1,3,4-triphosphate 5'/6' kinase (TPK1), mRNA
2771 5987	10732		2.33	7.0E-67	AW162232_1	EST_HUMAN	EST075022_1 Schneider fetal brain 00014 Homo sapiens cDNA clone IMAGE-2782083 3' similar to gbmAS7104
6583 5723	10854		8.35	6.0E-67	X88868_1	NT	H.sapiens mRNA for acetyl-CoA carboxylase
788 5850	11110		1.88	6.0E-67	Z17227_1	NT	Homo sapiens mRNA for transmembrane receptor protein
1277 64008	11580		0.89	6.0E-67	Y14320_1	NT	Homo sapiens PMP29 gene, exons 3,4,5,6 & 7
3147 82288	13453		1.28	6.0E-67	4508434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3418 8881	13718		1.21	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3419 8881	13719		1.21	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4097 92226	14381		0.88	6.0E-67	AI168201_2	NT	Homo sapiens chromosome 21 segment HS21C001
4097 92226	14362		0.88	6.0E-67	AI168201_2	NT	Homo sapiens chromosome 21 segment HS21C001
4673 91789	14834		2.84	6.0E-67	7857020	NT	Homo sapiens Dkfp34P211 protein (DKFP-34P211), mRNA
4673 91789	14935		2.84	6.0E-67	7857020	NT	Homo sapiens Dkfp34P211 protein (DKFP-34P211), mRNA
5157 10257	15395		0.89	6.0E-67	AF016888_1	NT	Homo sapiens B-ATF gene, complete cds
5157 10257	16398		0.89	6.0E-67	AF016888_1	NT	Homo sapiens B-ATF gene, complete cds
3208 6357	13518		2.83	5.0E-67	AF056850_1	NT	Homo sapiens T cell receptor beta locus, TCRBV773A2 to TCRBV1232 region
1333 8462	11642		3.95	4.0E-67	RC0819_1	EST_HUMAN	RC0221_1.1 Scares adult brain N2BH/B5BY Homo sapiens cDNA clone IMAGE-187253_5'
2774 5792	10828		1.33	3.0E-67	AA333768_1	EST_HUMAN	EST37803 Embryo, 9 week Homo sapiens cDNA 5' end
3435 8577	13737		1.12	3.0E-67	BE008440_1	EST_HUMAN	RC4-BT0311-141188-011-h06 B10311 Homo sapiens cDNA
4863 61779	14923		2.28	3.0E-67	AW889169_1	EST_HUMAN	MRQ-SU0062-04050-008-f01 SNQ058 Homo sapiens cDNA
4690 8808			0.92	3.0E-67	AL168270_2	NT	Homo sapiens chromosome 21 segment HS21C001
184 5379	10520		1.33	2.0E-67	BE548354_1	EST_HUMAN	Iw16699_x1 NCI_OCBP_Lu24 Homo sapiens cDNA clone IMAGE-3183138 3' similar to WP-F23H119
848 55897	111683		3.92	2.0E-67	AW816405_1	EST_HUMAN	CE08617_;
1103 62244			1.98	2.0E-67	AF167460_1	NT	QV4-570234-181199-037-405 ST0234 Homo sapiens cDNA
							Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe seq ID	Exon seq ID No:	ORF seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1892	7011	12232	1.51	2.0E-67	BE305037.1	EST_HUMAN	ba72c05.y1 NIH MGCG_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O34832 084892
1892	7011	12233	1.61	2.0E-67	BE305037.1	EST_HUMAN	ba72c05.y1 NIH MGCG_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O34832 084892
2221	7333	12589	1.11	2.0E-67	11422946	NT	Homo sapiens hypothetical protein J4462023.2 (J4462023.2), mRNA
2221	7333	12687	1.11	2.0E-67	11422946	NT	Homo sapiens hypothetical protein J4462023.2 (J4462023.2), mRNA
2384	7170	12723	2.48	2.0E-67	AF305661.1	NT	Homo sapiens KRB zinc finger protein ZFQR mRNA, complete cds
2409	7616	12765	2.21	2.0E-67	4758795	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRCG1), mRNA
3449	8591	13765	3.62	2.0E-67	A626765.1	EST_HUMAN	z08f001.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:7453392 3'
3977	6111	14259	2.44	2.0E-67	AL168360.2	NT	Homo sapiens chromosome 21 segment HS21/C100
250	5441	10581	4.73	1.0E-67	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (precursor protein: Alzheimer disease) (APP), mRNA
708	5683	11010	1.9	1.0E-67	AA102784.1	EST_HUMAN	z501650.81 Soares, fetal liver, spleen, INFNL_S1 Homo sapiens cDNA clone IMAGE:2448015 3'
4870	9196	14940	0.8	1.0E-67	BF432447.1	EST_HUMAN	na65f08.x1 Soares_NSF_F8_9W_OT_P_A_P_S1 Homo sapiens cDNA clone IMAGE:3
2156	7269	12517	4.77	8.0E-68	BE870732.1	EST_HUMAN	601448568F1 NIH_M/GC_65 Homo sapiens cDNA clone IMAGE:38322854 5'
3848	8884	14139	5.22	8.0E-68	AA209456.1	EST_HUMAN	z082110.11 Strategene HNT neuron (R8317233) Homo sapiens cDNA clone IMAGE:348163 5' similar to SAV_SULAC_Q07550 SAV PROTEIN.
3848	8884	14140	5.22	8.0E-68	AA209456.1	EST_HUMAN	z082110.11 Strategene HNT neuron (R8317233) Homo sapiens cDNA clone IMAGE:348163 5' similar to SAV_SULAC_Q07550 SAV PROTEIN.
1899	7018		1.22	6.0E-68	AW508942.1	EST_HUMAN	U1-H-BN0-ab<0-0-U1.r1 NIH_M/GC_50 Homo sapiens cDNA clone IMAGE:3078824 5'
603	7866	11113	0.72	6.0E-68	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
803	7586	11119	0.72	6.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
820	5673	11135	3.62	5.0E-68	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
820	5673	11136	3.62	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2741	7836	13088	38.26	5.0E-68	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
3125	8277	13433	2.97	6.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4162	8278		0.76	6.0E-68	4826987	NT	Homo sapiens retroblastoma-binding protein 2 (RBBP2), mRNA
2493	7602	12849	1.27	4.0E-68	11421988	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2493	7602	12850	1.27	4.0E-68	11421988	NT	Homo sapiens transcription factor NRF (NRF), mRNA
3084	8217		1.12	4.0E-68	AW207003.1	EST_HUMAN	U1-H-B11_and<0-0-U1.s1 NCI CGAP_Suds3 Homo sapiens cDNA clone IMAGE:2721309 3'
4960	10688		18.6	4.0E-68	P04406	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
3636	8177	13932	5.79	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
2825	10313		32.61	2.0E-68	D00522.1	NT	Cricetulus longicaudatus mRNA for EF-1 epsilon, complete cds

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description	
3988 9132	14278	0.7	2.0E-68	BE376786.1	EST_HUMAN	7F16D2.1 NCI_CGAP_CL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:Q308228 Q308228	HYPOTHETICAL_68.8 KO PROTEIN_N;	
4653 9770	14918	2.05	2.0E-68	AB086681.1	NT	Homo sapiens gene for extrin receptor type II B, complete cds		
284 5482	10624	11.03	1.0E-68	AW816405.1	EST_HUMAN	QV4-ST0234-181189-037-035 ST0234 Homo sapiens cDNA		
2232 7344	12698	1.34	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds		
2232 7344	12699	1.34	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds		
2720 7815	13071	1.15	1.0E-68	AW461832.1	EST_HUMAN	U+HB3-ek4-0-0-U1.61 NCI_CGAP_SubB Homo sapiens cDNA clone IMAGE:2737272 3'		
3985 9119	142638	1.54	1.0E-68	BE285032.1	EST_HUMAN	6011177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'		
5055 10157	15288	1.98	1.0E-68	BE285032.1	EST_HUMAN	6011177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 6'		
20 6231	10343	8.71	9.0E-69	5001876	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBCE) mRNA		
20 6231	10344	8.71	9.0E-69	6031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBCE) mRNA		
1020 6710	11335	1.68	9.0E-69	6021980	NT	Homo sapiens 26S proteasome-associated peptid homolog (POH) mRNA		
1020 6710	11338	1.68	9.0E-69	6031980	NT	Homo sapiens 26S proteasome-associated peptid homolog (POH) mRNA		
4100 8228	14986	0.69	8.0E-69	4757887	NT	Homo sapiens vraf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA		
3387 8512			1.14	8.0E-69	AJ237744.1	NT	Homo sapiens RIBR gene (partial), exon 12	
518 6584			0.98	4.0E-69	AI873630.1	EST_HUMAN	Wm26n11.x1 NCI_CGAP_Utk Homo sapiens cDNA clone IMAGE:2437125 3'	
384 5593	10739	5.27	3.0E-69	BE268012.1	EST_HUMAN	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3561362 5'		
609 67639	10898	1.98	3.0E-69	AF221712.1	NT	Homo sapiens Smad4- and Oil-interacting zinc finger protein mRNA, partial cds		
1570 68538						yd08e02.11 Seares infant brain NIH Homo sapiens cDNA clone IMAGE:24880 5' similar to SP:AA8838		
4940 10050	16188	0.97	3.0E-69	AB037732.1	NT	AA8838 SPEGF III=EGF REPEAT-CONTAINING FIBROELLIN-LIKE PROTEIN - SEA URCHIN ;		
5128 9189	14230	0.95	3.0E-69	AI755888.1	EST_HUMAN	Wf88g08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385768 3'		
124 6571	10718	2.22	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha/beta protein gene, partial cds		
124 5571	10719	2.22	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha/beta protein gene, partial cds		
404 6571	10718	4.69	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha/beta protein gene, partial cds		
404 6571	10719	4.69	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha/beta protein gene, partial cds		
1893 7012	12234	2.34	2.0E-69	BE267857.1	EST_HUMAN	601106444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3550174 5'		
2808 7862		3.38	2.0E-69	AA431167.1	EST_HUMAN	zv771g02.11 Seares testis_NHT Homo sapiens cDNA clone IMAGE:781682 5'		
1718 6845	12048	1.61	1.0E-69	AF053788.1	NT	Rattus norvegicus brain specific catenulin-binding protein CBP80 mRNA, partial cds		
2319 7037	12072	2.34	8.0E-70	AA230363.1	EST_HUMAN	ne13d12.1 NCI_CGAP_P-1 Homo sapiens cDNA clone IMAGE:1008023		
4352 9874	14812	1.7	8.0E-70	L77668.1	NT	Homo sapiens DGS-I mRNA, 3' end		
1825 6948	12169	3.57	7.0E-70	AI497807.1	EST_HUMAN	lm8901.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2168306 3'		
1825 6948	12170	3.57	7.0E-70	AI497807.1	EST_HUMAN	lm8901.x1 NCI_CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2168306 3'		

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1835	7054	12276	1.88	7.0E-70	AA282855.1	EST_HUMAN	Z16904..1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'
2058	7172		6.1	7.0E-70	EE316885.NT	Homo sapiens Lmnr suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA	
4202	8327	14459	3.42	7.0E-70	4757723.NT	Homo sapiens endoylevel cyclase 3 (ADCY3) mRNA	
872	6023	11104	3.49	6.0E-70	4502168.NT	Homo sapiens amyloid beta (A4) precursor protein (protease neutral), Alzheimer disease (APP) mRNA	
2126	7239	12482	6.8	6.0E-70	MS0688.1	Human Ku (p70/p80) subunit mRNA, complete cds	
2478	7684	12834	2.07	6.0E-70	8923889.NT	Homo sapiens Cif-N-acetylneuraminate acid synthase (LOC55307) mRNA	
2523	7842	12871	3.33	5.0E-70	7662307.NT	Homo sapiens KIAA0792 gene product (KIAA0792) mRNA	
2623	7842	12872	3.33	5.0E-70	7662307.NT	Homo sapiens KIAA0792 gene product (KIAA0792) mRNA	
1802	6730	11921	5.33	3.0E-70	BE071786.1	RC0-BT0522-0717286-011-e12 BT0522 Homo sapiens cDNA	
1802	6730	11922	5.33	3.0E-70	BE071786.1	RC0-BT0522-0717286-011-e12 BT0522 Homo sapiens cDNA	
6137	10237	16373	0.94	3.0E-70	AJ271738.1	Homo sapiens Xq pseudobautosomal region; segment 22	
37	6248	10398	1.24	2.0E-70	AF02872.1	NT	Hom sapiens phosphatidylserine 4 kinase 230 (PK230) mRNA, complete cds
687	6845	10885	13.85	2.0E-70	N42161.1	EST_HUMAN	Y07410..1 Scores melanocyte 2N14-H Homo sapiens cDNA clone IMAGE:270522 5' similar to SW-D3H1_RAT_P29268_3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR;
687	6845	10886	13.85	2.0E-70	N42161.1	EST_HUMAN	Y07410..1 Scores melanocyte 2N14-H Homo sapiens cDNA clone IMAGE:270522 5' similar to SW-D3H1_RAT_P29268_3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR;
703	6880	11009	2.61	2.0E-70	AI248899.1	EST_HUMAN	Q51h01..1 Scores Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1022	6163	11329	1.73	2.0E-70	8923668.NT	Homo sapiens hypothetical protein FLJ20788 (FLJ20788) mRNA	
1180	6320	11498	4.33	2.0E-70	7661983.NT	Homo sapiens KIAA0168 gene product (KIAA0168) mRNA	
1188	6320	11499	4.33	2.0E-70	7661983.NT	Homo sapiens KIAA0168 gene product (KIAA0168) mRNA	
1764	6880	12086	1.41	2.0E-70	AL1632022.NT	Hom sapiens chromosome 21 segment HS21C002	
2288	7407		4.84	2.0E-70	AA054010.1	EST_HUMAN	Z4894..1 Scores retina N264HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:3AG_HNL1A P03405_GAG POLYPROTEIN;
2460	7584	12817	1.35	2.0E-70	AB011173.1	Hom sapiens mRNA for KIAA0621 protein, partial cds	
3787	8934	14081	2	2.0E-70	AL133207.2	New human gene mapping to chromosome X	
4023	9153	14298	4.93	2.0E-70	M69181.1	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds	
4184	62260	14428	0.9	2.0E-70	L78810.1	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds	
4184	62260	14427	0.9	2.0E-70	L78810.1	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds	
3374	8519		3.07	1.0E-70	4507474.NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-glutamate-gamma-methionyltransferase) (TGm3) mRNA	
2192	7304	12554	31.81	6.0E-71	AF0568322.1	Homo sapiens SP100-LHM nuclear autoantigen (SP100) mRNA, complete cds	
4092	62221	14358	1.07	6.0E-71	AW816405.1	QY4-ST0234-181188-037405 ST0234 Homo sapiens cDNA	
100	5309	10448	0.9	4.0E-71	4507582.NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA	

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
347	65310	108688	331.53	4.0E-71	AF157826.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
347	65310	108689	331.63	4.0E-71	AF157828.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2845	80000	13169	1.01	4.0E-71	770544.4	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2845	80000	13169	1.01	4.0E-71	770541.4	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2853	80008	131683	2.01	4.0E-71	4505880	NT	Homo sapiens plasmalogen (PLG) mRNA
4408	85228	148683	6.18	4.0E-71	AF0568322.1	NT	Homo sapiens SIP10-HMG nuclear autoantigen (SP100) mRNA, complete cds
4971	10079	15216	5.78	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SDU), mRNA
1233	6564	11637	6.91	2.0E-71	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C068
637	51788	108332	1.78	1.0E-71	AI077827.1	EST_HUMAN	cyt5e03_61 Soenes _senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:16655916 3' similar to LOR1_b2 LOR1 repetitive element;
941	6069	11257	3.28	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1101	6239	11402	3.42	1.0E-71	AE026890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 16 and complete cds
1346	8474	11654	8.13	1.0E-71	AF0128972.1	NT	Homo sapiens phosphatidylglycerol 4-kinase 230 (PGK230) mRNA, complete cds
2078	7181	12434	3.22	1.0E-71	AB1017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2078	7181	12435	3.22	1.0E-71	AB1017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2854	7762	13001	2.34	1.0E-71	7657163	NT	Homo sapiens hairy enhancer-of-split related with YRPW motif-like (HEY1), mRNA
3484	8825	13782	2	1.0E-71	AF198685.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3682	8723	13880	6.81	1.0E-71	AF248219.1	NT	Homo sapiens SNAK protein kinase SNAK mRNA, complete cds
3682	8723	13881	6.81	1.0E-71	AF248219.1	NT	Homo sapiens SNAKE protein kinase SNAK mRNA, complete cds
3628	8765	13920	0.83	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library_Upreregulated Transcripts Homo sapiens cDNA clone 02_15 similar to Homo sapiens chromosome 18
3628	8765	13921	0.83	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library_Upreregulated Transcripts Homo sapiens cDNA clone 02_15 similar to Homo sapiens chromosome 19
3722	8860	14013	2.47	1.0E-71	AF218804.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 19.
4449	8568	14709	1.82	1.0E-71	D28476.1	NT	Human mRNA for KIAA0046 gene, complete cds
407	5574	10721	0.89	9.0E-72	AB57635.1	EST_HUMAN	WB85d3.x1 NCI_OGA_P_Lu19 Homo sapiens cDNA clone IMAGE:2423198 3' similar to TRQ088705 O88705
407	5574	10722	0.89	9.0E-72	AB57635.1	EST_HUMAN	WB85d3.x1 NCI_OGA_P_Lu19 Homo sapiens cDNA clone IMAGE:2423198 3' similar to TRQ088705 O88705
4088	9216	14850	1.61	7.0E-72	4501686	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4088	9216	14851	1.61	7.0E-72	4501688	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4088	6216	14352	1.61	7.0E-72	4501886	NT	
62	5273	10407	2.16	6.0E-72	BF333707.1	EST_HUMAN	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
62	5273	10408	2.15	5.0E-72	BF333707.1	EST_HUMAN	QVO-CS0010-150500-388-911 CS0010 Homo sapiens cDNA
63	5273	10407	8.82	8.0E-72	BF333707.1	EST_HUMAN	QVO-CS0010-150500-388-911 CS0010 Homo sapiens cDNA
63	5273	10408	8.82	5.0E-72	BF333707.1	EST_HUMAN	QVO-CS0010-150500-388-911 CS0010 Homo sapiens cDNA
1140	6277		1.83	6.0E-72	L11845.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
4780	8803		1.2	4.0E-72	11034844	NT	Homo sapiens hypothetical protein J11057B20.2 (D11057B20.2), mRNA
19	52320	10342	2.05	3.0E-72	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
604	6054		0.93	3.0E-72	AA723523.1	EST_HUMAN	aaH63008_61 Socres testis DNA clone 1310280 3'
1158	6282	11455	7.41	3.0E-72	UJ16308.1	NT	Human chondroitin sulfate proteoglycan veristicin V0 splice-variant precursor peptide mRNA, complete cds
1158	6282	11453	7.41	3.0E-72	UJ16308.1	NT	Human chondroitin sulfate proteoglycan veristicin V0 splice-variant precursor peptide mRNA, complete cds
1188	63320	11497	1.48	3.0E-72	UJ09226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1188	63320	11498	1.48	3.0E-72	UJ09226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1634	6861	11847	1.1	3.0E-72	BE242161.1	EST_HUMAN	TCAA1P1E1262 Pedicellit acute myelogenous leukemic cell (FAB M1) Bayor-HGSC project TCAA Human
3046	82020	133258	10.8	3.0E-72	AJ225043.1	NT	Human sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3262	84111	13573	2.73	3.0E-72	88223548	NT	Human sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3801	8838	14083	2.78	3.0E-72	\$T7688.1	NT	TCR V delta 2-C alpha T-cell receptor delta and C epsilon fusion gene (alternatively spliced, splice junction)
4395	86115	14658	1.1	3.0E-72	AF143382.1	NT	Human sapiens fibroblast-like pitkin (TXNL) gene, exon 3
4395	86116	14867	1.1	3.0E-72	AF143382.1	NT	Human sapiens fibroblast-like pitkin (TXNL) gene, exon 3
4518	86316	14781	2.83	3.0E-72	11416180	NT	Human sapiens hypothetical protein (FLJ11127), mRNA
4732	8845	14990	1.34	3.0E-72	AF167572.1	NT	Human sapiens protein methyltransferase (IPBP1) mRNA, complete cds
4732	8845	14691	1.34	3.0E-72	AF167572.1	NT	Human sapiens protein methyltransferase (IPBP1) mRNA, complete cds
4889	10010	15165	1.06	3.0E-72	AI864337.1	EST_HUMAN	WS81608_61 NCI CGAP - GIC8 Homo sapiens cDNA clone IMAGE:2307264 3'
2087	7183	12423	1.08	1.0E-72	AA846225.1	EST_HUMAN	ab3dd0221 Socres testis_ parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1387395 3'
1472	6590	11785	1.63	9.0E-73	AW374988.1	EST_HUMAN	MRO-CT0063-071098-002-4-11 CT0063 Homo sapiens cDNA
1040	6160	11345	1.57	8.0E-73	AW071755.1	EST_HUMAN	Q65606_61 NCI CGAP_Bm26 Homo sapiens cDNA clone IMAGE:25010688 3' similar to TR-Q656050
1423	68556	11737	2.38	8.0E-73	AI024877.1	EST_HUMAN	0339108_61 Socres testis_NHT Homo sapiens cDNA clone IMAGE:16339743 3'
1135	6272	11438	1.92	7.0E-73	88223280	NT	Human sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit BLAST) Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3283	8432	13594	0.89	7.0E-73	AL163206.2	NT	Human sepiens chromosome 21 segment HS21C009
4821	10031		1.81	7.0E-73	AL163228.2	NT	Human sepiens chromosome 21 segment HS21C022
163	6350		2.18	8.0E-73	AL1632219.2	NT	Human sepiens chromosome 21 segment HS21C018
1346	8475	11656	2.17	3.0E-73	AWB43789.1	EST_HUMAN	CMB-CN0044-280100-1B4-F08 cDNA clone IMAGE
1873	68983	122118	1.47	3.0E-73	114S6913	NT	Human sepiens homeo-binding protein (HEBP) mRNA
1873	68983	122119	1.47	3.0E-73	114S5913	NT	Human sepiens homeo-binding protein (HEBP) mRNA
852	6003	11174	2.63	2.0E-73	AF436897.1	NT	Human sepiens BASS1 (BASS1) mRNA, partial cds
1950	7088		3.28	2.0E-73	AWB68981.1	EST_HUMAN	RC3-LNN0088-270400-011->04 NN0068 Human sepiens cDNA
2271	7381		1.08	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3161	6312	13473	3.88	2.0E-73	4502582	NT	Human sepiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3537	8879	13840	0.63	2.0E-73	7691539	NT	Human sepiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3537	8879	13841	0.63	2.0E-73	7691539	NT	Human sepiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
4411	8831		1.08	2.0E-73	AL163283.2	NT	Human sepiens chromosome 21 segment HS21C033
1783	6619	12129	2.37	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1000480 5'
2458	7562	12814	1.65	1.0E-73	AF168349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
739	5895	11047	2.05	8.0E-74	4557128	NT	Human sepiens CD38-like 4 (CD38L4) mRNA
1853	7070	12284	2.19	7.0E-74	AJ001689.1	NT	Human sepiens NKGD2 gene, exon 10
3309	8458	13818	1.22	7.0E-74	AL163248.2	NT	Human sepiens chromosome 21 segment HS21C048
1128	8261	11426	3.48	6.0E-74	AF105907.1	NT	Human sepiens S104 gene, partial cds; P5' and hypothermic protein genes, complete cds; and S171 gene, partial cds
2284	7403	12654	89.23	6.0E-74	BE38821F1_NIH_M/GC_44 Human sepiens cDNA clone IMAGE-3605453 6'	EST_HUMAN	601283521F1_NIH_M/GC_44 Human sepiens cDNA clone IMAGE-3605453 6'
2284	7403	12655	89.23	6.0E-74	BE38826.1	EST_HUMAN	601283521F1_NIH_M/GC_44 Human sepiens cDNA clone IMAGE-3605453 6'
2827	7882	13144	1.2	6.0E-74	AW014039.1	EST_HUMAN	UHH-B10-seih-03-0-4II.1 NT NCI CGAP_Sub1 Human sepiens cDNA clone IMAGE-27053365 3'
2827	7882	13146	1.2	6.0E-74	AW014039.1	EST_HUMAN	UHH-B10-seih-03-0-4II.1 NT NCI CGAP_Sub1 Human sepiens cDNA clone IMAGE-27053365 3'
3692	8830	13984	1.39	6.0E-74	BE048846.1	EST_HUMAN	Int64e11.X1 NCI CGAP_Kid11 Human sepiens cDNA clone IMAGE-3132332 3'
3692	8830	13985	1.39	6.0E-74	BE048846.1	EST_HUMAN	Int64e11.X1 NCI CGAP_Kid11 Human sepiens cDNA clone IMAGE-3132332 3'
5011	10114	16244	1	6.0E-74	4758135	NT	Human sepiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5011	10114	16245	1	6.0E-74	4758135	NT	Human sepiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
903	60558	11225	2.51	5.0E-74	AW0203886.1	EST_HUMAN	dtf17c98.Y1 Morton Fetal Cochlea Human sepiens cDNA clone IMAGE-2483704 5'
2683	7769		6.84	5.0E-74	AV362766.1	EST_HUMAN	PMB-C70289-271099-001-H07 C70289 Human sepiens cDNA

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 Table 4  
 Single Exon Probes Expressed In BT474 Cells

Probe seq ID No:	Exon seq ID No:	ORF seq ID NC:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
277	54683	10609	5.66	4.0E-74	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
853	6004	11175	11.32	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1018 protein, partial cds
1888	7083	12307	1.19	4.0E-74	AB026888.1	NT	Homo sapiens DNA, DLECT1 to ORC1L4 gene region, section 12/DLECT1, ORC1L3, ORC1L4 genes, complete cds)
1886	7083	12308	1.19	4.0E-74	AB026889.1	NT	Homo sapiens DNA, DLECT1 to ORC1L4 gene region, section 12/DLECT1, ORC1L3, ORC1L4 genes, complete cds)
2084	7180	12419	11.24	4.0E-74	45031622	NT	Homo sapiens proteasome (prosome, macrophain) subunit, beta type, 1 (PSMB1) mRNA
2084	7180	12420	11.24	4.0E-74	45031692	NT	Homo sapiens proteasome (prosome, macrophain) subunit, beta type, 1 (PSMB1) mRNA
2123	7238	12481	1.98	4.0E-74	AB032894.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2404	7510	12760	7.18	4.0E-74	AJ008978.1	NT	Homo sapiens PLP gene
3053	8216	13370	6.84	4.0E-74	AJ009376.1	NT	Homo sapiens chromosome 21 segment HS21C010
3514	86555	13821	0.83	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C047
4038	9169	14310	1	4.0E-74	AL163247.2	NT	Homo sapiens KIAA0568 gene product (KIAA0568), mRNA
4680	6848	14784	1.71	4.0E-74	7662163	NT	Homo sapiens mRNA for transmembrane receptor protein
4568	9704	14842	0.87	4.0E-74	Z17227.1	NT	Homo sapiens hydroxacy-Coenzyme A thiolesterase/3-ketocyste-Coenzyme A thiolesterase
5057	10169	16280	1.18	4.0E-74	4604328	NT	Hydrolase (infunctional protein), beta subunit (HADHB) mRNA
5057	10159	16291	1.18	4.0E-74	4504326	NT	Homo sapiens hydroxacy-Coenzyme A thiolesterase/3-ketocyste-Coenzyme A thiolesterase
959	8107	11276	397.42	2.0E-74	7663491	NT	Hydrolase (infunctional protein), beta subunit (HADHB) mRNA
959	8107	11277	397.42	2.0E-74	7663491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1177	6312	11480	1.04	2.0E-74	AF020392.1	NT	Human endogenous retrovirus HERV-K-T47D
1248	6378	11557	3.01	2.0E-74	A1950528.1	EST_HUMAN	Q951e07_X1_NCI_CGAP_L128 Homo sapiens cDNA clone IMAGE:2547204-3' similar to SW/GS85_HUMAN Q08378 GOLGIN_65; contains element MER22 repetitive element;
1668	6738	11829	3.81	2.0E-74	4885168	NT	Homo sapiens epidermal growth factor receptor (avan erythroblast leukaemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1668	6738	11830	3.81	2.0E-74	4885168	NT	Homo sapiens epidermal growth factor receptor (avan erythroblast leukaemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
2568	78687	12822	7.73	2.0E-74	A1557280.1	EST_HUMAN	PT1.1_15_G11.1 tumor2 Homo sapiens cDNA 3'
4993	10089	15229	2.72	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
4993	10089	15230	2.72	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
52	5264	10391	2.53	1.0E-74	7657334	NT	Homo sapiens Mitisheper/NIK-related kinase (MINK), mRNA
335	6518	10654	3.25	1.0E-74	AW616405.1	EST_HUMAN	QVA5_T0234-1811864-337-f05 ST0234 Homo sapiens cDNA
499	5666	10801	1.38	1.0E-74	8922820	NT	Homo sapiens hypothetical protein FLJ11028, mRNA

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe seq ID No:	Exon seq ID No:	ORF seq ID No:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
508	5872	10808	13.77	1.0E-74	X02344.1	NT	Human sepiens beta 2 gene
689	6761	10839	1.72	1.0E-74	450820	NT	Human sepiens zinc finger protein 239 (ZNF239) mRNA
1000	6146	111313	2.39	1.0E-74	AL168246.2	NT	Human sepiens chromosome 21 segment HS21C046
2209	73220	12571	3.57	1.0E-74	AB012058.1	NT	Human sepiens DNA for Human P2Y6, complete cds
3117	82659	13425	3.47	1.0E-74	4758597	NT	Human sepiens membrane kinase, alpha, class 2A, member 1 (MAN2A1), mRNA
3885	8031	141190	0.87	1.0E-74	4504116	NT	Human sepiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3895	8031	141191	0.87	1.0E-74	4504116	NT	Human sepiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3941	80777	14231	6.64	1.0E-74	AL168268.2	NT	Human sepiens chromosome 21 segment HS21C038
4039	9170	14311	0.9	1.0E-74	BE083060.1	EST_HUMAN	RC2-BT0842-270300-019-f06 BT0842 Homo sapiens cDNA h273n08.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE-3213663 3' similar to WP-B0511.12
4241	8861	14489	0.72	1.0E-74	BE467769.1	EST_HUMAN	CE17361;
2807	7708		2.28	8.0E-75	AF476228.1	NT	Human sepiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
2269	7408	12859	1.55	6.0E-75	AB187446.1	EST_HUMAN	W638n08.x1 NCI CGAP_Pt22 Homo sapiens cDNA clone IMAGE-2417654 3' similar to gb:M4123_cds4
108	58112	10451	1.9	4.0E-75	BE081533.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN (HUMAN); QV1-H2T0522-210200-079-e022 BT0532 Homo sapiens cDNA y850n08.r1 Seacrest melanocyte 2b1bHM Homo sapiens cDNA clone IMAGE-259056.6'
4583	58226		1.35	4.0E-75	N38757.1	EST_HUMAN	CMB-AN0057-150400-325-411 N10057 Homo sapiens cDNA
1778	6592	12110	1.14	4.0E-75	AV897230.1	EST_HUMAN	601303888F1 NIH_3T3 cell IMAGE-3638344.5'
2811	7987	13127	6.48	4.0E-75	AB09464.1	EST_HUMAN	Human sepiens hypodermal proteolipid protein (FLJ10747) mRNA
2483	8824	13791	1.18	4.0E-75	8822897	NT	Human sepiens HTR2A serine protease (PRSS811) gene, complete cds
1003	8149	11316	3.28	3.0E-75	AF157623.1	NT	Human sepiens HTR2A serine protease (PRSS811) gene, complete cds
1004	8149	11316	2.31	3.0E-75	AF157623.1	NT	Human sepiens HTR2A serine protease (PRSS811) gene, complete cds
1850	6871	12192	1.97	3.0E-75	AB011153.1	NT	Human sepiens mRNA for KIAA0587 protein, partial cds
2400	75058	12765	2.07	3.0E-75	4759163	NT	Human sepiens synapsosomal-associated protein, 29kD (SNAP29) mRNA
2883	8148	13303	0.81	3.0E-75	AL168201.2	NT	Human sepiens chromosome 21 segment HS21C001
3172	8823	13484	1.18	3.0E-75	AB011153.1	NT	Human sepiens mRNA for KIAA058 protein, partial cds
3332	8478	13842	0.65	3.0E-75	M72353.1	NT	Human calcium-dependent phosphotyrosine-binding protein (PLA2) mRNA, complete cds
3332	8478	13843	0.65	3.0E-75	M72353.1	NT	Human calcium-dependent phosphotyrosine-binding protein (PLA2) mRNA, complete cds
4139	9287	14407	1.34	3.0E-75	D87675.1	NT	Human sepiens DNA for amyloid precursor protein, complete cds
4414	8634	14873	1.22	3.0E-75	7682421	NT	Human sepiens KIAA0571 protein (KIAA0571), mRNA xg60022.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE-2632707 3' similar to contains PTR7.H1
2278	7388	12633	15.13	1.0E-75	AW168135.1	EST_HUMAN	PTR7 repetitive element;
2912	80868	13239	3.84	1.0E-75	X52221.1	NT	H_sepiens ERCC2 gene, exons 1 & 2 (partial)
43	5255	10375	7.93	9.0E-76	AB852848.1	EST_HUMAN	W63010.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE-2307163 3' similar to TR-O76235 O76235 TRAP1;

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
43	5255	10378	7.83	8.0E-76	A1852648.1	EST_HUMAN	wis0b10_x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:075235 075236
638	6086	11283	0.77	8.0E-76	4504374.1	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
838	6088	11284	0.77	8.0E-76	4504374.1	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
778	6930	11089	2.61	7.0E-76	5016022	NT	Homo sapiens dihydropeptidase dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutamate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3276	84265	13588	2.66	7.0E-76	AF056460.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3282	8431	13583	6.25	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 76 (LY76) mRNA, and translated products
4350	9472	14689	4.75	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4350	9472	14610	4.75	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1237	6387	7279	8.0E-76	BE306253.1	EST_HUMAN	601312015F1 NIH MSG-44 Homo sapiens cDNA clone IMAGE:30558737 5'	
1947	7055	12288	28.0	8.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1947	7056	12289	28.9	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1947	7055	12290	28.9	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
628	6788	10920	1.68	3.0E-76	BF316282.1	EST_HUMAN	U+HBW1-a02-b04-c04-d04-e04-f04-g04-h04-i04 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083882 3'
628	6788	10921	1.68	3.0E-76	BF316282.1	EST_HUMAN	U+HBW1-a02-b04-c04-d04-e04-f04-g04-h04-i04 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083882 3'
1612	6740	11634	11.26	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1612	6740	11935	11.26	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3410	8653	13711	5.9	3.0E-76	BF375689.1	EST_HUMAN	RC6-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3410	8553	13712	5.9	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
4056	9185	14327	1.33	3.0E-76	BE348693.1	EST_HUMAN	h67712_x1 NCI_CGAP_Luz24 Homo sapiens cDNA clone IMAGE:3151823 3' similar to TR:094888 094888
279	6468	10611	1.69	2.0E-76	DB4295.1	NT	KIAA0792 PROTEIN ;
340	8523	10838	2.51	2.0E-76	DB4285.1	NT	Human mRNA for possible protein TPRL1, complete cds
340	5523	10839	2.51	2.0E-76	DB4285.1	NT	Human mRNA for possible protein TPRL1, complete cds
460	5628		1.09	2.0E-76	4557682	NT	Homo sapiens Immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
888	5750	10878	2.7	2.0E-76	4503944	NT	Homo sapiens Glucagon (GCG) mRNA
1032	6173	11341	1.80	2.0E-76	4788053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1650	6878	11855	1.65	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1650	6878	11866	1.85	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
2804	7880	13123	1.86	2.0E-76	P23266	SWISSPROT	Olfactory receptor-like protein F3
3279	8428	13560	2.04	2.0E-76	AA445982.1	EST_HUMAN	ZM64602.61 Scores basis_NTT Homo sapiens cDNA clone IMAGE:780888 3' similar to SW:ITB5_HUMAN P13884 INTEGRIN BETA-6 SUBUNIT PRECURSOR ;

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Table 4

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3278	8428	13891	2.04	2.0E-76	AA445982.1	EST_HUMAN	ZM84602.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:780888 3' similar to SW:ITBS_5_HUMAN
3749	8886	14037	0.6	2.0E-76	AA400700.1	EST_HUMAN	ZJ79811.1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:742386 6 similar to WP:R05D3.2
4108	5468	10611	1.33	2.0E-76	DB4285.1	NT	Human mRNA for possible protein TPFDI, complete cds
4825	10335	15176	5.93	2.0E-76	AW878618.1	EST_HUMAN	QV3-O70028-22030-132-b1 OT0028 Homo sapiens cDNA
4273	8397	14538	4.94	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4273	8397	14537	4.94	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
183	6377	10518	4.2	8.0E-77	R83144.1	EST_HUMAN	Yp110b2.1t Scores breast_3NBt-Bst Homo sapiens cDNA clone IMAGE:187165 5' similar to SPANK_HUMAN Q01484 ANKRYIN, BRAIN VARIANT 1
4498	9815	14756	1.32	8.0E-77	Bf205161.1	EST_HUMAN	6018689265F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4108603 5'
1834	7053	12275	1.51	7.0E-77	AA925755.1	EST_HUMAN	2A91501.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2388	7494	12747	8.1	7.0E-77	4505844. NT	Hom sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA	
2388	7494	12748	8.1	7.0E-77	4505844. NT	Hom sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA	
280	6460	10589	3.18	6.0E-77	4504600. NT	Hom sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA	
1143	6280	11444	1.27	6.0E-77	AW957753.1	EST_HUMAN	ESTM8823 MAGE gene sequences. IMAGE: Homo sapiens cDNA
1567	6888	11874	2.81	6.0E-77	AI204086.1	EST_HUMAN	Q97112.x1 Scores fetus_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745083 3'
1239	8389	11542	1.81	5.0E-77	AF041015.1	NT	7_Homo sapiens glutathione (GSH) gene, exon 2
1369	6497	11680	2.47	5.0E-77	4557250	NT	Homo sapiens dipeptidyl and metallopeptidase domain 10 (ADAM10) mRNA
2648	7744	12897	2.86	6.0E-77	AF182688.1	NT	Homo sapiens transducin-like kinase 1 (TLK1) mRNA, complete cds
2725	7820	13075	2.76	5.0E-77	4503160	NT	Hom sapiens culin 1 (CUL1) mRNA
3508	8449	13816	1.22	5.0E-77	8334510	NT	Hom sapiens ubiquitin specific protease 18 (USP18), mRNA
4913	10023	16167	2.57	5.0E-77	AL043953.1	EST_HUMAN	DKF4p434G1728_J1_434 (synonym: hsc3) Homo sapiens cDNA clone DKF4p434G1728 5'
3678	8817	13974	1.05	4.0E-77	AL449768.1	EST_HUMAN	AL449768 Homo sapiens fetal brain (Striatus GS) Homo sapiens cDNA
1974	7091	12320	1.98	3.0E-77	6730038	NT	Hom sapiens SET domain and mother transposase fusion gene (SETMAR) mRNA
1974	7091	12321	1.98	3.0E-77	5750038	NT	Hom sapiens SET domain and mother transposase fusion gene (SETMAR) mRNA
1359	6488	11688	2.58	2.0E-77	AV784817.1	EST_HUMAN	AV784617 MDS Homo sapiens cDNA clone MDSBTF10 5'
1442	6570	11757	9.84	2.0E-77	AW897712.1	EST_HUMAN	RC3-BN0053-1/0200-011-f01 BN0053 Homo sapiens cDNA
2094	7209	12455	2.55	2.0E-77	7708315	NT	Hom sapiens C-G179 protein (LOC51634), mRNA
2558	7043	12610	3.86	2.0E-77	AB037836.1	NT	Hom sapiens mRNA for KIAA1415 protein, partial cds
2566	7843	12811	3.86	2.0E-77	AB037836.1	NT	Hom sapiens mRNA for KIAA1416 protein, partial cds
4006	9139	14280	2.06	2.0E-77	BE044316.1	EST_HUMAN	BE044316 S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GA32_HUMAN P10284 RETROVIRUS-RELATED GAG POLYPEPTIDE;

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Table 4

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4390 8510	14852	0.8	2.0E-77	AI613618.1	EST_HUMAN	W2202_X1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR:CG65245 O65245 F21E10.7 PROTEIN ;	
4390 8510	14863	0.8	2.0E-77	AI613619.1	EST_HUMAN	W2202_X1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR:CG65245 O65245 F21E10.7 PROTEIN ;	
4569 8887		1.29	2.0E-77	4504068 NT		Homo sapiens glutamicoxaloacetic transaminase 2, mitochondrial (espartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA	
4734 8847	148983	3.28	2.0E-77	AA853025.1	EST_HUMAN	ns88g12_s1 NCI CGAP_P72 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47814 60S RIBOSOMAL PROTEIN L29. [1] contains element MSR1 repetitive element;	
42 5253	10371	0.91	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds	
42 5253	10372	0.91	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds	
270 5460	10600	3.44	1.0E-77	4502168 NT		Homo sapiens amyloid beta (A4) precursor protein (protease neuri-1, Alzheimer disease) (APP), mRNA	
270 5460	10601	3.44	1.0E-77	4502168 NT		Homo sapiens amyloid beta (A4) precursor protein (protease neuri-1, Alzheimer disease) (APP), mRNA	
878 7903	11199	5.89	1.0E-77	4502168 NT		Homo sapiens amyloid beta (A4) precursor protein (protease neuri-1, Alzheimer disease) (APP), mRNA	
878 7803	11200	5.89	1.0E-77	4502168 NT		Homo sapiens amyloid beta (A4) precursor protein (protease neuri-1, Alzheimer disease) (APP), mRNA	
1922 7041	12262	2.1	1.0E-77	AW058119.1	EST_HUMAN	W16305_X1 Socres_thymus_NH-F1 Homo sapiens cDNA clone IMAGE:2538160 3'	
2421 76228	12779	1.28	1.0E-77	AB029024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds	
3017 8171	13327	2.24	1.0E-77	4503090 NT		Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DEGR1), mRNA	
4330 8462	14583	3.21	1.0E-77	7706299 NT		Homo sapiens CGI-60 protein (LOC512626), mRNA	
4488 9817	14758	17.67	1.0E-77	AJ228041.1	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA	
4619 9737	14875	1.92	1.0E-77	6552322 NT		Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA	
4662 8778	14922	1.6	1.0E-77	AJ273014.1	EST_HUMAN	gi08904_X1 NCI CGAP_K12 Homo sapiens cDNA clone IMAGE:1881110 3'	
4851 8863	16103	1.07	1.0E-77	11418424 NT		Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA	
4944 8996	14734	0.87	1.0E-77	4768053 NT		Homo sapiens cAMP responsive element binding protein 1 (CREB1), mRNA	
6031 10153	16284	1.49	1.0E-77	7681849 NT		Homo sapiens KIAA0005 gene product (KIAA0005), mRNA	
5051 10163	15285	1.49	1.0E-77	7681849 NT		Homo sapiens KIAA0005 gene product (KIAA0005), mRNA	
82 5201	10431	1.88	6.0E-78	AU18785.1	EST_HUMAN	AU18785 HEMBA1 Homo sapiens cDNA clone HEMBA104354 5'	
82 5201	10432	1.88	6.0E-78	AU18789.1	EST_HUMAN	AU18789 HEMBA1 Homo sapiens cDNA clone HEMBA104354 5'	
215 5409	10549	1.15	5.0E-78	11422488 NT		Homo sapiens hypothetical protein FLJ11316, mRNA	

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2631	7634	12882	4.52	5.0E-78	AW673424.1	EST_HUMAN	be5410c3_3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900406 5' similar to WP:Y4836A6 CE22121;
3268	8511	13878	3.9	5.0E-78	M65386.1	NT	Human collagenase type IV (COL3A1) gene, exon 6
1138	6275	11459	1.7	4.0E-78	AL043314.2	EST_HUMAN	DKFZp43N0323_71_434 (synonym: hhs23_71_434) Homo sapiens cDNA clone DKFZp43N0323 6'
1533	68620	11848	1.38	4.0E-78	AL355641.1	NT	New human gene mapping to chromosome 22
							wr97b12xr1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2466616 3' similar to SW:WAP_PIG
1661	6768	11894	1.52	4.0E-78	AB85094.1	EST_HUMAN	O46655 WHEY ACIDIC PROTEIN PRECURSOR;
2286	7405	12857	22.41	4.0E-78	AF107405.1	NT	Homo sapiens pre-mRNA splicing factor (SFPS3) mRNA, complete cds
4259	9421	14653	1.82	4.0E-78	7865878	NT	Homo sapiens synaptin (LOC308163) mRNA
4740	8853	14599	1.57	4.0E-78	4505809	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha poly peptide (PIK4CA) mRNA
4740	8853	15000	1.57	4.0E-78	4505808	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha poly peptide (PIK4CA) mRNA
158	5353	10492	2.72	3.0E-78	AF095601.1	NT	Homo sapiens eRF3 gene, complete cds
158	5353	10493	2.72	3.0E-78	AF095601.1	NT	Homo sapiens eRF3 gene, complete cds
2279	7359	12639	1.84	3.0E-78	4502142	NT	Homo sapiens apoptosis inhibitor 3 (API3) mRNA
2353	7429	12150	1.38	3.0E-78	7708705	NT	Homo sapiens SH3 and PX domain-containing protein SH3PXY1 (SH3PXY1) mRNA
3169	8350	13513	0.95	3.0E-78	4507184	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
3744	8882	1.85	3.0E-78	AF140604.1	EST_HUMAN	AU140604 PLACE:3006373 6'	
3783	8870	14078	0.74	3.0E-78	4507334	NT	Homo sapiens synaptosomal 1 (SNW1), mRNA
4080	8890	14078	0.82	3.0E-78	4507334	NT	Homo sapiens synaptosomal 1 (SNW1), mRNA
3068	81261		2.33	2.0E-78	UD04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
3989	9123	1.51	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end	
4687	8783	14827	3.72	9.0E-79	11625881	NT	Homo sapiens peptide YY (PYY), mRNA
4833	8645	16088	3.54	9.0E-79	BE000837.1	EST_HUMAN	RC2-BN0074-080300-014-012 BN0074 Homo sapiens cDNA
3723	8861	140114	1.12	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4468	8887	14725	1.44	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
4468	8887	14726	1.44	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
5123	10228	15363	0.67	8.0E-79	8567387	NT	Homo sapiens peroxisome-targeting 3 (PTER3), mRNA
3235	8395	13647	11.83	7.0E-79	BE618848.1	EST_HUMAN	60147276871 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875857 3'
3168	8307		1.48	4.0E-79	88222325	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
311	5497	10587	1.68	3.0E-79	AF114488.1	NT	Homo sapiens Intersector short isoform (ITSN) mRNA, complete cds
979	6125	11265	3.13	3.0E-79	AF232708.1	NT	Homo sapiens cell-line (Sa220) a chloride ion current inducer protein (Cln) gene, complete cds
3072	8225	13376	1.84	3.0E-79	U08410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
285	6474		0.82	2.0E-79	H63129.1	EST_HUMAN	y48f03_s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2086413'
633	5794	10928	1.36	2.0E-79	BE3188926.1	EST_HUMAN	601169416F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:2511107 5'

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
626 6077	11248	2038	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA	
1037 61783		0.89	2.0E-79	AI623747.1	EST_HUMAN	h1B107_1 NC1 CGAP_Pz28 Homo sapiens cDNA clone IMAGE:2118635 3'	
1789 6924	12134	0.97	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA	
1789 6924	12135	0.97	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA	
1888 7006	12226	2	2.0E-79	7662255	NT	Homo sapiens KIAA0703 gene product (KIAA0703), mRNA	
2132 7248	12490	5.6	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rod, alpha (PDE8A), mRNA	
2132 7248	12491	5.8	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rod, alpha (PDE8A), mRNA	
2176 7289	12538	2.84	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAFF1 (Fasff gene)	
2281 7440	12853	8.4	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds	
2845 7648	12857	2.34	2.0E-79	8823248	NT	Homo sapiens hypothetical protein FLJ20276 (FLJ20276), mRNA	
2845 7648	12858	2.34	2.0E-79	8823248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA	
2877 7774	13025	1.18	2.0E-79	AB023154.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds	
4136 9284	14403	1.27	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAFF1 (Fasff gene)	
6187 10294	15431	1.23	2.0E-79	11421686	NT	Homo sapiens sodium calcium exchanger (NCX03), mRNA	
3124 8278	13431	7.99	8.0E-80	AA725848.1	EST_HUMAN	el2305.61 Scarecs testis_NH7 Homo sapiens cDNA clone 1943848 3'	
3124 8278	13432	7.98	9.0E-80	AA725848.1	EST_HUMAN	el2305.61 Scarecs testis_NH7 Homo sapiens cDNA clone 1343848 3'	
3587 8727		1.21	8.0E-80	U946387.1	NT	Homo sapiens Y chromosome spermatozoan candidate protein (RBM) pseudogene mRNA, partial cds	
4834 10044	15164	1.07	7.0E-80	HO46918.1	EST_HUMAN	Y49802.1 Scarecs placenta Nb2/HP Homo sapiens cDNA clone IMAGE:152067 5'	
901 6051	11221	2.38	8.0E-80	AI422197.1	EST_HUMAN	Q16765 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;	
1655 67783	11976	2.83	8.0E-80	U64698.1	NT	Homo sapiens NRD, converted mRNA, complete cds	
2272 7382	12829	3.33	8.0E-80	6831084	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA	
2272 7382	12830	3.33	8.0E-80	6831084	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA	
4259 9384	14519	1.98	8.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds	
4259 9384	14520	1.99	8.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds	
588 5748	10877	34.83	5.0E-80	4505228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA	
834 6988	11168	2.98	6.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBB) mRNA, complete cds	
826 5998	11167	2.98	6.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBB) mRNA, complete cds	
1191 6325		0.97	5.0E-80	X61647.1	NT	H_sapiens neox1 gene (exon 12)	
1488 6595		1.14	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21CC83	
2341 7448	12702	1.25	6.0E-80	U85353.1	NT	Human 13mbt protein homolog mRNA, complete cds	
2408 7614	12764	1.88	6.0E-80	ABC87855.1	NT	Homo sapiens mRNA for KIAA1424 protein, partial cds	

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2755	7849	13104	8.85	5.0E-80	4504292	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
4013	9148	14287	0.97	5.0E-80	AB016038.1	NT	Homo sapiens HM1-1 mRNA for beta-1,4 mannosidase, complete cds
4013	9148	14288	0.97	5.0E-80	AB016038.1	NT	Homo sapiens HM1-1 mRNA for beta-1,4 mannosidase, complete cds
4833	10043	15183	1.92	5.0E-80	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
214	8408		10.59	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4876	9782	14838	1.3	3.0E-80	BF085009.1	EST_HUMAN	PM0-GN0018-040900-0012-E03 Gt0018 Homo sapiens cDNA
4883	8894		3.82	3.0E-80	BE817486.1	EST_HUMAN	QV4-BN0283-040800-241-q10 BN0283 Homo sapiens cDNA
1810	6853	12148	3.63	2.0E-80	R35321.1	EST_HUMAN	Y065608.1 Scars infant brain NIH Homo sapiens cDNA clone IMAGE:380650 5'
1871	6891	12216	3.89	2.0E-80	AL444821.1	EST_HUMAN	RE74B7 subtracted ratna cDNA library Homo sapiens cDNA clone RE74B7
2047	7183	12402	16.22	2.0E-80	AL043116.2	EST_HUMAN	DKFZp424D1323_1' 434 (synonym: hsa33) Homo sapiens cDNA clone DKFZp424D1323 5'
338	6521		1.4	1.0E-80	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
800	5854	11114	1.98	1.0E-80	AF231020.1	NT	Homo sapiens chromosome 21 unknown mRNA
1858	7075		1.44	1.0E-80	AI732656.1	EST_HUMAN	nr011f12.5 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:1078405 3' similar to contains OFR_H1 OFR repetitive element.
4440	5859	14701	1.01	1.0E-80	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
5111	10212	15349	1.01	1.0E-80	4597810	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor gamma 2 (GABRG2) mRNA
4368	9487	14830	6.13	6.0E-81	BE266829.1	EST_HUMAN	60111970F1 NIH MGIC_16 Homo sapiens cDNA clone IMAGE:3362840 5'
4368	9487	14831	5.13	6.0E-81	BE266828.1	EST_HUMAN	60111970F1 NIH MGIC_16 Homo sapiens cDNA clone IMAGE:3362840 5'
2169	7311	12683	7.48	6.0E-81	BE265042.1	EST_HUMAN	60112650DF1 NIH MGIC_8 Homo sapiens cDNA clone IMAGE:33454580 5'
218	6412	10551	0.61	4.0E-81	AF262257.1	NT	Homo sapiens CRP2 binding protein mRNA, partial cds
700	5857	11005	1.37	4.0E-81	AI521435.1	EST_HUMAN	nr0002.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q83560 Q83560
1833	6958	12178	1.73	4.0E-81	AW078612.1	EST_HUMAN	nr08802.x1 NCI CGAP_Co14 Homo sapiens cDNA clone IMAGE:3035807 3' similar to SW:CGPG_BOVIN_P63620 COATOMER GAMMA SUBUNIT ;
3150	8501	13481	3.42	4.0E-81	AB037788.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
3608	8747	13803	0.89	4.0E-81	AW004608.1	EST_HUMAN	nr000203.x1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:O43816 O43816 STRAITIN ;
4132	8280	14597	2.2	4.0E-81	AF263306.1	NT	Homo sapiens rat3 interacting protein variant 2 mRNA, partial cds
4132	8280	14598	2.2	4.0E-81	AF263306.1	NT	Homo sapiens rat3 interacting protein variant 2 mRNA, partial cds
1271	6400	11572	10.35	3.0E-81	Y18800.1	NT	Homo sapiens NF2 gene
1271	6400	11573	10.35	3.0E-81	Y18800.1	NT	Homo sapiens cullin NF2 gene
2351	7458	12713	4.34	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2860	8114	13276	5.69	3.0E-81	4506280	NT	Homo sapiens pliotrophin (heparin binding growth factor 8, neutrite growth-promoting factor 1) (PTN) mRNA

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2860	8114	13277	5.98	3.0E-81	4506230	NT	Homo sapiens plakophilin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2794	7851	13118	2.9	2.0E-81	BE74638.1	EST_HUMAN	601474072F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3877121 5'
2794	7851	13117	2.9	2.0E-81	BE74638.1	EST_HUMAN	601474072F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3877121 5'
3754	8891	14042	0.8	2.0E-81	AW611542.1	EST_HUMAN	hgB5p013X NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
1431	6598	11741	1.18	1.0E-81	W26539.1	EST_HUMAN	33F3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4480	9608	14748	3.07	1.0E-81	AA040370.1	EST_HUMAN	2445109.1 Scareas, pregnant uterus, NIH3T3 NIH3T3 fibroblast synthesis - frt4y; PR:552437 SB2437 COP diacylglycerol synthase - frt4y;
4614	9732	14889	6.85	1.0E-81	BE047898.1	EST_HUMAN	Iz45c04_NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2281628 5'
12	5223	10335	6.88	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
103	6223	10335	3.89	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
261	5451	10590	3.03	8.0E-82	U05988.2	NT	Human CRFB4 gene, partial cds
815	50658	11129	2.28	8.0E-82	U05988.1	NT	Human CRFB4 gene, partial cds
888	60938	11209	1.2	8.0E-82	U05988.1	NT	Human CRFB4 gene, partial cds
1501	6228	11616	1.33	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1670	6789	11896	1.21	8.0E-82	6715601	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4222	6347	14480	0.71	8.0E-82	88223432	NT	Homo sapiens hypothetical protein FLJ20481 (FLJ20481) mRNA
1463	6590		1.1	7.0E-82	BF035327.1	EST_HUMAN	60145931F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882088 5'
2728	7023	13078	1.6	7.0E-82	AU144050.1	EST_HUMAN	ALU44050 HEMBA_Homo sapiens cDNA clone HEMBA1000752 3'
1683	6814	12012	61.3	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
275	5485	10507	14.68	3.0E-82	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nonch-ll, Alzheimer disease) (APP), mRNA
701	50598	11006	2.28	3.0E-82	BE006706.1	EST_HUMAN	RC2-BN120-01040-013-02 BN120 Homo sapiens cDNA clone 1343848 3'
788	65942	11102	8.05	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
871	6122	11193	8.74	3.0E-82	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nonch-ll, Alzheimer disease) (APP), mRNA
1062	6203		63.03	3.0E-82	AA725848.1	EST_HUMAN	al23865.81 Scareas, testis, NIH Homo sapiens cDNA clone IMAGE:1343848 3'
13822	...6491	11673	1.14	3.0E-82	AW876073.1	EST_HUMAN	RCBP10001-10010-021-502 PT0001 Homo sapiens cDNA
1478	6505	11781	2.32	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21/G085
1807	7028	12248	1.31	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN005-28070-018-504 BN005 Homo sapiens cDNA
3265	8405		1.94	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTTR2) mRNA
695	61767	10884	1.4	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds
686	5787	10885	1.4	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds

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 Table 4  
 Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1700	6828	12028	2.13	2.0E-82	AL0468390.1	EST_HUMAN	DKFZP434M117 NT 434 (synonym: fts3) Homo sapiens cDNA clone DKFZP434M117 6'
2948	8102	13207	0.7	2.0E-82	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3823	8959	14107	1	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4212	9337	14470	0.98	2.0E-82	4504118	NT	Homo sapiens glutamate receptor, ionotropic, ketone 1 (GRK1) mRNA
4531	8949	14795	1.11	2.0E-82	AB028018.1	NT	Homo sapiens mRNA for KIAA1056 protein, partial cds
4531	8949	14796	1.11	2.0E-82	AB028018.1	NT	Homo sapiens mRNA for KIAA1056 protein, partial cds
4841	9553	15068	2.94	2.0E-82	AF045555.1	NT	Homo sapiens Wscr1 (WBSCR1) and Wscr6 (WBSCR6) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5084	10166	16209	1.42	2.0E-82	4507650	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6) mRNA
6094	10166	16300	1.42	2.0E-82	4507650	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6) mRNA
5910	6752	10819	1.35	1.0E-82	11546921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5) mRNA
1211	6343	11592	1.98	1.0E-82	BE885108.1	EST_HUMAN	6015108598F1 NIH MGIC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1289	6418	11652	4.73	1.0E-82	BE084388.1	EST_HUMAN	RC4-BT0310-110300-016-F10 B710310 Homo sapiens cDNA
1280	6419	11683	1.7	1.0E-82	AB011102	NT	Homo sapiens mRNA for KIAA0588 protein, partial cds
1421	6548	11728	3.26	8.0E-83	BE383975.1	EST_HUMAN	601285348F1 NIH MGIC_20 Homo sapiens cDNA clone IMAGE:3614382 5'
1695	7871	12023	2.23	8.0E-83	NG6851.1	EST_HUMAN	ZBp812.s1 Seares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:285823 3'
1384	8493	11674	1.88	7.0E-83	AW385629.1	EST_HUMAN	QV4-L10016-271288-088-f11 L10016 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contignt Aa
2629	7884		1.62	7.0E-83	AA6846855.1	EST_HUMAN	no1201.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contignt Aa
4784	8997		6.92	7.0E-83	BF221613.1	EST_HUMAN	7p37q7.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3647883 3' similar to TRC8Y316 Qv7318
403	5570	10717	1.49	6.0E-83	NA3320.1	NT	Human platelet Chytochrome b/b (GPbIIb) gene, exons 2-29
1787	6922	12132	2.43	6.0E-83	AW573088.1	EST_HUMAN	h38103.s1 Seares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833825 3' similar to SW:yBEB_HAEIN P44471 HYPOTHEICAL PROTEIN HIC0034.;
3023	8177	0.93	6.0E-83	AF231618.1	NT	Homo sapiens chromosome 21 unknown mRNA	
3548	8959	13851	0.75	6.0E-83	11430241	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379) mRNA
846	8994	1.61	6.0E-83	U178883.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 6	
2042	7875		8.24	5.0E-83	AF008305.1	NT	Homo sapiens 26S proteasome regulatory subunit (SU32) mRNA, complete cds
3616	8755	13911	2.15	5.0E-83	AL133207.2	NT	Novel human gene mapping to chromosome X
3883	6010	14178	1.77	5.0E-83	4886180	NT	Homo sapiens decoyribonuclease (DNASE1), mRNA
5062	10184	16207	11.94	5.0E-83	4657013	NT	Homo sapiens catelase (CAT) mRNA
5062	10164	15298	11.94	5.0E-83	4357013	NT	Homo sapiens catelase (CAT) mRNA
639	5800	10934	1.69	4.0E-83	AF224669.1	NT	Homo sapiens matmosidase, beta A, hyoscyamus (MANBA) gene, and tubiquitin-conjugating enzyme E2D 3 (UBED3) genes, complete cds

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Table 4

## Single Exon Probes Expressed in BT474 Cells.

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T <sub>Cap</sub> ) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
898 6144			3.25	3.0E-83	AA988311.1	EST_HUMAN	EST78542 Placenta1 Homo sapiens cDNA similar to similar to endogenous retrovirus ERVb np87607_s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR12 THR
2738 7832			1.06	3.0E-83	AA982654.1	EST_HUMAN	Q8ZG05_s1 Soares testis_NHT_Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR-Q9ZB14
1812 6395	12160		2.11	2.0E-83	AA983492.1	EST_HUMAN	Q8ZG05_s1 Soares testis_NHT_Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR-Q9ZB14
1812 6395	12161		2.11	2.0E-83	AA983492.1	EST_HUMAN	Q8ZG05_s1 Soares testis_NHT_Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR-Q9ZB14
1930 7049	12270		2.01	2.0E-83	NA68951.1	EST_HUMAN	Q8ZG05_s1 Soares fetal liver spleen 1NFL3 Homo sapiens cDNA clone MAGE:2865923 3'
2162 7276	12222		0.87	2.0E-83	AB033098.1	NT	Home sapiens mRNA for KIAA1272 protein, partial cds
2814 7970	13129		2.0E-83	2.0E-83	BE828694.1	EST_HUMAN	RC8-E10448-28050-015-H12_E10048 Homo sapiens cDNA
3252 8402			1.97	2.0E-83	11420834	NT	Home sapiens cDNA clone (Unpublished) like 1 (SALL1), mRNA
3755 8952			0.7	2.0E-83	AI163202.2	NT	Home sapiens chromosome 21 segment HS21C002
4313 8435	14570		4.13	2.0E-83	AF202878.1	NT	Home sapiens hemopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4620 9738	14878		9.02	2.0E-83	7706398	NT	Home sapiens armyn repeat-containing protein ASB-2 (LOC51676), mRNA
4620 9738	14877		9.02	2.0E-83	7706398	NT	Home sapiens armyn repeat-containing protein ASB-2 (LOC51676), mRNA
1419 6548	11726		3.86	1.0E-83	4504326	NT	Home sapiens hydronoxyl-Coenzyme A thiolesterase/Coenzyme A thiolesterase/enoyl-Coenzyme A hydratase (Infunctional protein), beta subunit (HADHB) mRNA
1419 6548	11727		3.68	1.0E-83	4504326	NT	Home sapiens hydronoxyl-Coenzyme A thiolesterase/Coenzyme A thiolesterase/enoyl-Coenzyme A hydratase (Infunctional protein), beta subunit (HADHB) mRNA
2817 7716	12870		4.89	1.0E-83	BE883360.1	EST_HUMAN	601507315F1 NIH_3T3C71 Homo sapiens cDNA clone IMAGE:39088754 5'
3163 8314	13476		0.93	1.0E-83	7622349	NT	Home sapiens cell recognition molecule Cesp12 (KIAA0888), mRNA
3847 8883	14138		7.16	1.0E-83	AF053168.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4223 8348	14481		2.31	1.0E-83	Z25822.1	NT	H. sapiens gene for mitochondrial dodecanoyl-CoA delta-isomerase, exon 3
4857 8669	15114		1.58	1.0E-83	4502168	NT	Home sapiens amyloid beta (A4) precursor protein (protease neutral), Alzheimer disease (APP), mRNA
3774 8901	14084		3.43	7.0E-84	BE801209.1	EST_HUMAN	601676023F1 NIH_3T3C71 Homo sapiens cDNA clone IMAGE:39068863 6'
1289 6228	11600		4.09	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0118-20050-011-005 FN0119 Homo sapiens cDNA
1289 6228	11601		4.09	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0118-20050-011-005 FN0119 Homo sapiens cDNA
2374 7480	12734		3.37	6.0E-84	AA176574.1	EST_HUMAN	aa88ca03.61 Strategate schizo brain S11 Homo sapiens cDNA clone IMAGE:371020 3'
712 68650	11017		0.8	5.0E-84	AA382811.1	EST_HUMAN	ESTB694 Testis Homo sapiens cDNA 5' end
2885 8139			1.7	6.0E-84	AF09718.1	NT	Home sapiens chromosome 3 subfragments region
1385 6513	11694		0.87	4.0E-84	AB097735.1	NT	Home sapiens mRNA for KIAA1314 protein, partial cds
1418 6545	11725		3.03	4.0E-84	AI688321.1	EST_HUMAN	wa7fc04_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302088 3' similar to SW:NRDC_HUMAN_OA3847 NARDILYSIN PRECURSOR ;

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4928 10038	15173		0.98	4.0E-84	4505928	NT	Human sapiens polymerase (DNA-directed), alpha (70KD) (POLA2), mRNA
4929 10039	15179	1.84	4.0E-84	Af068601.2	NT	Human sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds	
5129 10229	15364	1.04	4.0E-84	AA011549.1	EST HUMAN	CE02165 GTP-BINDING ADP-RIBOSYLATION FACTOR; 20620/7.71 Scores 6_ests_NH1 Homo sapiens cDNA clone IMAGE:742548 6 similar to WP:F2285.1	
314 55010	10840	1.87	3.0E-84	Af026201.1	NT	Human sapiens Bach 1 protein homolog mRNA, partial cds	
1884 70811	12305	2.9	3.0E-84	5453855	NT	Human sapiens pericentriolar material 1 (PCM1) mRNA	
2008 7123	12359	7.05	3.0E-84	AL068680.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains	
3730 8897	14021	8.04	3.0E-84	AF014469.1	NT	Human sapiens X-linked juvenile retinoschisis precursor protein (XLRS1) mRNA, complete cds	
2096 7211	12458	3.39	2.0E-84	BE1695397.1	EST HUMAN	CMT-B/T0785-18050-272-408 BT0785 Homo sapiens cDNA	
2098 7211	12469	3.39	2.0E-84	BE0986397.1	EST HUMAN	CMT-B/T0785-18050-272-408 BT0785 Homo sapiens cDNA	
2809 8053	13235	9.32	2.0E-84	Af068643.1	NT	Human sapiens myelin basic protein 1-like (MBT1-) mRNA, complete cds	
2831 8085	13252	1.4	2.0E-84	Y09211.1	NT	H. sapiens DNA for endogenous retrovirus retroviral like element	
4760 8873	15024	1.01	2.0E-84	BT308618.1	EST HUMAN	601887684F1 NIH MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5'	
4760 8873	15025	1.01	2.0E-84	BT308618.1	EST HUMAN	601887684F1 NIH MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5'	
310 6498	10639	1.31	1.0E-84	AF114488.1	NT	Human sapiens Intersectin short isoform (ITS) mRNA, complete cds	
5483 5713	10847	54.29	1.0E-84	4507852	NT	Human sapiens Ywba3 3-monooxygenase/trypophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA	
718 5878		1.02	1.0E-84	11427681	NT	Human sapiens complement component 5 (C5) mRNA	
1297 8426	11593	5.12	1.0E-84	AA084376.1	EST HUMAN	Iam85b1.1 s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:16288385 3'	
2048 7182	12401	1.84	1.0E-84	BE3592137.1	EST HUMAN	601368006F1 NIH MGC_44 Homo sapiens cDNA clone IMAGE:3628257 5'	
2205 7317	12567	2.18	1.0E-84	11427187	NT	Human sapiens pericentriolar material 1 (PCM1) mRNA	
3732 8870	14023	2.48	1.0E-84	AA128851.1	EST HUMAN	nt!1206.81 NC_0094P_SS1 Homo sapiens cDNA clone IMAGE:12339106 3'	
4394 9514	14655	4.48	1.0E-84	A1220044.1	NT	Human sapiens B59 kb carting between AML1 and CBR1 on chromosome 21(q22; segment 13	
4688 9784	14928	3.07	1.0E-84	AL048314.2	EST HUMAN	DKFZp434N0323 1/434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N0323 5'	
4688 9784	14929	3.07	1.0E-84	AL048314.2	EST HUMAN	DKFZp434N0323 1/434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N0323 5'	
4887 9514	14656	2.2	1.0E-84	AL0225041.1	NT	Human sapiens 859 kb carting between AML1 and CBR1 on chromosome 21(q22; segment 13	
966 6115		1.98	9.0E-85	AL1683209.2	NT	Human sapiens chromosome 21 segment HS21C009	
1074 6214	11377	7.67	9.0E-85	U51432.1	NT	Human sapiens nuclear protein Skp mRNA, complete cds	
1074 6214	11378	7.67	9.0E-85	U51432.1	NT	Human sapiens nuclear protein Skp mRNA, complete cds	
1591 6720	11939	0.83	9.0E-85	M33282.1	NT	Human plasmalogens gene, exon 7	
1591 6720	11910	0.98	9.0E-85	M33282.1	NT	Human plasmalogens gene, exon 7	
1888 6817	120163	2.58	9.0E-85	7657020	NT	Human sapiens DKFZp434P211 protein (DKFZp434P211) mRNA	
4888 6898	16145	0.91	9.0E-85	AL168268.2	NT	Human sapiens chromosome 21 segment HS21C088	
1137 6214	11433	8.3	7.0E-85	LD05094.1	NT	Human sapiens ribosomal protein L27 mRNA, complete cds	

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Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2314	7422	12673	1.61	5.0E-85	AL163284.2	NT	Human sapiens chromosome 21 segment HS21C084
1303	6433	11507	1.63	3.0E-85	AF0886157.1	NT	Human sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1790	6516	12123	6.48	3.0E-85	T97486.1	EST_HUMAN	y469p9.7 Scores fetal liver cDNA clone IMAGE clone cDNA clone IMAGE:121604 5'
4262	8414	14649	1.03	3.0E-85	BE207189.1	EST_HUMAN	601198704F2 NIH JMG C_7 Homo sapiens cDNA clone IMAGE:3533616 5'
4872	8883	15129	1.65	3.0E-85	11024655	NT	Human sapiens F-box only protein 24 (FBXO24), mRNA
4872	8883	15130	1.66	3.0E-85	11024655	NT	Human sapiens F-box only protein 24 (FBXO24), mRNA
884	6111	11281	0.88	2.0E-85	7857286	NT	Human sapiens KIAA0829 probe Mez2 interacting nuclear target (MINT) homolog (KIAA0829), mRNA
1042	6183	11349	3.03	2.0E-85	AF248540.1	NT	Human sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1412	6339	11719	1.62	2.0E-85	7708206	NT	Human sapiens CGI-201 protein (LOC51340), mRNA
1429	6556	11739	5.67	2.0E-85	5174775	NT	Human sapiens apolipoprotein C-II (APOC2) mRNA
1429	6556	11739	5.67	2.0E-85	5174775	NT	Human sapiens apolipoprotein C-II (APOC2) mRNA
2212	7224	12674	1.76	2.0E-85	U10626.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2783	6471		6.16	2.0E-85	7657488	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2894	8149	13309	1.39	2.0E-85	M39838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4310	8432	14587	4.68	2.0E-85	4505880	NT	Human sapiens plasminogen (PLG) mRNA
4888	8887	15143	0.89	2.0E-85	AL163284.2	NT	Human sapiens chromosome 21 segment HS21C084
2263	7373		2.12	1.0E-85	BE18408.1	EST_HUMAN	601165416F1 NIH JMG C_7 Homo sapiens cDNA clone IMAGE:3948918 5'
2370	7476	12730	4.1	1.0E-85	BE16382.1	EST_HUMAN	601462817F1 NIH JMG C_7 Homo sapiens cDNA clone IMAGE:3868021 5'
2370	7476	12731	4.1	1.0E-85	BE618592.1	EST_HUMAN	601462817F1 NIH JMG C_7 Homo sapiens cDNA clone IMAGE:3868021 5'
1438	6886		20.84	9.0E-85	BE274217.1	EST_HUMAN	601120778F1 NIH JMG C_20 Homo sapiens cDNA clone IMAGE:2857680 5'
837	6895	11251	0.94	7.0E-85	AA686801.1	EST_HUMAN	gj8888.81 Scores_pariathyroid_tumor_NHPA Homo sapiens cDNA clone IMAGE:1403559 3
837	6895	11252	0.94	7.0E-85	AA686801.1	EST_HUMAN	gj8888.81 Scores_pariathyroid_tumor_NHPA Homo sapiens cDNA clone IMAGE:1403559 3
1289	6427	11599	4.58	6.0E-85	4505482	NT	Human sapiens oxoglutarate dehydrogenase (lipoylase) (OGDH) mRNA
208	6402	10848	3.84	4.0E-85	BE64773.1	EST_HUMAN	6010726394F1 NIH JMG C_12 Homo sapiens cDNA clone IMAGE:3458830 5'
4265	8090	14528	0.98	3.0E-85	BE867703.1	EST_HUMAN	601443262F1 NIH JMG C_85 Homo sapiens cDNA clone IMAGE:3847485 5'
284	6454	10592	1.31	2.0E-85	AA306284.1	EST_HUMAN	EST1777232 Jurkat T-cells VI Homo sapiens cDNA 5' end
413	5581		2.4	2.0E-85	AL1632203.2	NT	Human sapiens chromosome 21 segment HS21C003
-1182	6328	11483	1.68	2.0E-85	N58977.1	EST_HUMAN	Y21608.81 Scores_multiple_sclerotsis_2NDHMSP Homo sapiens cDNA clone IMAGE:283478 5'
1505	6892	11618	1.43	2.0E-85	4759827	NT	Human sapiens neutrophil III (NRXN3) mRNA
1605	6532	11619	1.43	2.0E-85	4759827	NT	Human sapiens neutrophil III (NRXN3) mRNA
2174	7287	12535	1.95	2.0E-85	8635487	NT	Human endogenous retrovirus, complete genome
2249	7359	12816	3.27	2.0E-85	AB033103.1	NT	Human sapiens mRNA for KIAA1277 protein, partial cds
3397	8641	13707	1.44	2.0E-85	AW988142.1	EST_HUMAN	EST378215 MAGE sequence(s), MAGI Homo sapiens cDNA

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3727	8884	140117	2.82	2.0E-88	AF158778.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAT-delta) mRNA, complete cds
3727	8884	140118	2.82	2.0E-88	AF168778.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAT-delta) mRNA, complete cds
4014	9147		2.64	2.0E-88	AW516742.1	EST HUMAN	Indigo-1 NCI CGAP_GC9 Homo sapiens cDNA clone IMAGE:20186423
4756	9869	150119	2.51	2.0E-88	AF055490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5043	10145	15274	1.35	2.0E-88	4505778	NT	Homo sapiens phosphomannose kinase, epsilon 1 (muscle) (PKM1), mRNA
1610	6738	11832	2.78	1.0E-88	4828555	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (UBQD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA
3141	8282	13449	1.38	1.0E-88	6453649	NT	Homo sapiens fibrillin 5 (FBXN5) mRNA
3220	8371	13534	2.89	1.0E-88	LD0492.1	NT	Human gamma-d glutamyl transpeptidase mRNA, complete cds
3278	8427	13688	1.23	1.0E-88	AL168208.2	NT	Homo sapiens chromosome 21 segment HS21 C008
3278	8427	13589	1.25	1.0E-88	AL168209.2	NT	Homo sapiens chromosome 21 segment HS21 C009
3917	9053	14213	0.89	1.0E-88	7708161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
3917	8063	14214	0.89	1.0E-88	7708161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4238	8363	14498	4.73	1.0E-88	AL168300.2	NT	Homo sapiens chromosome 21 segment HS21 C100
4896	10007	15152	1.27	1.0E-88	AF100751.1	NT	Homo sapiens FK506-binding protein FKBP23 isoform mRNA, complete cds
479	5846	10787	81.05	8.0E-87	X62246.1	NT	Oncocidius mRNA for elongation factor 1 alpha
3513	8654	13829	1.08	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
6173	10270	16411	0.63	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
1160	6299	11461	2.39	5.0E-87	AA382911.1	EST_HUMAN	EST382914. Testis I Homo sapiens cDNA 5' end
867	6114	11283	0.86	4.0E-87	AL1683210.2	NT	Homo sapiens chromosome 21 segment HS21 C010
1174	6309	11478	18.49	4.0E-87	AE0317835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1439	8566	11751	0.99	4.0E-87	R78139.1	EST HUMAN	Y80101.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145578 5' similar to contains Altu repetitive element
2024	7141	12381	1	4.0E-87	AB007925.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds
2389	7505	12753	1.48	4.0E-87	77062889	NT	Homo sapiens CG1-60 protein (LOC51626), mRNA
2389	7606	12764	1.48	4.0E-87	77062889	NT	Homo sapiens CG1-60 protein (LOC51626), mRNA
3446	8588	13761	1.75	4.0E-87	5174874	NT	Homo sapiens myeloidlymphoid or mixed-lineage leukemia (mlle) (Drosophila homolog); translocated to 4 (MLL7) mRNA
2737	7831	13085	6.83	2.0E-87	48856420	NT	Homo sapiens Naphthimidol group (mammalian chitosanase) protein 4 (NMG4) mRNA
2914	8688		0.68	2.0E-87	B53272920.1	EST HUMAN	Q76BN10148-0598010-264-e03 B53272920.1 Homo sapiens cDNA
3763	8800	14052	0.78	2.0E-87	AU116935.1	EST HUMAN	AU116935.1 HEMBA1 Homo sapiens cDNA clone HEMBA10003307 6'
4889	10000	16148	0.6	2.0E-87	BF376311.1	EST HUMAN	CMB-TN0038-150300-332-H08 TN0038 Homo sapiens cDNA
4941	10051	16189	1.37	2.0E-87	BE176478.1	EST HUMAN	RCE-H70580-203030-031-C94 HT1080 Homo sapiens cDNA
1184	7669		1.7	1.0E-87	7706683	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1441	6568	11753	1.93	1.0E-87	AW381977.1	EST HUMAN	PM2-CT0285-141089-001-#04 CT0286 Homo sapiens cDNA
1441	6598	11754	1.93	1.0E-87	AW381977.1	EST HUMAN	PM2-CT0285-141089-001-#04 CT0286 Homo sapiens cDNA
3688	8227	1269	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cytophilin	
3715	8553	14007	2.98	1.0E-87	4758827	NT	Human repetitive element III (NRXN3) mRNA
1107	6245	11408	6	9.0E-88	AF074485.1	NT	Human sapiens double stranded RNA activated protein kinase (PRK) gene, exon 12
1358	6485	11685	2.83	9.0E-88	AB037820.1	NT	Human sapiens mRNA for KIAA1388 protein, partial cds
1368	6485	11686	2.83	9.0E-88	AB037820.1	NT	Human sapiens mRNA for KIAA1389 protein, partial cds
2111	72228	12468	1.12	9.0E-88	7681701	NT	Human sapiens DKFZP588P1522 protein (DKFZP588P1522), mRNA
3807	8746	13802	1.03	9.0E-88	AL183209.2	NT	Human sapiens chromosome 21 segment HS21C009
4243	8568	14501	3.03	9.0E-88	X91928.1	NT	H. sapiens ECE-1 gene (exon 9)
4243	8568	14502	3.03	9.0E-88	X91928.1	NT	H. sapiens ECE-1 gene (exon 9)
4889	10085	16226	1.01	9.0E-88	AB026888.1	NT	Human sapiens DNA, DLEC1 to ORC1L4 gene region, section 7/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
1842	6593	234	6.0E-88	7681887	NT	Human sapiens KIAA0063 gene product (KIAA0063), mRNA	
2603	7702	12859	8.44	5.0E-88	NB83389.1	EST HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 F similar to ZINC FINGER PROTEIN HZF1
2870	8124	15209	0.88	5.0E-88	AF114488.1	NT	Human sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2882	8138	13300	0.63	5.0E-88	AF114488.1	NT	Human sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2882	8138	13301	0.63	5.0E-88	AF114488.1	NT	Human sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3370	8515		2.52	5.0E-88	AB683217.1	EST HUMAN	wd88468.1 NCI_CGAP Li-24 Homo sapiens cDNA clone IMAGE:2338789 3' similar to contains Atu repetitive element contains element MER22 MER22 repetitive element ;
3523	6594	13831	0.87	5.0E-88	AF114488.1	NT	Human sapiens Intersectin short isoform (ITSN) mRNA, complete cds
4705	8221	14868	0.62	5.0E-88	AF114488.1	EST HUMAN	PM01-TN0028-050800-004-#10 TN0028 Homo sapiens cDNA
1334	6483	11643	1.8	4.0E-88	BF091228.1	EST HUMAN	PM1-TN0028-050900-004-#10 TN0028 Homo sapiens cDNA
1334	6483	11844	1.8	4.0E-88	BF091228.1	EST HUMAN	PM1-TN0028-050900-004-#10 TN0028 Homo sapiens cDNA
739	6586	11038	2.2	3.0E-88	11645800	NT	Human sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1824	6597		1.79	3.0E-88	4508020	NT	Human sapiens zinc finger protein 268 (ZNF268) mRNA
2813	8087	13240	4.81	3.0E-88	N68951.1	EST HUMAN	Z44812.1 Soore's fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:235923 3'
4219	8344	14474	0.88	3.0E-88	4501912	NT	Human sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA
4219	9344	14475	0.68	3.0E-88	4501912	NT	Human sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA
-4457	9576		3.87	3.0E-88	11428310	NT	Human sapiens Calsenilin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1038	6178	11343	1.32	2.0E-88	7305188	NT	Human sapiens SNARE protein kinase SNAK mRNA, complete cds
1638	6755	11859	1.88	2.0E-88	AF246219.1	NT	Human sapiens SNARE protein kinase SNAK mRNA, complete cds
1762	6598	12094	4.8	2.0E-88	AF246219.1	NT	Human sapiens SNARE protein kinase SNAK mRNA, complete cds

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4403 9823	14684	1.89	2.0E-89	5031668	NT	Human sapiens dynamin, exocystinal, light polypeptide 4 (DNAL4), mRNA	
2897 7783	13044	1.51	8.0E-89	BE311557.1	EST_HUMAN	601114240871 NIH_3T3C_14 Human sapiens cDNA clone IMAGE:35001188 5'	
432 6601	10747	1.21	7.0E-89	7657213	NT	Human sapiens harmonically upregulated neu tumor-associated kinase (HUNK), mRNA	
432 6601	10748	1.21	7.0E-89	7657213	NT	Human sapiens harmonically upregulated neu tumor-associated kinase (HUNK), mRNA	
4853 6685	16110	3.03	7.0E-89	4557590	NT	Human sapiens complement component 8, beta polypeptide (C8B), mRNA	
4908 100118	16162	3.98	7.0E-89	AL048748.1	EST_HUMAN	DKIF2p34E246 nt 434 (synonym: hsa33) Human sapiens cDNA clone DKIF2p434E246 5'	
1024 6165	11331	1.26	6.0E-89	6803114	NT	Human sapiens inner membrane protein, mitochondrial (mitofillin) (MMT), mRNA	
2165 7307	12557	4.18	6.0E-89	4506124	NT	Human sapiens carboxy-terminal protein kinase PRP4, homolog (PRP4), mRNA	
2411 7517	12768	3.33	6.0E-89	4507788	NT	Human sapiens ubiquitin-conjugating enzyme E2L_3 (UBE2L3), mRNA	
2411 7517	12767	3.33	6.0E-89	4507788	NT	Human sapiens ubiquitin-conjugating enzyme E2L_3 (UBE2L3), mRNA	
3511 8652	13818	1.12	6.0E-89	7681817	NT	Human sapiens HSPC168 protein (HSPC168), mRNA	
4607 6725	14860	3.88	6.0E-89	AB507866.2	NT	Human sapiens mRNA for KIAA0406 protein, partial cds	
4607 6725	14861	3.88	6.0E-89	AB507866.2	NT	Human sapiens mRNA for KIAA0406 protein, partial cds	
5148 10248	16328	0.69	6.0E-89	6806918	NT	Human sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	
6148 10248	16327	0.69	6.0E-89	6806918	NT	Human sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	
6058 10160	15282	3	6.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Bayfor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2E0383	
5058 10160	15293	3	6.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Bayfor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2E0383	
2842 7897	13153	1.53	3.0E-89	AW976181.1	EST_HUMAN	EST388280 IMAGE sequences, MAGN Human sapiens cDNA	
122 6575	10723	0.76	2.0E-89	7708870	NT	Human sapiens PXR26 protein (PXR26), mRNA	
122 6575	10724	0.78	2.0E-89	7708870	NT	Human sapiens PXR26 protein (PXR26), mRNA	
523 9894	10823	0.87	2.0E-89	AB3037763.1	NT	Human sapiens mRNA for KIAA1342 protein, partial cds	
						cp88c08_x1 Scores: NFL_T_GBC_S1 Human sapiens cDNA clone IMAGE:18430222 3' similar to d0:404131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Abu repetitive element.	
2847 8002	13162	1.46	2.0E-89	AI222095.1	EST_HUMAN	Human sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds	
4118 9244	14380	1.49	2.0E-89	AF089897.1	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11	
4125 9253	14391	6.08	2.0E-89	X58742.1	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11	
4125 9253	14392	6.06	2.0E-89	X58742.1	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11	
4328 9448	14981	1.08	2.0E-89	AL163203.2	NT	Human sapiens chondrocanine 21 segment HS21C003	
4474 8953	14732	1.18	2.0E-89	AI007378.1	NT	Human sapiens GGT gene, exon 5	
1084 6205	11367	3.39	8.0E-90	AI163246.2	NT	Human sapiens chromosome 21 segment HS21C0046	
1085 6205	11367	3.22	8.0E-90	AI163246.2	NT	Human sapiens chromosome 21 segment HS21C0048	
1333 7914	11845	6.98	8.0E-90	BE670561.1	EST_HUMAN	7636105x1 NCI CGAP_Lu24 Human sapiens cDNA clone IMAGE:3284583 3'	

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1335	7914	11848	6.89	8.0E-90	BE670561.1	EST_HUMAN	7636f08_x1 NCI_CGAP_Li24 Homo sapiens cDNA clone IMAGE:3284583 3'
637	5939		7	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha 1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3040	8193	13349	1.25	6.0E-90	X91926.1	NT	H_sapiens_ECE-1 gene (exon 6)
3040	8194	13350	1.25	6.0E-90	X91926.1	NT	H_sapiens_ECE-1 gene (exon 6)
4204	6329	14481	7.5	6.0E-90	89223298	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4204	6329	14482	7.5	6.0E-90	89223298	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
150	6347		33.35	6.0E-90	AB035344.1	NT	Homo sapiens TCOL6 gene, exon 1-10
1185	6329	11498	3.1	6.0E-90	UB9226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1681	6854	12176	1.41	6.0E-90	A1222985.1	EST_HUMAN	q986c03_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:18430222 3' similar to gba:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Ali repetitive element
1681	6854	12178	1.41	5.0E-90	A1222985.1	EST_HUMAN	q986c03_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:18430222 3' similar to gba:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Ali repetitive element
2625	7628	12876	1.38	5.0E-90	AF114497.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
4513	8831	14776	0.98	6.0E-90	4806354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4641	8759	14806	0.88	6.0E-90	AL135549.1	EST_HUMAN	DKFZp762p1616_17 702 (synonym: hmg2) Homo sapiens cDNA clone DKFZp762p1616_5'
300	5489	10629	2.48	4.0E-90	AF231820.1	NT	Homo sapiens chromosome 21 unknown mRNA
300	5489	10630	2.48	4.0E-90	AF231820.1	NT	Homo sapiens chromosome 21 unknown mRNA
1097	6226	11391	3.88	4.0E-90	4505318	NT	Homo sapiens myostatin phosphatase, target subunit 1 (MYP11), mRNA
1708	6831	12033	8.69	4.0E-90	X99033.1	NT	H_sapiens genes encoding discoidin receptor tyrosine kinase, exon 16
2824	7880	13140	0.63	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2824	7880	13141	0.63	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2895	8150	13310	1.03	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2895	8150	13311	1.03	4.0E-90	6806918	NT	Homo sapiens genes encoding discoidin receptor tyrosine kinase, exon 16
4628	6744	14888	6.2	4.0E-90	DB3765.1	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4768	6879	16028	2.82	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for NEC22 gene, exon 8
4787	8800	15944	1.88	4.0E-90	WA96887.1	NT	Human phytomone converting enzyme (KIAA1244) protein, partial cds
211	8406	10548	3	2.0E-90	B5537913.1	EST_HUMAN	6511687378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1175	6310	11477	23.89	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonsisomic chromosomal) protein 17 (HMG17), mRNA
1175	6310	11478	23.89	2.0E-90	6031748	NT	Homo sapiens high-mobility group (nonsisomic chromosomal) protein 17 (HMG17), mRNA
3822	8958	14108	1.81	2.0E-90	AI188213.1	EST_HUMAN	q954c02_x1 Scores_placenta_816weeks_2NbHPbeta6W Homo sapiens cDNA clone IMAGE:1713410 3' similar to SW.OL.F3.NOUSE P22275 OLFACTORY RECEPTOR OR3 ;

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Table 4  
Single Exon Probes Expressed in

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit Accession No.	Top Hit Database Source
4885	88986	15142	7.01	4.8	1.0E-80	5728855 NT	Homo sapiens GRB2-related adapter protein (Grb2-associated binder protein) [GRAP] mRNA	
274	5484	10806	3.01	1.0E-80	AF231920.1 NT	Homo sapiens amyloid beta (A4) precursor protein (protease matin-1, Alzheimer disease) (APP) mRNA		
372	7862	10805	2.12	1.0E-80	AF231920.1 NT	Homo sapiens chromosome 21 unknown mRNA		
373	7883	10636	2.12	1.0E-80	AF231920.1 NT	Homo sapiens chromosome 21 unknown mRNA		
693	6850	10894	1.7	1.0E-80	AJ237689.1 NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial		
693	6850	10895	1.7	1.0E-80	AJ237689.1 NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial		
728	6884	11033	12.83	1.0E-80	AF284760.1 NT	Homo sapiens ALR-like protein mRNA, partial cds		
728	6884	11034	12.83	1.0E-80	AF284760.1 NT	Homo sapiens ALR-like protein mRNA, partial cds		
1111	6249	4388	4.88	1.0E-80	4507828 NT	Homo sapiens Knippe-like factor 7 (ubiquilin) (KLF7) mRNA		
1310	6440	11616	2.9	1.0E-80	AF098164.1 NT	Homo sapiens protein phosphatase 2A/B gamma subunit gene, exon 3		
1310	6440	11617	2.9	1.0E-80	AF098164.1 NT	Homo sapiens protein phosphatase 2A/B gamma subunit gene, exon 3		
1881	6810	5.61	1.0E-80	BE3788884.1 EST HUMAN	BT0115963H22_NLH_MG_C52_Homo sapiens cDNA clone IMAGE3511118.5			
1808	7027	12247	2.4	1.0E-80	11420514 NT	Homo sapiens similar to SALL1 (sal (Drosophila) like) (LOC571187) mRNA		
2816	7972	13132	6.74	1.0E-80	6005720 NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2) mRNA		
3830	89868	14118	0.85	1.0E-80	AB020710.1 NT	Homo sapiens mRNA for KIAA0863 protein, partial cds		
3830	89868	14119	0.85	1.0E-80	AB020710.1 NT	Homo sapiens soluble interleukin-1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 8 and complete cds, alternatively spliced		
4401	9521	14682	1.31	1.0E-80	AF167340.1 NT	Homo sapiens cDNA clone 381.3'		
4168	9264	14432	5.3	8.0E-91	D12234.1 EST HUMAN	HUM0005381 Liver HepG2 cell line. Homo sapiens cDNA clone 381.3'		
1457	6584	11772	1.01	7.0E-91	AF052768.1 NT	Rattus norvegicus brain specific contactin-binding protein CIBP80 mRNA, partial cds		
3456	8593	13762	2.08	5.0E-91	AA702784.1 EST HUMAN	ZB05064.11 Scores fetal liver, spleen. Homo sapiens cDNA clone MAGE448016.3'		
4480	9809	14747	1.1	6.0E-91	AU148539.1 EST HUMAN	AU145339 7794A1 Homo sapiens cDNA clone Y78AA10020287.6'		
4490	9809	14748	1.1	6.0E-91	AU148539.1 EST HUMAN	Homo sapiens chromosome 22 open reading frame 6 (C22ORF6) mRNA		
4777	6880	15035	1.24	6.0E-91	7110834 NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5) mRNA		
7777	9890	15036	1.24	6.0E-91	7110834 NT	Homo sapiens lysophosphatidic acid acyltransferase delta (LPAAT-delta) mRNA, complete cds		
3185	8339	13488	11.3	4.0E-91	AF168778.1 NT	Homo sapiens lysophosphatidic acid acyltransferase delta (LPAAT-delta) mRNA, complete cds		
3185	8336	13499	11.3	4.0E-91	AF168778.1 NT	Homo sapiens lysophosphatidic acid acyltransferase delta (LPAAT-delta) mRNA, complete cds		
1829	6758	11952	2.26	3.0E-91	11430183 NT	Homo sapiens adult carrier family 4, anion exchanger, member 3 (SLC4A3) mRNA		
1829	6758	11953	2.26	3.0E-91	11430183 NT	Homo sapiens adult carrier family 4, anion exchanger, member 3 (SLC4A3) mRNA		
1802	7872	12140	1.35	3.0E-91	AF265655.1 NT	Homo sapiens ubiquitin-conjugating B1R domain enzyme APOLLO mRNA, complete cds		
3321	8468	13631	1.48	3.0E-91	AL168285.2 NT	Homo sapiens chromosome 21 segment HS21.C083		
3444	8856	13748	2.88	3.0E-91	AB033104.1 NT	Homo sapiens mRNA for KIAA1278 protein, partial cds		
2858	13749	2.88	3.0E-91	AB033104.1 NT	Homo sapiens mRNA for KIAA1278 protein, partial cds			

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No.	Exon Seq ID No.	ORF Seq ID No:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3767	8304	14057	2.23	3.0E-91	AFO84630.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4584	8882	14821	3.8	3.0E-91	MS08383.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4984	10072	15208	1.05	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4884	10072	15210	1.05	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
47	6268	10883	3.17	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1248	8379	11553	9.58	1.0E-91	AW449748.1	EST_HUMAN	U1H-B13_ate-d-01-0-U_81 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733280 3'
1245	8378	11552	10.34	9.0E-92	AJ001689.1	NT	Homo sapiens NK32D gene, exon 10
1245	8376	11553	10.34	9.0E-92	AJ001689.1	NT	Homo sapiens NK32D gene, exon 10
88	5287	10438	5.9	8.0E-92	W26387.1	EST_HUMAN	2833 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
283	5472	10814	6.48	8.0E-92	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614687 5'
6083	10185	15323	1.06	8.0E-92	AW157671.1	EST_HUMAN	TR-068302_OSG302_KU4005 PROTEIN :contains element MER22 repetitive element:
234	7886	10566	1.01	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
234	7886	10567	1.01	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
589	5781		1	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Serine/threonine nucleated isoform mRNA, complete cds
1284	6413	11589	2.65	7.0E-92	4502384	NT	Homo sapiens B-cell CLLymphoma 7b (BCL7B) mRNA
2169	7282	12529	10.41	7.0E-92	6031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2169	7282	12529	10.41	7.0E-92	6031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2833	7638	12884	1.27	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2887	7784	13032	10.39	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S165E), mRNA
2716	7811	13068	1.19	7.0E-92	AB31007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3327	10306	13635	0.76	7.0E-92	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3327	10306	13636	0.76	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4581	6878	14818	1.17	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2880 nt]
4581	6878	14819	1.17	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2880 nt]
1600	6728		1.37	6.0E-92	BE390982.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3805018 5'
2727	7822	13077	3.88	3.0E-92	BE808714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3802839 5'
24	5226	10349	1.34	2.0E-92	4501688	NT	Homo sapiens activin A receptor, type IIb (ACVR2B) mRNA
174	5368	10508	3.34	2.0E-92	11422946	NT	Homo sapiens hypothetical protein d482023.2 (D482023.2), mRNA
174	5368	10509	3.34	2.0E-92	11422946	NT	Homo sapiens hypothetical protein d482023.2 (D482023.2), mRNA
748	5904	11059	4.61	2.0E-92	BE289180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
748	5904	11060	4.61	2.0E-92	BE289190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1729 68569			1.9	2.0E-92	ST78653.1	NT	mg-mnas-related [Human, Genomic, 2416 nt] wk27d07_51 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12344
1940 7059	12281		2.6	2.0E-92	AIR1819.1	EST HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN :
1940 7059	12282		2.8	2.0E-92	AIR1819.1	EST HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN :
1897 7084	12309		1.97	2.0E-92	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1897 7084	12310		1.97	2.0E-92	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
2040 7157	12397		7.63	2.0E-92	45068860	NT	Homo sapiens syncoilin 4 (an�tiglycan, syndecan) (SDCA) mRNA
2620 7719	12873		14	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2780 6798	11692		1.09	2.0E-92	11418424	NT	Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
2780 6798	11693		1.09	2.0E-92	11418424	NT	Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
3597 8736	13689		1.18	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3597 8736	13689		1.18	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3683 69002	13958		6.99	2.0E-92	5603180	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp80-organizing protein) (STIP1), mRNA
4263 63089	145263		1.72	2.0E-92	MT0976.1	NT	[Human endogenous retroviral DNA (4-1), complete retroviral segment]
4979 10087			2.28	2.0E-92	AL040437.1	EST HUMAN	DKFZp434C0414 .71 43 (synonym: fibs3) Homo sapiens cDNA clone DKFZp434C0414 15
1861 6881	12204		1.77	1.0E-92	R78078.1	EST HUMAN	Y80608.71 Seacrest placenta N12-P Homo sapiens cDNA clone IMAGE:145574 5'
1861 6881	12205		1.77	1.0E-92	R78078.1	EST HUMAN	Y80608.71 Seacrest placenta N12-P Homo sapiens cDNA clone IMAGE:145574 5'
2065 7181	12421		63.38	1.0E-92	45068838	NT	Homo sapiens ribosomal protein, large, P1 (RPUP1) mRNA
2022 7139	12379		2.17	0.0E-93	AL121681.1	EST HUMAN	ALU121681.1 MAMMA1 MAMMA1000738 5'
2038 7154			26.89	9.0E-93	AA316723.1	EST HUMAN	EST1884414 HCC cell line (metastasis to liver in mouse) 11 Homo sapiens cDNA 5' end similar to ribosomal protein L29
4312 9434	14669		1.42	9.0E-93	AAJ121681.1	EST HUMAN	ALU121681 MAMMA1 MAMMA1000738 5'
243 6434	10573		6.68	7.0E-93	AA231818.1	NT	Homo sapiens chromosome 21 unknown mRNA
3047 8201	13367		0.67	6.0E-93	11626178	NT	Homo sapiens T-cell lymphoma in reaction and metastasis 1 (TIAM1), mRNA
1381 6619	11689		4.35	5.0E-93	AB014611.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1415 6542	11720		13.62	5.0E-93	AB74184.1	EST HUMAN	WCD08-08_01 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2314870 3'
1415 6542	11721		13.62	5.0E-93	AB74184.1	EST HUMAN	WCD08-08_01 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2314870 3'
1835 7927	12180		1.01	5.0E-93	AJ287710.1	NT	Homo sapiens mRNA for CD22L5 proto kinase, (CD22L5 gene), isoform 2
3218 8369	13632		4.85	6.0E-93	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin 2x50e0f9.61 Seacrest testis_NHT Homo sapiens cDNA clone IMAGE:785688 3' similar to SW:CLPA_RAT
83 5262			4.53	4.0E-93	AA459893.1	EST HUMAN	P37397 CALPONIN_ACIDIC ISOFORM ;
444 6612	10757		1.44	4.0E-93	4557878	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar BLAST E Value	(Top) Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit No.	Top Hit Database Source
444	6612	10768	1.44	4.0E-83	4557870 NT	Homo sapiens Interferon gamma receptor 1 (IFNGR1) mRNA		
772	6926	11084	2.88	4.0E-83	7657454 NT	Homo sapiens pescadillo (zabranish) homolog 1, containing BRCT domain (PEST), mRNA		
772	5926	11085	2.88	4.0E-83	7657454 NT	Homo sapiens pescadillo (zabranish) homolog 1, containing BRCT domain (PEST), mRNA		
1185	6319	11487	1.84	4.0E-83	8922858 NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA		
1978	7089	12327	2.62	4.0E-83	AF047877.1	Homo sapiens dystrophin (DMD) gene, deletion breakpoint 1-3 in Intron 5		
2225	7331	12591	1.18	4.0E-83	AF157476.1	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds		
2375	7481	12795	1.31	4.0E-83	AL103301.2	Homo sapiens chromosome 21 segment HS21C101		
3553	8894	13856	0.85	4.0E-83	7705398 NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA		
4022	9164	14288	1.47	4.0E-83	4504854 NT	Homo sapiens Interleukin 18 receptor 1 (IL18R1) mRNA		
5009	8394	13856	0.85	4.0E-83	7705398 NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA		
34228	8768	13923	9.7	3.0E-83	BF690680.1	EST HUMAN	602246854F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332038 5'	
36228	8768	13924	8.7	3.0E-83	BF690680.1	EST HUMAN	602246854F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332038 5'	
5052	10154		0.94	3.0E-83	AF231681.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds	
187	63182	10523	26.63	2.0E-83	AB016810.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds	
187	63182	10524	28.53	2.0E-83	AB016810.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds	
321	66017	10848	19.27	2.0E-83	AL168285.2	NT	Homo sapiens chromosome 21 segment HS21C085	
322	65017	10848	6.78	2.0E-83	AL168285.2	NT	Homo sapiens chromosome 21 segment HS21C085	
2121	7236	12479	2.73	2.0E-83	U40783.1	NT	Human C14-associational RS cyclophilin CARS-Cyp mRNA, complete cds	
2461	7655	12818	1.71	2.0E-83	BF252882.1	EST HUMAN	601175886F1 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:3368220 5'	
89	5303	10448	2.59	1.0E-83	AF238897.1	NT	Homo sapiens CTR1 pseudogene	
89	5303	10448	2.66	1.0E-83	AF238897.1	NT	Homo sapiens hypothetical protein (D32BE19.C1.1), mRNA	
6116	66892	10816	18.63	1.0E-83	7657016 NT	Homo sapiens hypothetical protein FLJ20281 (FLJ20281), mRNA		
658	5760	10889	3.83	1.0E-83	AI148755.1	EST HUMAN	cytobiotin N1 CGAP_C11 Homo sapiens cDNA clone IMAGE:1672593 3' similar to TR-Q8Z384 QR22384 ZINC FINGER PROTEIN :	
873	6024	11195	7.63	1.0E-83	AF287676.1	NT	Homo sapiens DNA for arylidyl precursor protein, complete cds	
1240	6370	11643	8.84	1.0E-83	6922370 NT	Homo sapiens hypothetical protein FLJ20281 (FLJ20281), mRNA		
1240	6370	11544	8.84	1.0E-83	6922370 NT	Homo sapiens hypothetical protein FLJ20281 (FLJ20281), mRNA		
1350	6479	11658	1.17	1.0E-83	AB0446783.1	NT	Homo sapiens mRNA for KIAA1663 protein, partial cds	
1352	6481	11680	1.18	1.0E-83	AF167703.1	NT	Homo sapiens cysteine-rich repeat-containing protein SE2 precursor, mRNA, complete cds	
2318	7427	12878	5.52	1.0E-83	AF231984.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds	
2440	7844	12788	1.52	1.0E-83	AF055068.1	NT	Homo sapiens MHC class 1 region	
2477	7682		1.11	1.0E-83	AL137200.1	NT	Novel human gene mapping to chromosomes 1	

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit No.	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2782	8428	11602	2.86	1.0E-83	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone [MAGE:3532865 5'	Homo sapiens cDNA clone [MAGE:3532865 5'
2782	8429	11603	2.88	1.0E-83	BE297389.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone [MAGE:3532865 5'	Homo sapiens cDNA clone [MAGE:3532865 5'
2899	8053	13222	3.67	1.0E-83	DB7675.1	NT		Homo sapiens DNA for amyloid precursor protein, complete cds
3201	8362		1.58	1.0E-83	Af231081.1	NT		Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4407	8527	14887	1.98	1.0E-83	AI163284.2	NT		Homo sapiens chromosome 21 segment HS21C084
3935	8071	14227	1.85	6.0E-94	AF142482.1	NT		Homo sapiens transcription enhancer factor-5 mRNA, complete cds
1894	6976		21.16	4.0E-94	LG50394.1	NT		Homo sapiens ribosomal protein L27 mRNA, complete cds
2618	7717	12971	1.78	4.0E-94	4656008	NT		Homo sapiens respiratory subunit 10 (PPP1R10) mRNA
3649	8788	13942	1.02	4.0E-94	AW197851.1	EST_HUMAN	XN891123  Soares_NFL_T_GBC_ST1 Homo sapiens cDNA clone [MAGE:2701679 3'	XN891123  Soares_NFL_T_GBC_ST1 Homo sapiens cDNA clone [MAGE:2701679 3'
3849	8788	13943	1.02	4.0E-94	AW197851.1	EST_HUMAN	XN891123  Soares_NFL_T_GBC_ST1 Homo sapiens cDNA clone [MAGE:2701679 3'	XN891123  Soares_NFL_T_GBC_ST1 Homo sapiens cDNA clone [MAGE:2701679 3'
4985	8901	14947	2.97	4.0E-94	AI691312.1	EST_HUMAN		INFLATION NQI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TRQ162635 Q162635 PROTEIN TYROSINE PHOSPHATASE :
6038	6768	10897	3.14	3.0E-94	AB022785.1	NT		Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
719	6878	11023	1.3	3.0E-94	4592568	NT		Homo sapiens complement component B (C5) mRNA
17761	8377	12082	1.29	3.0E-94	AF167708.1	NT		Homo sapiens cysteine-rich repeat-containing protein SS2 precursor, mRNA, complete cds
17761	6877	12083	1.29	3.0E-94	AF167706.1	NT		Homo sapiens cysteine-rich repeat-containing protein SS2 precursor, mRNA, complete cds
1782	69008	12116	2.04	3.0E-94	4597586	NT		Homo sapiens E1A binding protein p300 (EP300) mRNA
4160	9298	14421	0.7	3.0E-94	AA484905.1	EST_HUMAN	ZW639081  Soares_total_fetus_Nb2HFB_Bv Homo sapiens cDNA clone IMAGE:774782 5'	ZW639081  Soares_total_fetus_Nb2HFB_Bv Homo sapiens cDNA clone IMAGE:774782 5'
144	5341	10485	3.43	1.0E-94	BE285714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone [MAGE:3531038 5'	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone [MAGE:3531038 5'
3081	8214	13387	2.13	1.0E-94	BE283433.1	EST_HUMAN	601111686F1 NIH_MGC_16 Homo sapiens cDNA clone [MAGE:3352559 5'	601111686F1 NIH_MGC_16 Homo sapiens cDNA clone [MAGE:3352559 5'
3081	8214	13388	2.13	1.0E-94	BE283483.1	EST_HUMAN		TUBULIN ALPHA-1 CHAIN (HUMAN):
4338	8468	14696	0.89	1.0E-94	9506682	NT		Homo sapiens hypochloric protein (FLJ220746), mRNA
4757	9870	15020	4.78	1.0E-94	AI9041151.1	EST_HUMAN	CMTB03-060288-076 BT043 Homo sapiens cDNA	CMTB03-060288-076 BT043 Homo sapiens cDNA
3134	8225	13441	2.81	9.0E-95	AF027302.1	NT		Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3134	8225	13442	1.02	9.0E-95	7682027	NT		Homo sapiens KIAA0256 gene product (KIAA0256), mRNA
4509	9628	14771	1.81	8.0E-95	A769898.1	EST_HUMAN	W69864  X1 NC1 CGAP_L124 Homo sapiens cDNA clone IMAGE:2340603 3' similar to gb:K00568	TUBULIN ALPHA-1 CHAIN (HUMAN):
4509	9628	14772	1.81	8.0E-95	AI700888.1	EST_HUMAN		Homo sapiens DNA for amyloid precursor protein, complete cds
273	5463	10504	12.32	7.0E-95	D87675.1	NT		Homo sapiens DNA for amyloid precursor protein, complete cds
273	5463	10505	12.32	7.0E-95	D87676.1	NT		Homo sapiens DNA for amyloid precursor protein, complete cds
4345	9497	14605	4.92	7.0E-95	M95708.1	NT		Homo sapiens Ly-6-like protein (CD69) mRNA, complete cds

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## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4391 9511				1.36	7.0E-95 AL163246.2	NT	Homo sapiens chromosomes 21 segment HS21C048
1658 6784	11977	4.12	2.0E-65	7882027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA	
1658 6784	11978	4.12	2.0E-85	7882027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA	
1846 7083	12287	1.73	2.0E-95	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sarcoma fundus dystrophy, pseudodiflammatory) (TIMP3)	mRNA
1848 7083	12281	2.79	2.0E-95	BE393873.1	EST_HUMAN	80_1312161F1_NIH_MGC_44_Homo_sapiens_cDNA_clone IMAGE:36588802 5'	
2403 7609	12759	1.47	2.0E-95	5453685	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA	
2403 7609	12759	1.47	2.0E-95	5453685	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA	
2442 7348	12789	1.77	2.0E-85	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	
2484 7688	12837	2.67	2.0E-95	4758423	NT	Homo sapiens Glycoside cleavage system protein H (anthromethyl carrier) (GCSH) mRNA	
3156 8231	13444	2.69	2.0E-95	AF016452.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds	
3550 8691	13852	2.81	2.0E-95	7705890	NT	Homo sapiens unconventional myosin-16 (LOC51168), mRNA	
3550 8691	13853	2.81	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-16 (LOC51168), mRNA	
3600 8739	13852	2.18	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1368 protein, partial cds	qm01c02_x1_Scenes_NhNMpu_S1_Homo_sapiens_cDNA_clone IMAGE:1680546 3' similar to WPT23G7.4
3731 8869	14022	3.84	2.0E-95	AL280264.1	EST_HUMAN	CE03705;	
4339 9461	14638	1.82	2.0E-95	7657185	NT	Homo sapiens hypothetical protein (HS922B1A), mRNA	
5021 10123	15255	2.79	2.0E-95	7861879	NT	Homo sapiens KIAA0137 gene product (KIAA0137), mRNA	
441 7890	10754	1.39	8.0E-98	BE807607.1	EST_HUMAN	60_1497008F1_NIH_MGC_70_Homo_sapiens_cDNA_clone IMAGE:36589761 5'	
441 7890	10755	1.39	8.0E-98	BE807607.1	EST_HUMAN	60_1497008F1_NIH_MGC_70_Homo_sapiens_cDNA_clone IMAGE:36589761 5'	
3886 8022	14178	1.23	7.0E-98	AF231920.1	NT	Homo sapiens chromosomes 21 unknown mRNA	
2240 7351	12603	3.03	6.0E-98	BE171984.1	EST_HUMAN	MR04HT0569-2502020-002-d07 HT0569 Homo_sapiens cDNA	
3229 8449	13608	0.92	8.0E-98	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C01	
3484 8603	13770	38.6	8.0E-98	M26873.1	NT	Human glyoxaldehyde-3-phosphate dehydrogenase pseudogene 3 transcript	
6150 10287	15423	1.28	6.0E-98	AF422283.1	EST_HUMAN	I441d3_1_NCI_COAP_Bin23_Homo_sapiens_cDNA_clone IMAGE:20588757 3'	
318 6804	10842	2.15	5.0E-98	AB0326998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds	
843 6994	11163	3.36	6.0E-98	AB0326998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds	
843 6994	11164	3.36	6.0E-98	AB0326998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds	
2533 7684		2.01	5.0E-98	11416787	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA	
4877 9988		1.63	5.0E-98	260812.1	NT	H. sapiens DNA for monooxygenase oxidase type A (7) (partial)	
5150 10250	16389	0.68	5.0E-98	AF2264760.1	NT	Homo sapiens ALR-J-like protein mRNA, partial cds	
4162 9238		8.24	3.0E-98	HB88668.1	EST_HUMAN	y87h2L Scenes fetal liver spleen 1NF-LS Homo_sapiens cDNA clone IMAGE:212327 5'	
414 6582		3.71	2.0E-98	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (metanome-associated) (CSPG4), mRNA	

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
746	5902	11056	1.52	2.0E-98	AL_163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1804	69226	12142	1.43	2.0E-98	7706205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
41223	98317	14981	1.05	2.0E-98	BE148204.1	EST_HUMAN	RC3-HT0230-040500-110-802 HT0230 Homo sapiens cDNA
620	6780	10869	2.02	1.0E-98	4826883	NT	Homo sapiens neuron cell adhesion molecule (NRCAM) mRNA
620	5780	10910	2.02	1.0E-98	4826883	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
670	68229	10859	5.58	1.0E-98	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1791	69017	12124	8.41	1.0E-98	AW055054.1	EST_HUMAN	EST387124 MAGE sequences, MAGC Homo sapiens cDNA
1781	68177	12125	6.41	1.0E-98	AW055054.1	EST_HUMAN	EST387124 MAGE sequences, MAGC Homo sapiens cDNA
2246	7876	12614	1.72	1.0E-98	U51472.2	NT	Felis catus superfamily myosin heavy chain (sMyHC) mRNA, complete cds
33098	84456	13817	0.98	6.0E-97	BF245204.1	EST_HUMAN	601863712F1 NIH MGIC 57 Homo sapiens cDNA clone IMAGE-4081202 6'
839	60937	11255	3.71	4.0E-97	BE004438.1	EST_HUMAN	CMD-BN0108-170300-283-006 BN0108 Homo sapiens cDNA
849	60937	11255	1.34	4.0E-97	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidearginine deiminase type II, complete cds
949	60937	11268	1.34	4.0E-97	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidearginine deiminase type II, complete cds
1814	70333	12263	4.55	4.0E-97	5453572	NT	Homo sapiens brevetinin A-inhibited guanine nucleotide-exchange protein 2 (B1C2), mRNA
240	54322	10571	2.11	3.0E-97	AB0322898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
876	60286	11197	14.13	3.0E-97	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease neprilin-1, Alzheimer disease) (APP), mRNA
875	60288	11198	14.13	3.0E-97	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease neprilin-1, Alzheimer disease) (APP), mRNA
1482	7818	11788	1.45	3.0E-97	4758813	NT	Homo sapiens N-myrc (and STAT) interactor (NMI), mRNA
2416	7877	12772	2.12	3.0E-97	U36265.1	NT	Human delta-prime-adaptin (PAM22) gene, exon 7
3243	83393	13555	0.89	3.0E-97	5174478	NT	Homeo sapiens pericentrin (PCNT) mRNA
4747	98860	15009	28	1.0E-97	4503470	NT	Homeo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
802	60532	11222	6.13	9.0E-98	BE080973.1	EST_HUMAN	PM4-BT0724-010400-008-412 BT0724 Homo sapiens cDNA
1280	84309	11584	1.08	9.0E-98	8338092	NT	Homeo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
48405	9763		1.26	9.0E-98	8400716	NT	Homeo sapiens nebulin (NEB), mRNA
1381	66099	11680	1.03	8.0E-98	AB033768.1	NT	Homeo sapiens NPAD-odony10 mRNA for peptidylarginine deiminase type I, complete cds
1675	67033	11892	1.32	8.0E-98	6031810	NT	Homeo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1575	67033	11893	1.32	8.0E-98	5031810	NT	Homeo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1739	6863	12070	5.86	8.0E-98	AB017007.1	NT	Homeo sapiens PMS2L-16 mRNA, partial cds
1739	6863	12071	5.83	8.0E-98	AB017007.1	NT	Homeo sapiens PMS2L-16 mRNA, partial cds
3773	89110	14063	6.28	8.0E-98	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
2168	7271	12519	1.29	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124.3.4 (downregulated in lung carcinoma) Homo sapiens cDNA clone 1B
2572	7672	12827	2.89	3.0E-98	AB014607.1	NT	Homeo sapiens mRNA for KIAA0707 protein, partial cds

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**Table 4**  
**Single Exon Probes Expressed in BT474 Cells**

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit No.	Top Hit Accession	Top Hit Database Source	Top Hit Descriptor
2712	7807		3.52	3.0E-98	AA077498.1	EST_HUMAN	7B18H10_1 Chromosome 7 Fetal Brain cDNA Library/Homo sapiens cDNA clone '7B18H101'	
734	58190	11042	1.37	2.0E-98	EE281694.1	EST_HUMAN	6011494-88F1 NIH MC_G19 Homo sapiens cDNA clone IMAGE-3502245 5'	
2071	7187	12428	2.46	2.0E-98	EE294287.1	EST_HUMAN	6011725B8F1 NIH MC_G17 Homo sapiens cDNA clone IMAGE-3528134 5'	
2219	7331	12584	3.31	2.0E-98	AL1832022	NT	Homo sapiens chromosome 21 segment HS21C002	
3109	62622	13416	1	2.0E-98	AB032377.1	NT	Homo sapiens hCHK1 gene for checkpoint kinase, exon 2	
3109	82362	13417	1	2.0E-98	AB032377.1	NT	Homo sapiens hCHK1 gene for checkpoint kinase, exon 2	
4081	8210	14347	1.2	2.0E-98	88233308	NT	Homo sapiens hypothetical protein FLJ20333 (FLJ20333), mRNA	
4272	83198	14535	0.69	2.0E-98	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	
4317	8439	14572	3.11	2.0E-98	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA	
4795	89038	15047	1.63	2.0E-98	AF218802.1	NT	Homo sapiens attractin precursor (ATTRN) gene, exon 18	
4785	89038	16048	1.63	2.0E-98	AF218802.1	NT	Homo sapiens attractin precursor (ATTRN) gene, exon 18	
5122	10223	15357	0.86	2.0E-98	AI200857.1	EST_HUMAN	qf203_x1_Searcs_tests_NtH Homo sapiens cDNA clone IMAGE-1784633 3' similar to SW-CYT_COTJA	
6122	10223	15358	0.86	2.0E-98	AI200857.1	EST_HUMAN	qf203_x1_Searcs_tests_NtH Homo sapiens cDNA clone IMAGE-1784633 3' similar to SW-CYT_COTJA	
405	5572	10720	80.3	1.0E-98	AB852007.1	EST_HUMAN	P29816 60S RIBOSOMAL PROTEIN L23A. ;	
484	5622	10785	3.16	1.0E-98	AW888861.1	EST_HUMAN	PM0-BN0055-100300-001-006 BN0055 Homo sapiens cDNA	
1809	6932	12147	55.14	1.0E-98	NA9818.1	EST_HUMAN	y23051.1 Searcs fetal liver spleen 1NIF-S Homo sapiens cDNA clone IMAGE-243585 5' similar to PIR-SS54204 S54204 ribosomal protein L29 - human ;	
471	6633	10780	0.84	8.0E-99	UJ10991.1	NT	Human G2 protein mRNA, partial cds	
3885	8001	14169	1.67	6.0E-99	AW976384.1	EST_HUMAN	ES1388473 MAGE ressequences, MAGN Homo sapiens cDNA	
4713	8829	14972	1.06	6.0E-99	4502680	NT	Homo sapiens CD34 antigen (CD34) mRNA	
8220	6069	11234	0.63	5.0E-99	UJ35464.1	NT	Human protein C inhibitor (PC1-B) mRNA, complete cds	
9220	6069	11236	0.63	5.0E-99	UJ35464.1	NT	Human protein C inhibitor (PC1-B) mRNA, complete cds	
1888	7085	12311	1.27	5.0E-99	Y11368.1	NT	H. sapiens IMPA gene, exon 8	
4537	8865	14809	2.03	5.0E-99	AF098680.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S342 to TCRBV12522 region	
4694	9810	14957	1.03	5.0E-99	AF286555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLO mRNA, complete cds	
4694	9810	14958	1.06	5.0E-99	AF286555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLO mRNA, complete cds	
1243	6374		26.58	2.0E-99	AW214782.1	EST_HUMAN	xp0203_x1_NCI_CQAP_HN9 Homo sapiens cDNA clone IMAGE-2738874 3' similar to gBM31212 MYOSIN	
3242	83392	13554	1.49	2.0E-99	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds	
4516	9834	14779	1.05	2.0E-99	AF085703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds	

Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit No.	Top Hit Assessment No.	Top Hit Database Source	Top Hit Descriptor
313	5459	10539	1.14	1.0E-69	AF114487.1	NT	Homo sapiens Intersector long isoform (ITSN) mRNA, complete cds	
377	65545	10569	1.28	1.0E-69	11526180	NT	Homo sapiens Gα-binding protein transcription factor, alpha subunit (Gα <sub>i</sub> ) (GABPA), mRNA	
1430	6557	111740	6.38	1.0E-69	M310538.1	NT	Human KU (670kDa) subunit mRNA, complete cds	
1571	6639	118888	2.04	1.0E-69	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds	
1571	6639	116877	2.04	1.0E-69	AF182523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds	
1832	7051	122772	1.04	1.0E-69	45033730	NT	Homo sapiens FK506-binding protein 6 (38kD) (FKBP6) mRNA, and translated products	
1832	7051	122773	1.04	1.0E-69	45033730	NT	Homo sapiens FK506-binding protein 8 (36kD) (FKBP8) mRNA, and translated products	
3857	8210	133864	0.84	1.0E-69	JR3171.1	NT	Human interferon-α/β receptor (IFN-α/βR-Rec) mRNA, complete cds	
4359	8481	148119	2.23	1.0E-69	AF058018.1	NT	Homo sapiens fatty acid ester hydrolase (FAAH) gene, exon 14	
4359	8481	148220	2.23	1.0E-69	AF058018.1	NT	Homo sapiens fatty acid ester hydrolase (FAAH) gene, exon 14	
1	6214	10326	1.7	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047	
2	6214	10326	2.2	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047	
87	6277	104111	1.08	1.0E-100	11418230	NT	Homo sapiens Testis-specific Xk-related protein on Y (XkSY) mRNA	
87	5277	10412	1.08	1.0E-100	11418230	NT	Homo sapiens Testis-specific Xk-related protein on Y (XkSY) mRNA	
164	5360	105600	0.88	1.0E-100	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008	
315	5501	10841	1.28	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049	
341	6524	10860	2.31	1.0E-100	T056987.1	EST_HUMAN	EST02879 Fetal brain, Stratagene (cat#86287006) Homo sapiens cDNA clone IMAGE:2722/6432	
438	56015		1.62	1.0E-100	AF043528.1	NT	Homo sapiens X-linked arthritroic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	
489	6857		10.45	1.0E-100	X83631.1	NT	G. gorilla DNA for ZNF80 gene homolog	
509	6875	108099	1.98	1.0E-100	BE180509.1	EST_HUMAN	RC3-HTD026-040500-022-b109 HT0625 Homo sapiens cDNA	
1020	6161	11326	2.65	1.0E-100	7661686	NT	Homo sapiens DKFZP2000610122 protein (DKFZP2000610122), mRNA	
1020	6161	11327	2.55	1.0E-100	7661685	NT	Homo sapiens DKFZP2000610122 protein (DKFZP2000610122), mRNA	
1448	6574	11760	1.25	1.0E-100	BF530758.1	EST_HUMAN	S02072084F1 NCI CGAP Bin87 Homo sapiens cDNA clone IMAGE:4215039 5	
1561	6839		1.33	1.0E-100	AW207655.1	EST_HUMAN	UH-B1-afk-07-0-U1s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722/643	
1658	6894	11881	1.14	1.0E-100	AI202057.1	EST_HUMAN	P81081 CYSTATIN; qPCR209 XI Soares testis_NFT Homo sapiens cDNA clone IMAGE:1764333 3 similar to SW-CYT_COTJA	
1876	6895	12220	1.36	1.0E-100	AB09329894.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds	
2415	7521	12771	1.03	1.0E-100	X92468.1	NT	H. sapiens mRNA for IFN-γ-gamma (PKC-0)	
2628	7784	13015	1.76	1.0E-100	11416878	NT	Homo sapiens KIAA0857 protein (KIAA0857), mRNA	
2880	8145		3.49	1.0E-100	D11078.1	NT	Homo sapiens Rch12 gene, retinoblastoma-like element	
4183	8309	14446	1.33	1.0E-100	AF057354.1	NT	Homo sapiens myeloblastosis-related protein 1a mRNA, partial cds	
4214	9339	14471	2.03	1.0E-100	4603792	NT	Homo sapiens follistatin-stimulating hormone receptor (FSFR) mRNA	
5078	10177	16311	3.28	1.0E-100	5032104	NT	Homo sapiens small optic (obs) (Oscophila) homolog (SOLH) mRNA	

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Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6078	10177	16312	3.28	1.0E-100	6032104 NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA	
70	5285	10424	1.2	1.0E-101	7110714 NT	Homo sapiens SEC14 (S. cerevisiae) like 2 (SEC14L2), mRNA	
76	6285	10425	1.2	1.0E-101	7110714 NT	Homo sapiens SEC14 (S. cerevisiae) like 2 (SEC14L2), mRNA	
684	5942	10881	2.68	1.0E-101	AB007915.2 NT	Homo sapiens mRNA for KIAA0448 protein, partial cds	
702	5958	11001	6.65	1.0E-101	7110734 NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA	
702	5959	11008	6.66	1.0E-101	7110734 NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA	
771	5925	11083	3.3	1.0E-101	7657454 NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	
854	6005	11178	1.67	1.0E-101	4603914 NT	Homo sapiens phosphatidylglycerol kinase family transference, phosphotidylycholine sintetase, phosphotidylylaminodiazole synthetase (GART) mRNA	
926	8074	11242	0.74	1.0E-101	220856.1 NT	Homo sapiens of carcino-embryonic antigen heavy chain gene	
988	8132	11303	17.11	1.0E-101	BF581218.1 EST HUMAN	602158474F1 NIH 3T3 cDNA clone IMAGE:4287291 5'	
1034	6185	11359	1.18	1.0E-101	65221450 NT	Homo sapiens SEC14 (S. cerevisiae) like 2 (SEC14L2), mRNA	
1689	6725	11917	1.18	1.0E-101	59221450 NT	Homo sapiens GBC_58 gamma-1, GBC_58	
1598	6725	11918	1.18	1.0E-101	59221450 NT	Homo sapiens GBC_58 gamma-1, GBC_58	
1758	6884	12097	1.22	1.0E-101	7682183 NT	Homo sapiens KIAA0688 gene product (KIAA0688), mRNA	
1758	6884	12092	1.22	1.0E-101	7682183 NT	Homo sapiens KIAA0688 gene product (KIAA0688), mRNA	
1849	7067	12282	1.42	1.0E-101	4502898 NT	Homo sapiens cathepsin D-like protease A1 (pancreatic) (CPA1) mRNA	
2048	7164	12403	3.43	1.0E-101	BE843070.1 EST HUMAN	RC3-ST0281-160800-018-H09 ST0281 Homo sapiens cDNA	
2329	7838	12689	1.77	1.0E-101	6728892 NT	Homo sapiens A Kinase (PRKA) enhancer protein 6 (AKAP6), mRNA	
2570	7680	12835	5.26	1.0E-101	X72983.1 NT	H. sapiens EW5 gene, exon 6	
2708	7901	13052	3	1.0E-101	AJ231744.1 NT	Homo sapiens RIBIIR gene (partial), exon 12	
2708	7801	13054	3	1.0E-101	AJ231744.1 NT	Homo sapiens RIBIIR gene (partial), exon 12	
2822	8073	12448	1.0E-101	AJ252312.1 NT	Homo sapiens generic downstream Rhesus box		
3168	8337	13500	2.75	1.0E-101	4885270 NT	Homo sapiens gamma-9-laminin/matrix transferase 1 (GGM1) mRNA	
3225	8375	1236	1.0E-101	BF038327.1 EST HUMAN	601458351F1 NIH 3T3 cDNA clone IMAGE:38620368 5'		
3362	8607	13674	1.88	1.0E-101	AW865668.1 EST 3737629 WAGE-like sequences, MGI Homo sapiens cDNA		
3381	13053	1.65	1.0E-101	AJ231744.1 NT	Homo sapiens RIBIIR gene (partial), exon 12		
3381	7801	13054	1.65	1.0E-101	AJ231744.1 NT	Homo sapiens RIBIIR gene (partial), exon 12	
3683	8622	13978	0.74	1.0E-101	AF079289.1 NT	Homo sapiens Na+/H+ exchanger isoform 2 (NHE2) mRNA, complete cds	
3854	8690	14148	4.69	1.0E-101	AB022785.1 NT	Homo sapiens ASH22, gene, complete cds, similar to <i>Drosophila</i> ash2 gene	
6017	10119	16262	1.61	1.0E-101	6921460 NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTM2A1), mRNA	
5017	10119	16253	1.61	1.0E-101	6921460 NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTM2A1), mRNA	
38	5249	10367	1.38	1.0E-102	AF012872.1 NT	Homo sapiens phosphotidylinositol 4-kinase 230 (PIK230) mRNA, complete cds	
339	6622	10857	5.21	1.0E-102	AL163303.2 NT	Homo sapiens chromosome 21 segment HS2/C103	

Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe Seq ID No:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
617	5777	10908	1.27	1.0E-102	BE262470.1	EST_HUMAN	601108282F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
775	6929	11088	0.88	1.0E-102	4657534 NT		Homo sapiens down-regulated in adenoma (DRA) mRNA
1118	6263	11420	5.62	1.0E-102	M10876.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1272	6401	11574	1.69	1.0E-102	11437148 NT		Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 6 (SLC2A9), mRNA
1272	6401	11575	1.69	1.0E-102	11437148 NT		Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 6 (SLC2A9), mRNA
1427	6554	11736	490.48	1.0E-102	BE408447.1	EST_HUMAN	601260882F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3628501 5'
2286	7393	12648	4.12	1.0E-102	AH124869.1	EST_HUMAN	em00010_x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1639854 3' similar to SW_GG95_HUMAN_Q03879_GOLGIN-65.;
2286	7395	12647	4.12	1.0E-102	AH124869.1	EST_HUMAN	em00010_x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1639854 3' similar to SW_GG95_HUMAN_Q03879_GOLGIN-65.;
2822	7978	13137	0.7	1.0E-102	11419442 NT		Homo sapiens peroxisomal biogenesis factor 1 (PEX1), mRNA
2867	8152		0.70	1.0E-102	Y13582.1		Homo sapiens PRKY exon 7
3037	8191	13347	1.85	1.0E-102	7681978 NT		Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3111	8284	13418	5.87	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3111	8284	13419	6.87	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4210	6335	14467	1.54	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21 Q007
4389	9509	14651	1.83	1.0E-102	Y13582.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'
6097	10197	16335	1.04	1.0E-102	FR84488.1	EST_HUMAN	Y32504.11 Scares placenta N62HP Homo sapiens cDNA clone IMAGE:140384 5'
68	6278	10413	2.08	1.0E-102	SEB0906168.1	EST_HUMAN	601600405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:380123015 5'
68	6278	10414	2.08	1.0E-103	SEB0906168.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:380123015 5'
98	6305	10444	6.79	1.0E-103	DB07078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
205	5400	10542	3.51	1.0E-103	6483763 NT		Homo sapiens nucleolar protein (KED repeat) (NOP56) mRNA
882	6123	11283	0.84	1.0E-103	AJ278348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPP-E gene)
1247	6377	11556	6.89	1.0E-103	SEB77541.1	EST_HUMAN	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887878 5'
1609	6737	11831	3.26	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PI4K230) mRNA, complete cds
1817	7038	12266	1.53	1.0E-103	7657592 NT		Homo sapiens ERG-GATA-ASSOCIATED PROTEIN (SMPAP), mRNA
1877	7094	12323	0.89	1.0E-103	4502428 NT		Homo sapiens bone morphogenic protein 8 (osteogenic protein 2) (BMP8) mRNA
1877	7094	12324	0.89	1.0E-103	4502428 NT		Homo sapiens bone morphogenic protein 8 (osteogenic protein 2) (BMP8) mRNA
2281	7391	12642	4.8	1.0E-103	AU134891.1	EST_HUMAN	AU134891 PLACE-1 Homo sapiens cDNA clone PLACE-1000865 5'
2427	7531	12784	1.1	1.0E-103	AF050908.1	NT	Homo sapiens promyelocytic leukemic zinc finger protein (PLZF) gene, complete cds
2584	7685	12839	1.87	1.0E-103	N32770.1	EST_HUMAN	W910D8.61 Scares placenta 8to9weeks 2nHP86sW Homo sapiens cDNA clone IMAGE:2556989 3'
3041	8195		2.84	1.0E-103	BE144722.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
3361	8506	13873	3.62	1.0E-103	AW288246.1	EST_HUMAN	UHH-BW0-qH-11-Q-U1-st1 NCL_C3AP_Sub6 Homo sapiens cDNA clone IMAGE:2733165 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3421	8663	13720	0.97	1.0E-103	AB040582.1	NT	Human sapiens mRNA for KIAA1459 protein, partial cds
3735	8873		14.84	1.0E-103	AF023881.1	NT	Macaca mulatta cyclin A mRNA, complete cds
3771	8808	14061	1.86	1.0E-103	AA485983.1	EST HUMAN	ab10012.81 Strategic Lung (#337210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element;
3808	8946	14094	1.88	1.0E-103	11430876	NT	Homo sapiens neuronin 1 (NRP1), mRNA
3978	8112	14280	2.69	1.0E-103	T23683.1	EST HUMAN	seq440 dHB3mVA-Cat109+10-Biot Homo sapiens cDNA clone BAH3mVA-Cat109+10-Biot
2322	5428	10564	4.96	1.0E-104	AL037648.3	EST HUMAN	DKFZ584H1072_7_584 (synonym: fibar2) Homo sapiens cDNA clone DKFZ584H1072_6'
2322	6428	10565	4.96	1.0E-104	AL037549.3	EST HUMAN	DKFZ584H1072_7_584 (synonym: fibar2) Homo sapiens cDNA clone DKFZ584H1072_6'
1898	7015	12235	1.59	1.0E-104	4502428	NT	Homo sapiens bone morphogenic protein 8 (osteogenic protein 2) (BMP8), mRNA
2177	7290	12837	7.35	1.0E-104	AA192876.1	EST HUMAN	#222dd8_81 Strategic cokon (#337210) Homo sapiens cDNA clone IMAGE:897026 3' similar to gb274118_7 rat CDP Glycoprotein PRECURSOR (HUMAN);
2187	7293	12848	5.57	1.0E-104	BE744628.1	EST HUMAN	BD1577460F1 NIH MGIC_9 Homo sapiens cDNA clone IMAGE:332638_5
2349	7456	12710	1.14	1.0E-104	BF334221.1	EST HUMAN	RC1-CT0249-110800-214-112 CT0249 Homo sapiens cDNA
2349	7456	12711	1.14	1.0E-104	BF334221.1	EST HUMAN	RC1-CT0249-110800-214-112 CT0249 Homo sapiens cDNA
2414	7520	12770	7.5	1.0E-104	5031570	NT	Homo sapiens ARP2/actin-related protein 2, yeast) homolog (ACTR2), mRNA
2473	7577	12828	2.1	1.0E-104	7862125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2473	7677	12829	2.1	1.0E-104	7862125	NT	Human lymphocyte antigen CD56/MEM43 mRNA, complete cds
2836	7880	13150	7.41	1.0E-104	WS4871.1	NT	H. sapiens gene encoding phenylpyruvate tautomerase II
2882	8036		2.55	1.0E-104	Y11161.1	NT	EST_HUMAN AU33526 OVARC1 Homo sapiens cDNA clone EST_HUMAN
3246	8319	13568	1.02	1.0E-104	AU133028.1	EST_HUMAN	EST_171658 Adrenalf gland tumor Homo sapiens cDNA clone OWARC1000336_5'
3312	8517		2.01	1.0E-104	AA310438.1	EST_HUMAN	EST_171658 Adrenalf gland tumor Homo sapiens cDNA clone OWARC1000336_5'
3914	9050	14209	1.03	1.0E-104	AB032898.1	NT	Human sapiens mRNA for KIAA1172 protein, partial cds
4101	9230	14367	0.77	1.0E-104	F11745.1	EST_HUMAN	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4346	9479	14618	3.84	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4581	8699	14838	2.19	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4681	8699	14837	2.16	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
276	7861	10608	4.52	1.0E-105	4502138	NT	Homo sapiens amyloid beta (A4) precursor protein (precursor Me1S1), mRNA
424	6211	10323	39.88	1.0E-105	4505150	NT	Homo sapiens Meis1 (muse) homolog (MEIS1), mRNA
592	5764	10381	3.78	1.0E-105	AF023897.1	NT	Hom sapiens potassium channel subunit (HERG-3) mRNA, complete cds
592	5764	10382	3.78	1.0E-105	AF032897.1	NT	Hom sapiens potassium channel subunit (HERG-3) mRNA, complete cds
6923	6822		2.63	1.0E-105	AB020981.1	NT	Hom sapiens mRNA for cyclin B2, complete cds
1832	6985	12177	0.99	1.0E-105	AI163280.2	NT	Hom sapiens chromosome 21 segment HS21CD80
1931	7050	12271	1.54	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds

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Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2172	7285	12833	65.09	1.0E-105 AA318369.1	EST_HUMAN	EST20639_Spleen_1 Homo sapiens cDNA 5' end similar to autoinhibitory antigen Ku, p70/p50 subunit	
2302	7411		1.11	1.0E-105 BE891788.1	EST_HUMAN	601434491F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3819811-5'	
2683	7780		1.32	1.0E-105 AA684808.1	EST_HUMAN	nt010265s1 NCI_CGAP_Ptari Homo sapiens cDNA clone IMAGE:1100265_3'	
2978	8132		2.88	1.0E-105 AJ228041.1	NT	Homo sapiens 95% homolog between AML1 and CBF1 on chromosome 21;q22; segment 1/3	
3383	8479	13844	0.87	1.0E-105 7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA	
3333	8479	13845	0.87	1.0E-105 7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA	
4073	8220	14339	2.78	1.0E-105 AW981688.1	EST_HUMAN	EST373761_MAGE Homo sapiens cDNA	
4918	10026		4.61	1.0E-105 AL163208.2	NT	Homo sapiens chromosome 22 segment HS21C008	
6089	10189	15329	0.91	1.0E-105 AB018339.1	NT	Homo sapiens mRNA for KIAA0788 protein, partial cds	
6130	10230	16365	1.44	1.0E-105 AB020873.1	NT	Homo sapiens mRNA for KIAA0888 protein, complete cds	
149	6243		2.75	1.0E-105 AW563282.1	EST_HUMAN	UHFB-E00-ak4-9-07-0-U1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348_5'	
202	6397	10540	1.83	1.0E-105 AL1655055.1	EST_HUMAN	Iq78001X1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2215008_3	
640	5706	10840	1.77	1.0E-108 AW865638.1	EST_HUMAN	EST377829_MAGE resequences, MAGI_Homo sapiens cDNA	
602	5764	10892	1.69	1.0E-108 J00148.1	NT	Human dihydrofolate reductase pseudogene (psf-Hd1)	
603	5764	10892	2.18	1.0E-108 J00148.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds	
1638	66838	11852	1.63	1.0E-108 JAF145712.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds	
1716	8843	12046	3.28	1.0E-108 J48724.1	NT	hg4105_s1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:8973852_3' similar to contains element LTR3 repetitive element;	
1815	6938	12164	2.48	1.0E-106 AA527448.1	EST_HUMAN	hg4105_s1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:8973852_3' similar to contains element LTR3 repetitive element;	
1815	6938	12156	2.48	1.0E-106 AA527448.1	EST_HUMAN	LTR3 repetitive element;	
2114	7228	12471	1.68	1.0E-106 BE144298.1	EST_HUMAN	MRO-H10185-140200-008-40 H10185 Homo sapiens cDNA	
2285	7404	12635	12.07	1.0E-108 4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA	
2475	7579	12831	1	1.0E-106 AF003528.1	NT	Homo sapiens membrane protein BS-63 mRNA, complete cds	
2665	7668	12921	1.36	1.0E-108 UB4476.2	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA	
2567	7868	12923	1.3	1.0E-108 BE280201.1	EST_HUMAN	60143783F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3802461_5'	
2721	7816	13072	9.55	1.0E-108 AI276528.1	EST_HUMAN	ctf5h101x1 Scores_NhMPu_S1 Homo sapiens cDNA clone IMAGE:1878307_5'	
2785	6606	11755	2.61	1.0E-108 4604184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA regions	
2785	6569	11759	2.61	1.0E-108 4604184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA	
2840	7995	13153	1.51	1.0E-108 BE384298.1	EST_HUMAN	60143783F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3813818_5'	
2807	8040	13230	4.79	1.0E-108 AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds	
2807	8039	13231	4.79	1.0E-108 AB037747.1	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA	
3160	8311	13471	3.81	1.0E-108 6922865	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3160	8311	13472	3.81	1.0E-108	8822865	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3395	8500	13688	0.77	1.0E-108	AB008681.1	NT	Homo sapiens gene for acetyl receptor type IIb, complete cds
3422	8684	13724	1.96	1.0E-108	AB038104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3422	8584	13722	1.09	1.0E-108	AB038104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4012	9145	14285	7.75	1.0E-108	AV974650.1	EST_HUMAN	EST388875 IMAGE sequences, MAGN Homo sapiens cDNA
4012	9145	14288	7.75	1.0E-108	AV974650.1	EST_HUMAN	EST388876 IMAGE sequences, MAGN Homo sapiens cDNA
4031	9182	14304	1.28	1.0E-108	6729729	NT	Homo sapiens API5-like 1 (AP5L1), mRNA
4471	9590	14750	1.29	1.0E-108	AA825262.1	EST_HUMAN	ef7287.1t Scores NIHmPy_S1 Homo sapiens cDNA clone IMAGE:1047588 5'
4574	8892	14826	1.05	1.0E-108	BE144286.1	EST_HUMAN	NFR-HHT105-140200-008-d10 HT0168 Homo sapiens cDNA
233	6427		3.11	1.0E-107	AJ217356.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
282	6462		1.89	1.0E-107	X60459.1	NT	Human FNAR gene for interferon alphasbeta receptor
619	5779		4.12	1.0E-107	4828863	NT	Homo sapiens neuronal cell adhesion molecule (NCAM) mRNA
620	8789	10922	2.1	1.0E-107	AF165103.1	NT	Homo sapiens NY-REN-2B antigen mRNA, partial cds
814	6957	11128	2	1.0E-107	X60459.1	NT	Human FNAR gene for interferon alphasbeta receptor
887	6037	11268	2.88	1.0E-107	X60459.1	NT	Human FNAR gene for interferon alphasbeta receptor
970	6117	11288	10.71	1.0E-107	AF164121.1	NT	Homo sapiens sodium-dependent high-affinity diethyldithiocarbamate transporter (NaDC3) mRNA, complete cds
1282	6411	11597	2.27	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1683	6712	11803	3.68	1.0E-107	BF037405.1	EST_HUMAN	QV24-1T0540-120900-358-a05 HT0540 Homo sapiens cDNA
1784	6850	12058	2.27	1.0E-107	AF136276.1	NT	Homo sapiens cathepsin Z precursor (CTS2) gene, exon 3
1883	6974	12155	2.84	1.0E-107	AB001922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1883	6974	12168	2.84	1.0E-107	AB001922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2342	7449	12703	2.18	1.0E-107	AW842451.1	EST_HUMAN	PNM1-CN0031-180100-001-d03 CN0031 Homo sapiens cDNA
2342	7449	12704	2.18	1.0E-107	AW842451.1	EST_HUMAN	PNM1-CN0031-180100-001-d03 CN0031 Homo sapiens cDNA
2506	7609	12860	1.51	1.0E-107	BE732460.1	EST_HUMAN	601567616F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2506	7609	12861	1.51	1.0E-107	BE732460.1	EST_HUMAN	601567616F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2979	8133	13285	4.88	1.0E-107	AW842451.1	EST_HUMAN	PNM1-CN0031-180100-001-d03 CN0031 Homo sapiens cDNA
2979	8133	13286	4.88	1.0E-107	AW842451.1	EST_HUMAN	PNM1-CN0031-180100-001-d03 CN0031 Homo sapiens cDNA
3074	8227	13378	3.48	1.0E-107	5902097	NT	Homo sapiens SM173 (suppressor of nif1 two 3, yeast) homolog 2 (SM173-2), mRNA
3805	8942	14090	4.44	1.0E-107	AF020871.1	NT	Homo sapiens myobularin (MTM1) gene, exon 9
866	9104	11273	2.61	1.0E-108	BE286042.1	EST_HUMAN	601177016F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
1289	6398	11671	6.07	1.0E-108	Y16900.1	NT	Homo sapiens NF2 gene
2070	7186	12427	2.92	1.0E-108	BF028728.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3584839 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit No.	Top Hit Accession	Top Hit Database Source	Top Hit Descriptor
2311	7420	12870	1.13	1.0E-108	A1688040.1	EST_HUMAN		W91610_X1_NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
2311	7420	12871	1.13	1.0E-108	A1688040.1	EST_HUMAN		W91610_X1_NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
2405	7511	12781	65.48	1.0E-108	BE206894.1	EST_HUMAN		b62510_X1_NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863689 3' similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN); gb:J06277 Mouse hexokinase mRNA, complete cds (MOUSE);
2929	8083	13259	1.27	1.0E-108	60016978	NT		Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3331	8477	13840	0.63	1.0E-108	Af032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	
3331	8477	13841	0.63	1.0E-108	Af032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	
4129	9257	14295	1.35	1.0E-108	AW664438.1	EST_HUMAN		W12a11_X1_NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:28172060 3' similar to SW5BP1_MOUSE P56194 SH3-BINDING PROTEIN 3B_P-1.;
4500	9819	14760	5.12	1.0E-108	U72861.1	NT		Human hepatocyte nuclear factor 4-alpha gene, exon 2
4500	9819	14761	5.12	1.0E-108	U72861.1	NT		Human hepatocyte nuclear factor 4-alpha gene, exon 2
4772	9885	16031	2.17	1.0E-108	.76811879	NT		Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4897	10008	15153	1.08	1.0E-108	AV504789.1	EST_HUMAN		U1-HFBNO-align-04-0J11 NIH_MGC_30 Homo sapiens cDNA clone IMAGE:30380168 5'
4927	10037	16117	2.75	1.0E-108	AJ058006.1	NT		Homo sapiens PSN1 gene, alternative transcript
5118	10217	15352	0.67	1.0E-108	503-6824	NT		Home sapiens CCAT1-box-binding transcription factor (CBF2) mRNA
6141	10241	15377	1.15	1.0E-108	Y12490.1	NT		Homo sapiens mRNA for Cdc42-associated microtubule-binding protein (GMAP-210)
6149	10249	15388	1.48	1.0E-108	8400716	NT		Homo sapiens nebulin (NEB), mRNA
6204	10301		3.36	1.0E-108	AL169209.2	NT		Homo sapiens chromosome 21 segment HS221C019
41	6252	10370	2.06	1.0E-108	AW603116.1	EST_HUMAN		II.2_JJ10077-280-40-078-D06 UM077 Homo sapiens cDNA
84	5274	10409	3.96	1.0E-108	D86974.1	NT		Human mRNA for KIAA02220 gene, partial cds
216	5410	10550	0.72	1.0E-109	11422486	NT		Homo sapiens hypothetical protein FLJ111316 (FLJ111316), mRNA
225	8418	10555	4.64	1.0E-109	11438391	NT		Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCM1), mRNA
466	6834	10772	4.05	1.0E-109	4507712	NT		Homo sapiens tetrahydroopeptide repeat domain 2 (THC2) mRNA
598	6758	10888	26.83	1.0E-109	AB023216.1	NT		Homo sapiens mRNA for KIAA0598 protein, partial cds
698	6758	10987	28.83	1.0E-109	AB023216.1	NT		Homo sapiens mRNA for KIAA0598 protein, partial cds
1013	6168	11322	0.61	1.0E-109	AL1682249.2	NT		Homo sapiens chromosome 21 segment HS21C049
1206	6339	11508	37.97	1.0E-109	M2889.1	NT		Homo sapiens nucleolar phosphoprotein B23 (NP1), mRNA, complete cds
1206	6339	11508	20.28	1.0E-109	M2889.1	NT		Homo sapiens nucleolar phosphoprotein B23 (NP1), mRNA, complete cds
1656	6885	11872	2.97	1.0E-109	BE283973.1	EST_HUMAN		601188922F2 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2858636 5'
1656	6885	11873	2.97	1.0E-109	BE283973.1	EST_HUMAN		601188922F2 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2858636 5'
1884	7004	12223	9.05	1.0E-109	D13843.2	NT		Homo sapiens mRNA for KIAA0018 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
2228	7335	12589	1.78	1.0E-109	AL163284.2	NT	Human sapiens chromosome 21 segment HS2TC0684	
2231	7343	12597	3.7	1.0E-109	Y17123.1	NT	Human sapiens SNF5/INI1 gene, exon 6	
2587	7898	12943	4.69	1.0E-109	A1022328.1	EST_HUMAN	098501_X1 Scores: fetal_liver_spleen_1NF1S_S1 Human sapiens cDNA clone IMAGE:1684658 3' similar to TR002197 On2197 CIRCULATING CATHODIC ANTIGEN ;	
2587	7898	12944	4.89	1.0E-109	A1022328.1	EST_HUMAN	098501_X1 Scores: fetal_liver_spleen_1NF1S_S1 Human sapiens cDNA clone IMAGE:1684658 3' similar to TR002197 On2197 CIRCULATING CATHODIC ANTIGEN ;	
2588	7899	12945	1.95	1.0E-109	4604208	NT	Human sapiens guanylate cyclase activator TA (retina) (GUCA1A) mRNA	
3030	8184	138339	2.43	1.0E-109	N85190.1	EST_HUMAN	I2B16f Human fetal heart Lambda ZAP Express Human sapiens cDNA clone J2818 5' similar to ZINC FINGER PROTEIN ZNF43	
3369	8514	136891	1.01	1.0E-109	AW689192.1	EST_HUMAN	CMB-NN0068-160400-150-410 NN0068 Human sapiens cDNA	
3369	8514	136892	1.01	1.0E-109	AW689192.1	EST_HUMAN	CMB-NN0069-160400-150-410 NN0069 Human sapiens cDNA	
3503	8644	138110	1.13	1.0E-109	AF240598.1	NT	Human sapiens retinol dehydrogenase, homolog isoform-1 (RDH) mRNA, complete cds	
3545	8888	138448	0.88	1.0E-109	M31928.1	NT	Human sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10	
3545	8888	138449	0.88	1.0E-109	M31928.1	NT	Human sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10	
3819	8959			1.28	1.0E-109	BE148144.1	EST_HUMAN	MRO-HT0203-110400-108-504 HT0209 Human sapiens cDNA
3888	9103	142511	0.87	1.0E-109	AB011181.2	NT	Human sapiens mRNA for KIAA0809 protein, partial cds	
3988	9103	142622	0.87	1.0E-109	AB011181.2	NT	Human sapiens mRNA for KIAA0809 protein, partial cds	
4118	9248	14383	3.75	1.0E-109	A1655417.1	EST_HUMAN	ts88063_X1 NCI_CGAP_GC8 Human sapiens cDNA clone IMAGE:2239320 3' similar to WP:F53A2.8	
4383	8504	14647	2.77	1.0E-109	4504206	NT	Human sapiens guanylate cyclase activator TA (retina) (GUCA1A) mRNA	
4573	8691	14828	1.56	1.0E-109	7682983	NT	Human sapiens KIAA0777 gene product (KIAA0377), mRNA	
4904	10014	15158	0.88	1.0E-109	R15404.1	EST_HUMAN	3e48-306.11 Scores: infant brain 1NIB Human sapiens cDNA clone IMAGE:530587 5'	
6034	10138	15288	0.63	1.0E-109	BE283673.1	EST_HUMAN	601188922F2 NIH_MG3C_15 Human sapiens cDNA clone IMAGE:29159836 5'	
6034	10138	15269	0.63	1.0E-109	BE283673.1	EST_HUMAN	601188922F2 NIH_MG3C_16 Human sapiens cDNA clone IMAGE:29159836 5'	
3	6216	10327	0.76	1.0E-109	7649804	NT	Human sapiens deiodinases, iodothyronine, type II (DIO2), transcript variant 2, mRNA	
36	6247	10368	9.68	1.0E-110	5893079	NT	Human sapiens leucine zipper-like transcriptional regulator, 1 (LZTR1), mRNA	
38	6247	10368	3.68	1.0E-110	8893073	NT	Human sapiens leucine zipper-like transcriptional regulator, 1 (LZTR1), mRNA	
105	6216	10327	0.86	1.0E-110	7649804	NT	Human sapiens deiodinases, iodothyronine, type II (DIO2), transcript variant 2, mRNA	
282	5480	10822	0.76	1.0E-110	D87281.1	NT	Human mRNA for inward rectifier potassium channel, complete cds	
525	5651	10823	1.39	1.0E-110	U84550.1	NT	Human dytrotrevin (DTN) gene, exon 20	
1182	6317	11485	1.01	1.0E-110	5031620	NT	Human sapiens calcium receptor-like (CALCR) mRNA	
1283	6412	11683	2.49	1.0E-110	AB032253.1	NT	Human sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds	
1828	7045	12268	1.87	1.0E-110	BE378477.1	EST_HUMAN	601237545F1 NIH_MG3C_44 Human sapiens cDNA clone IMAGE:3609838 5'	
2050	7168		0.88	1.0E-110	BFE608886.1	EST_HUMAN	U1-H-B14-eos-b-05-0-U1-61 NCI_CGAP_Sub8 Human sapiens cDNA clone IMAGE:3085784 3'	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
2803	7959		0.88	1.0E-110	4503088 NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA		
3002	6412	11658	1.48	1.0E-110	AB032253.1	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds		
3059	9212		1.12	1.0E-110	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L-44-like ribosomal protein (L44), and F7FP3 (F7FP3) genes, complete cds	
4175	8301	14497	2.25	1.0E-110	M15918.1	NT	Human autoimmune antigen small nuclear ribonucleoprotein E pseudogene	
4803	9721	14856	231	1.0E-110	A017218.1	EST_HUMAN	cDNA clone IMAGE:1627083 3' similar to SW:N21_RAT P62851 NUCLEAR ENVELOPE/FORE MEMBRANE PROTEIN POM 121;	
4823	9744	14883	4.09	1.0E-110	AU117812	EST_HUMAN	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA102241 5' :	
4898	10086		2.28	1.0E-110	7682441 NT	Hom sapiens KIAA0022 protein (KIAA0022), mRNA		
6185	10283	15402	7.72	1.0E-110	A1781392.1	EST_HUMAN	chr4d02; y6 NCI_CQAP Kids Home sapiens cDNA clone IMAGE:1471779 5'	
170	5355		42.78	1.0E-111	U43701.1	NT	Human fibosomal protein L23a mRNA, complete cds	
193	5353	10531	0.61	1.0E-111	4758807 NT	Hom sapiens ras GTPase activating protein-like (GAP), mRNA		
733	6889		2.03	1.0E-111	BF035327.1	EST_HUMAN	601458331TF1 NIH MGIC_88 Homo sapiens cDNA clone IMAGE:38820888 5'	
742	6898	11086	3.32	1.0E-111	839092 NT	Hom sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA		
928	6076	11246	2.2	1.0E-111	M25142.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34	
3877	8816	13972	1.05	1.0E-111	6912841 NT	Hom sapiens sex comb on midleg homeobox 1 (SCMH1), mRNA		
3877	8819	13973	1.05	1.0E-111	6912841 NT	Hom sapiens sex comb on midleg homeobox 1 (SCMH1), mRNA		
4142	9270	14498	1.08	1.0E-111	7681569 NT	Hom sapiens DKFZP434D156 protein (DKFZP434D156), mRNA		
4506	9428	14563	4.63	1.0E-111	K02268.1	NT	Human enkephalin B (enkB) gene, exon 4 and 5' flanking and complete cds	
605	5765	10853	0.78	1.0E-112	4601864 NT	Hom sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA		
607	5797	10855	4.13	1.0E-112	U28103.1	NT	Human steroidogenic acute regulatory protein (StAR) gene, exon 5	
607	5797	10856	4.13	1.0E-112	U28103.1	NT	Human steroidogenic acute regulatory protein (StAR) gene, exon 5	
631	6791	10924	1.88	1.0E-112	BF509039.1	EST_HUMAN	U11-B14-ect-5'-0-1-U-61 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'	
631	6791	10925	1.88	1.0E-112	BF509039.1	EST_HUMAN	U11-B14-ect-5'-0-1-U-61 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'	
1002	8148	11816	1.22	1.0E-112	AF157623.1	NT	Hom sapiens HTRA serine protease (PRSS11) gene, complete cds	
1063	6294	11958	2.27	1.0E-112	P52142	ZINC FINGER PROTEIN 195		
1698	6826	12025	4.1	1.0E-112	7682126 NT	Hom sapiens KIAA0440 protein (KIAA0440), mRNA		
1698	6826	12026	4.1	1.0E-112	7682125 NT	Hom sapiens KIAA0440 protein (KIAA0440), mRNA		
2181	7284	12541	0.88	1.0E-112	A176825.1	EST_HUMAN	W08083.XI NCI_CGAP_Kdr/2 Homo sapiens cDNA clone IMAGE:24008111 3'	
2478	7583	12823	1.87	1.0E-112	BE868838.1	EST_HUMAN	601442874F1 NIH_MSC_85 Homo sapiens cDNA clone IMAGE:3946858 5'	
3050	8204		0.78	1.0E-112	4504118 NT	Hom sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA		
3381	8397	14184	0.88	1.0E-112	BE076073.1	EST_HUMAN	MR2-BT0390-05C300-113-09 BT0390 Homo sapiens cDNA	
4577	8689	14832	0.9	1.0E-112	4504118 NT	Hom sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA		
4717	8832	14975	5.79	1.0E-112	AB037832.1	NT	Hom sapiens mRNA for KIAA1411 protein, partial cds	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4717	8832	14976	8.78	1.0E-112	AB037832.1	NT	Human sepians mRNA for KIAA_1411 protein, partial cds
741	6897	11049	7.88	1.0E-113	AI365588.1	EST_HUMAN	ac850101_x1 Schiller meningioma Homo sepians cDNA clone IMAGE:1883625 3'
741	6897	11050	7.68	1.0E-113	AI365589.1	EST_HUMAN	ac850101_x1 Schiller meningioma Homo sepians cDNA clone IMAGE:1883625 3'
942	8090	11258	38.88	1.0E-113	M11985.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1555	6884	11871	3.48	1.0E-113	AI365588.1	EST_HUMAN	ac850101_x1 Schiller meningioma Homo sepians cDNA clone IMAGE:1883625 3'
1843	7813	12285	1.77	1.0E-113	AF240775.1	NT	Human sepians eIF4E-transporter mRNA, complete cds
2089	7202	12446	1.23	1.0E-113	BFG15218.1	EST_HUMAN	U4-H-BW1-am4-03-Q-U1 NC_CGAP_Sub7 Homo sepians cDNA clone IMAGE:3082878 3'
2431	75315	12278	4.68	1.0E-113	AJ005976.1	NT	Human sepians PIP gene
3107	8280	13414	3.18	1.0E-113	AJ223848.1	NT	Human sepians mRNA for putative RNA helicase, 3' end
6049	10151	15281	0.6	1.0E-113	5453562	NT	Human sepians activating transcription factor B (B-ATF), mRNA
6049	10151	15282	0.6	1.0E-113	5453562	NT	Human sepians activating transcription factor B (B-ATF), mRNA
57	52638	10397	3.85	1.0E-114	Y17151.2	NT	Human sepians mRNA for multidrug resistance protein 3 (ABCC3)
57	52638	10398	3.85	1.0E-114	Y17151.2	NT	Human sepians mRNA for multidrug resistance protein 3 (ABCC3)
57	52638	10399	3.86	1.0E-114	Y17151.2	NT	Human sepians mRNA for multidrug resistance protein 3 (ABCC3)
844	68015	10840	5.72	1.0E-114	T70831.1	EST_HUMAN	YD15c01 s1 Soares fetal liver spleen INFLS Homo sepians cDNA clone IMAGE:108288 3' similar to gb:AC1187 ALPH4-2-MACROGLLOBULIN PRECURSOR (HUMAN) contains Abu repetitive element
1072	6212	11376	4.74	1.0E-114	8923087	NT	Human sepians hypothetical protein FLJ20080 (FLJ20080), mRNA
1317	8446	11625	7.17	1.0E-114	78571628	NT	Human sepians ribosomal tumor deletion region protein 1 (RTDR1), mRNA
1654	67812	11675	3.61	1.0E-114	8631094	NT	Human sepians mitochondrial maintenance defective (S. cerevisiae) 3 (Mch3), mRNA
1688	68116	12013	10.86	1.0E-114	8671973	NT	Human sepians nucleophosin-like protein 1 (NLP-1), mRNA
2074	71190	12433	3.62	1.0E-114	BE171984.1	EST_HUMAN	MRO-H1453-230200-002-007 H1055 Homo sepians cDNA
2236	7348	126033	1.19	1.0E-114	AB002374.1	NT	Human mRNA for KIAA0578 gene, partial cds
2765	62854	10373	1.13	1.0E-114	AB033102.1	NT	Human sepians mRNA for KIAA1276 protein, partial cds
2766	62854	10374	1.13	1.0E-114	AB033102.1	NT	Human sepians mRNA for KIAA1276 protein, partial cds
3108	8291	13415	2.8	1.0E-114	X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3161	83012	13482	1.01	1.0E-114	BF205374.1	EST_HUMAN	601889821 NIH MGSC_19 Homo sepians cDNA clone IMAGE:4100214 5'
3891	8125	14270	1.35	1.0E-114	AF149773.1	NT	Human sepians NOD1 protein (NOD1) gene, exons 1, 2, and 3
4192	8318	14451	1	1.0E-114	AA574056.1	EST_HUMAN	nk1102.21 NC_CGAP_Co2 Homo sepians cDNA clone IMAGE:1013187 3' similar to gb:X68857_cde1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
4369	8480	14834	0.78	1.0E-114	JR3171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Ret) mRNA, complete cds
5118	10219	16353	1.43	1.0E-114	BE275324.1	EST_HUMAN	601122173F1 NIH MGSC_19 Homo sepians cDNA clone IMAGE:3440988 5'
22	5233	10347	10.03	1.0E-116	4758111	NT	Human sepians HLA-B associated transcript-1 (D6S51E) mRNA
125	5323	10468	4.96	1.0E-115	4505838	NT	Human sepians polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
128	6327		52.4	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
280	5478	10819	9.75	1.0E-115	AW604768.1	EST_HUMAN	QV4-LM0054-300300-168-508 UMM094 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:000538 000539
534	67000	10832	1.52	1.0E-116	AI339206.1	EST_HUMAN	TTF-I INTERACTING PEPTIDE 6; Q01610_1_XI_NCI_CGAP_GCA_Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:000538 000539
534	57000	10833	1.52	1.0E-115	AI339206.1	EST_HUMAN	TTF-I INTERACTING PEPTIDE 5; Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
787	6941	11100	1.26	1.0E-116	6174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
787	6941	11101	1.26	1.0E-115	6174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
789	6943	11103	186.08	1.0E-116	4503784	NT	Homo sapiens ferritin heavy polypeptide 1 (FTH1) mRNA
1574	8702	11690	1.49	1.0E-115	AF228180.1	NT	Homo sapiens alpha-aminoacidopeptidase synthase mRNA, complete cds
1574	8702	11691	1.49	1.0E-116	AF228180.1	NT	Homo sapiens alpha-aminoacidopeptidase synthase mRNA, complete cds
1840	6981	12184	1.89	1.0E-115	AJ277832.1	NT	Homo sapiens partial TTN gene for fibrin
2072	71883	12420	1.22	1.0E-116	BE745469.1	EST_HUMAN	Q015789387-1 NIH MGCC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2072	71883	12420	1.22	1.0E-116	BE745469.1	EST_HUMAN	Q015789387-1 NIH MGCC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2276	73885	12534	1.35	1.0E-115	AF231124.1	NT	Homo sapiens testican-1 mRNA, complete cds
2813	7889		1.84	1.0E-115	AV804759.1	EST_HUMAN	QV4-LM0054-300300-158-508 UMM094 Homo sapiens cDNA
30891	8244	13394	3.74	1.0E-116	AJ248922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 genes)
30891	8244	13395	3.74	1.0E-116	AJ248922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 genes)
3454	8596	13760	2.04	1.0E-116	AJ277832.1	NT	Homo sapiens partial TTN gene for fibrin
4016	9149	14291	4.51	1.0E-116	AB002348.2	NT	Homo sapiens mRNA for KIAAC550 protein, partial cds
4240	9305	14498	0.73	1.0E-116	AL197163.1	NT	Novel human gene mapping to chromosome X
4380	9501	14844	3.37	1.0E-116	69152659	NT	Homo sapiens sirt2-like 3 (SIRT3), mRNA
4413	9533	14872	3.17	1.0E-116	4758279	NT	Homo sapiens EphB4 (EPHB4) mRNA
4847	9766	14869	3.98	1.0E-116	AL0888857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BA/T2 genes
4847	9766	14910	3.36	1.0E-116	AL0888857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BA/T2 genes
4878	9890	15138	2.95	1.0E-116	AL163268.2	NT	Homo sapiens chromosome 21 segment 1S21C068
4878	9890	15137	2.85	1.0E-116	AL163268.2	NT	Homo sapiens chromosome 21 segment 1S21C068
5711	5735	10883	1.37	1.0E-116	BE275502.1	EST_HUMAN	Q011213477-1 NIH MGCC_20 Homo sapiens cDNA clone IMAGE:2888875 5'
6011	5855	11115	1.24	1.0E-116	4507334	NT	Homo sapiens synaptobatin 1 (SYN1), mRNA
850	6011		0.63	1.0E-116	4507334	NT	Homo sapiens synaptobatin 1 (SYN1), mRNA
1898	7116	12380	1.69	1.0E-116	5174478	NT	Homo sapiens peripherin (PCNT) mRNA
1898	7116	12351	1.69	1.0E-116	5174478	NT	Homo sapiens peripherin (PCNT) mRNA
2018	7138	12376	2.34	1.0E-116	AU133080 NT2R4 Homo sapiens cDNA clone NT2R4-001228 5'	EST_HUMAN	AU133080 NT2R4 Homo sapiens cDNA clone NT2R4-001228 5'
2088	7832	12447	1.18	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2058	7932	12449	1.19	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2284	7393	12844	1.09	1.0E-116	5453941	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2322	7430		1.27	1.0E-116	U78308.1	NT	Human olfactory receptor drift-7-201-1 (OR17-201-1) gene, olfactory receptor drift17-32 (OR17-32) gene and olfactory receptor pseudo drift17-01 (OR17-01) pseudogene, partial cds
2453	7537	12769	2.13	1.0E-116	AB016833.1	NT	Homo sapiens mRNA for KIAA07850 protein, partial cds
2698	7880	13043	4.58	1.0E-116	BE889258.1	EST HUMAN	601513337F1 NIH_ MGIC_71 Homo sapiens cDNA clone IMAGE3914600_6'
3154	8305	13484	6.48	1.0E-116	L77670.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3154	8305	13485	5.46	1.0E-116	L77510.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4357	9479	14817	2.21	1.0E-116	6031654	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4453	9572	14711	1.62	1.0E-116	AB028898.1	NT	Homo sapiens DNA, DLECT1 to ORC1L4 gene region, section 1/2 (DLECT1, ORC1L3, ORC1L4 genes, partial cds)
4826	9837	15078	1.69	1.0E-116	AB070686.1	EST HUMAN	PM-BT35-070469-016 BT135 Homo sapiens cDNA
5033	10135	15286	1.19	1.0E-116	U58108.1	NT	Mus musculus nebulin mRNA, partial cds
5033	10135	15267	1.19	1.0E-116	U58109.1	NT	Mus musculus nebulin mRNA, partial cds
557	5722	10853	9.68	1.0E-117	4828838	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1078	7909	11384	2.2	1.0E-117	AF124398.1	NT	Mus musculus fragile-X-related protein 1 (FXR1) gene, exons 13e through 15
1228	6360	11630	1.2	1.0E-117	AF284780.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1845	6968	12187	1.38	1.0E-117	M18818.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
2160	7305	12595	3.46	1.0E-117	AW897699.1	EST HUMAN	EST369769 MAGE-sequences, MAGE_Homo sapiens cDNA
3251	8401	13563	1.69	1.0E-117	AA978114.1	EST HUMAN	op32c-11.51 Scares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE1878548_3'
3665	9100	14249	5.62	1.0E-117	AA316723.1	EST HUMAN	EST1188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 6' end similar to ribosomal protein L28
4321	9443	14576	1.73	1.0E-117	8858584	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4550	9868	14810	3.06	1.0E-117	AL042120.1	EST HUMAN	DKFZp34C1120_f1_434 (synonym: Hts3) Homo sapiens cDNA clone DKFZp34C1120_f1
4692	9808	14954	1.03	1.0E-117	X89570.1	NT	H. sapiens mRNA for TPCR18 protein
4692	9808	14955	1.03	1.0E-117	X89570.1	NT	H. sapiens mRNA for TPCR18 protein
4778	9891	15037	10.23	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4778	9891	15038	10.23	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4839	8951	16086	1.5	1.0E-117	U88109.1	NT	Mus musculus nebulin mRNA, partial cds
4839	8951	15080	1.5	1.0E-117	U88109.1	NT	Mus musculus nebulin mRNA, partial cds
4917	10027	15169	3.3	1.0E-117	AB020873.1	NT	Homo sapiens mRNA for KIAA0886 protein, complete cds
69	5279	10416	7.76	1.0E-118	AF161500.1	NT	Homo sapiens HSPC151 mRNA, complete cds
91	6300	10439	1.53	1.0E-118	AL048854.1	EST HUMAN	DKFZp34C1056_f1_434 (synonym: Hts3) Homo sapiens cDNA clone DKFZp34C1056_f1
515	5681	10815	11.4	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (Q3288E) (C1;1), mRNA

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Probe seq ID NO:	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar (T <sub>Cop</sub> ) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
915 7004	11231		2.6	1.0E-113	5174880	NT	Human sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA	
2214 7226	12676		3.87	1.0E-113	BE389705.1	EST HUMAN	601281947F1 NIH_1MG_C_44 Homo sapiens cDNA clone IMAGE:3604019 5'	
2214 7326	12677		3.87	1.0E-113	BE389705.1	EST HUMAN	601281947F1 NIH_1MG_C_44 Homo sapiens cDNA clone IMAGE:3604019 5'	
2214 7326	12678		3.87	1.0E-113	BE389705.1	EST HUMAN	601281947F1 NIH_1MG_C_44 Homo sapiens cDNA clone IMAGE:3604019 5'	
2310 7419				18.78	1.0E-113	AW851728.1	EST HUMAN	EST368789 IMAGE sequences: MAGEB Homo sapiens cDNA
2703 7789	13050		6.32	1.0E-113	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds	
2703 7799	13051		6.32	1.0E-113	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds	
3080 8293			4.24	1.0E-113	Y13892.1	NT	Human sapiens PRKY exon 7	
3178 8328	13492		4.93	1.0E-116	A1347684.1	EST HUMAN	sp01105_x1 NCI CGAP Kids Homo sapiens cDNA clone IMAGE:1916769 3'	
3178 8328	13493		4.93	1.0E-113	A1347684.1	EST HUMAN	sp01105_x1 NCI CGAP Kids Homo sapiens cDNA clone IMAGE:1916769 3'	
3921 8057	14216		0.98	1.0E-113	AB024469.1	NT	Pongo pygmaeus DNA, similar to gene of HEV-N and MSRV, Isolate:CRW3-3	
4065 9195	14234		8.96	1.0E-113	D22660.1	NT	Human mRNA for ribosomal protein, complete cds	
4675 9791	14837		1.17	1.0E-113	11426783	NT	Human sapiens KIAA0748 gene product (KIAA0748) mRNA	
769 8891	11068		0.63	1.0E-119	AF170492.1	NT	Human sapiens chloride channel CLC4 (CLC4) mRNA, complete cds	
1039 7807	11344		1.69	1.0E-119	7705807	NT	Human sapiens CQL105 protein (LC05101) mRNA	
1837 7056	12277		3.67	1.0E-119	AB023147.1	NT	Human sapiens mRNA for KIAA0530 protein, partial cds	
3077 8230	13382		0.84	1.0E-119	8922205	NT	Human sapiens hypothetical protein FLJ10052; mRNA	
3825 8891	14219		1.07	1.0E-119	4504118	NT	Human sapiens endotopic, latendope, kalinus 1 (GRIK1) mRNA	
289 5487	10628		0.77	1.0E-120	4507334	NT	Human sapiens synaptobatin 1 (SYNU1) mRNA	
1043 6184	11350		2.38	1.0E-120	AF248540.1	NT	Human sapiens Intersectin 2 (SH3D1B) mRNA, complete cds	
1043 6184	11351		2.38	1.0E-120	AF248540.1	NT	Human sapiens Intersectin 2 (SH3D1B) mRNA, complete cds	
1434 8891	11744		6.03	1.0E-120	IN44873.1	EST HUMAN	YH01211 Soares metastacytis 2 Human Homo sapiens cDNA clone IMAGE:273768 5'	
1616 6743	11838		2.55	1.0E-120	AF167706.1	NT	Human sapiens cysteine-rich repeat-containing protein SB2 precursor, mRNA, complete cds	
1818 6841	12159		4.32	1.0E-120	4557280	NT	Human sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA	
2088 7213	12460		2.02	1.0E-120	AB011389.1	NT	Human sapiens gene for AF-6, complete cds	
2088 7213	12461		2.02	1.0E-120	AB011389.1	NT	Human sapiens gene for AF-6, complete cds	
2500 7804	12852		1.23	1.0E-120	4755124	NT	Human sapiens equinopoth 4 (AQP4), splice variant b, mRNA	
3289 5487	10828		1.13	1.0E-120	4507334	NT	Human sapiens synaptobatin 1 (SYNU1) mRNA	
4335 8457	14894		1.71	1.0E-120	AF056490.1	NT	Human sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds	
4335 8457	14895		1.71	1.0E-120	AF056490.1	NT	Human sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds	
4632 9750	14896		1.79	1.0E-120	AF098463.1	NT	Human sapiens stemlocatch (STC) gene, partial cds	
4632 9750	14897		1.79	1.0E-120	AF098463.1	NT	Human sapiens stemlocatch (STC) gene, partial cds	
72 5281	10419		0.87	1.0E-121	Y18000.1	NT	Human sapiens NF2 gene	
378 6554	10658		2.09	1.0E-121	AU134983.1	EST HUMAN	AU134983 PLACE1: Human sapiens cDNA clone PLACE1000889 5'	

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 Table 4  
 Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
722	7888	11026	1.11	1.0E-121	50321922 NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA	
1587	8718	11908	0.98	1.0E-121	AB011163.1	Homo sapiens mRNA for KIAA0581 protein, partial cds	
1669	7088	12312	1.31	1.0E-121	4755139 NT	Homo sapiens Insitol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant 8, mRNA	
1889	7088	12313	1.31	1.0E-121	4755139 NT	Homo sapiens Insitol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant 8, mRNA	
2083	7208	12464	1.15	1.0E-121	L76831.1	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds	
2540	7843	12892	1.37	1.0E-121	BF344378.1	EST_HUMAN	602014769F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4150286 5'
2540	7843	12893	1.37	1.0E-121	BF344378.1	EST_HUMAN	602014769F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4150286 5'
2838	8092	13259	1.11	1.0E-121	AF111682	EST_HUMAN	Homo sapiens Selenite palmitoyl transferase, subunit II gene, complete cds; and unknown genes
3053	8206	13364	5.8	1.0E-121	Y18208.1	NT	Homo sapiens HhB3 gene for hair keratin, exons 1 to 9
3053	8206	13362	6.9	1.0E-121	Y18208.1	NT	Homo sapiens HhB3 gene for hair keratin, exons 1 to 9
3624	8965	13832	1	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3624	8865	13833	1	1.0E-121	AB037768.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
9655	9794	13950	7.87	1.0E-121	AF165166.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
9704	8842	13897	0.7	1.0E-121	AB041651.1	EST_HUMAN	CMBT043-050208-075 BT043 Homo sapiens cDNA clone IMAGE:20105417 3'
4307	9429	14584	1.48	1.0E-121	AI263284.1	EST_HUMAN	Q55760 X1 NC1 CGAP_Pant Homo sapiens cDNA clone IMAGE:20105417
4861	10046	15205	2.74	1.0E-121	X91887.1	NT	H.sapiens ECE-1 gene (exon 17)
265	5455	10593	1.76	1.0E-122	11526176 NT	EST_HUMAN	Homo sapiens T-cell lymphoma invasion and metastasis 1 (Tiam1) mRNA, complete cds
334	5517	10653	2.2	1.0E-122	AF4114488.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (Tiam1) mRNA
366	6536	10877	1.88	1.0E-122	11526176 NT	EST_HUMAN	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
883	6933	11205	3.01	1.0E-122	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
1222	6354	11524	5.81	1.0E-122	M20707.1	NT	Human kappa-immunglobulin gamma-like pseudogene (Chr22:4) variable region (subgroup V kappa II)
1727	6834	12059	2.28	1.0E-122	11418424 NT	Human sapiens collagen, type XII, alpha 1 (COL12A1) mRNA	
1828	6949	12171	3.48	1.0E-122	BE806224.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898358 5'
2404	7588	12521	22.83	1.0E-122	BF316170.1	EST_HUMAN	6018863175F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126234 5'
2484	7588	12622	22.83	1.0E-122	BF316170.1	EST_HUMAN	6018863175F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126234 5'
2601	7858	13122	2.08	1.0E-122	AF204717.1	NT	Homo sapiens FYN domain-containing dual specificity protein phosphatase FYN-DSF2 mRNA, complete cds
4815	8827	15068	2.79	1.0E-122	4502168 NT	EST_HUMAN	Homo sapiens amyloid beta (A4) precursor protein (precursor neprilin), Alzheimer disease (APP), mRNA
4975	10085		1.84	1.0E-122	AW504845.1	EST_HUMAN	UJ-HFBN0-ell-e03-0-UJ1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3078848 5'

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 Table 4  
 Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
185	5380	10521	0.84	1.0E-123	U31519.1	NT	Human phosphoenolpyruvate carboxykinase (PCK1) gene, promoter region and partial cds
768	69222	11078	2.81	1.0E-123	BF345224.1	EST HUMAN	6202108058F1 NCI CGAP Brn67 Homo sapiens cDNA clone IMAGE:4163870 5'
768	69222	110590	2.61	1.0E-123	BF345224.1	EST HUMAN	6202108058F1 NCI CGAP Brn67 Homo sapiens cDNA clone IMAGE:4163870 5'
1014	61057	11923	4.65	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C04.9
1023	61064	11330	5.61	1.0E-123	5803114.1	NT	Homo sapiens inner membrane protein, mitochondrial (mitofillin) (MIFT), mRNA
1242	6372	11547	11.95	1.0E-123	4608818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B), mRNA, and translated products
1242	6372	11548	11.85	1.0E-123	4608818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B), mRNA, and translated products
2080	7205	12480	2.04	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2080	7205	12481	2.04	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2080	7205	12482	2.04	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2263	7402		1.8	1.0E-123	7705982	NT	Homo sapiens RAB9-like protein (LC0551209), mRNA
268	5466	10594	1.6	1.0E-124	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
269	5468	10595	1.6	1.0E-124	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
272	8482		1.67	1.0E-124	D87676.1	NT	Homo sapiens DNA for env/odd precursor protein, complete cds
485	5883	10782	2.1	1.0E-124	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C04.6
689	6848	10988	3.14	1.0E-124	AA397551.1	EST HUMAN	281104.11 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728710 5' similar to TR:G300482
689	5846	10989	3.14	1.0E-124	AA397551.1	EST HUMAN	281104.11 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728710 5' similar to TR:G300482
757	6912	11070	8.92	1.0E-124	AF165854.1	NT	Human putative ribosomal protein S1, mRNA
809	6982	11124	1.68	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
805	60355	11224	3.62	1.0E-124	77059448	NT	Homo sapiens hypothetical protein (HSPOC058), mRNA
1319	6448	11628	0.74	1.0E-124	11418092	NT	Homo sapiens ring finger protein (RNF), mRNA
1353	8492	11691	4.17	1.0E-124	AF214682.1	NT	Homo sapiens transporter 3 gene, exons 8-10, and complete cds
1353	8492	11692	4.17	1.0E-124	AF214682.1	NT	Homo sapiens glucose transporter 3 gene, exons 8-10, and complete cds
1827	6890	12172	3.71	1.0E-124	AJ317172.1	NT	Homo sapiens mRNA for nucleolar RNA-helicase (n6-1 genes)
2054	7170	12409	1.39	1.0E-124	BE870624.1	EST HUMAN	60149715F1 NIH MGC 89 Homo sapiens cDNA clone IMAGE:38363954 5'
2484	7558	12781	1.68	1.0E-124	AB024089.1	NT	Homo sapiens gene for B120, exon 11
3471	8613	13779	0.84	1.0E-124	S76884.1	NT	Homo sapiens ATP-sensitive inward rectifying K-channel subunit (KCNE1/BIR1) gene, exon
3471	8613	13780	0.84	1.0E-124	S76884.1	NT	Homo sapiens ATP-sensitive inward rectifying K-channel subunit (KCNE1/BIR1) gene, exon
3878	9012	14169	0.8	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
4051	9132	14324	0.73	1.0E-124	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4710	88283	149869	1.71	1.0E-124	A5024069.1	NT	Homo sapiens gene for B120, exon 11	
317	6903		11.1	1.0E-125	A5032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds	
425	6212	10324	3.94	1.0E-125	B574922.1	EST_HUMAN	60157780 F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3826885 5'	
643	6804	10838	0.84	1.0E-125	AI1106868.1	EST_HUMAN	HA008 Human fetal liver cDNA library Homo sapiens cDNA	
643	6804	10939	0.84	1.0E-125	AI1106866.1	EST_HUMAN	HA008 Human fetal liver cDNA library Homo sapiens cDNA	
726	5882	11030	1.81	1.0E-125	A5284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds	
861	6012	11183	3.17	1.0E-125	AA042813.1	EST_HUMAN	263607.51 Scores _pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486640 3' similar to gb:X65557_cds1_Olfactory receptor-like protein HGPNOTE (HUMAN);	
869	61465	11312	1.61	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010	
1155	6281	11454	-1.2	1.0E-125	7662278	NT	Homo sapiens KIAA0744 gene product histone deacetylase 7 (KIAA0744), mRNA	
1823	6946	12167	3.61	1.0E-125	AF015450.1	NT	Homo sapiens Urspringerpha mRNA, complete cds	
1823	6946	12168	3.61	1.0E-125	AF016450.1	NT	Homo sapiens Urspringerpha mRNA, complete cds	
2338	7445	12697	2.88	1.0E-125	AA011278.1	EST_HUMAN	263607.51 Scores _fetal liver spleen INFSL_S1 Homo sapiens cDNA clone IMAGE:428568 5'	
2474	7678	12830	2.08	1.0E-125	AA042813.1	EST_HUMAN	263607.51 Scores _pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486640 3' similar to gb:X65557_cds1_Olfactory receptor-like protein HGPNOTE (HUMAN);	
2559	7681	12814	1.68	1.0E-125	4504698	NT	Homo sapiens fibrin, alpha (INHA) mRNA	
2559	7681	12816	1.86	1.0E-125	4504696	NT	Homo sapiens fibrin, alpha (INHA) mRNA	
2558	7684	12818	11.32	1.0E-125	AI732565.1	EST_HUMAN	ch84402.56 NCI_CQAP_Kid5 Homo sapiens cDNA clone IMAGE:1477779 3'	
2681	10303	13289	1	1.0E-125	BED18009.1	EST_HUMAN	bb74fb8y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3043131 5' similar to TR:QB86804 QB86804	ZINC FINGER PROTEIN ;
3887	8973	14129	1.42	1.0E-125	AA042813.1	EST_HUMAN	263607.51 Scores _pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486640 3' similar to gb:X65557_cds1_Olfactory receptor-like protein HGPNOTE (HUMAN);	
4523	8841	14788	1.84	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA	
4623	8841	14789	1.94	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA	
4588	9706	14844	1.98	1.0E-125	BE515412.1	EST_HUMAN	6011411622 F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140788 5'	
774	6928	11087	2.04	1.0E-125	4758037	NT	Homo sapiens CDC-like kinase (CLK) mRNA	
777	6881	11080	1.04	1.0E-126	M618386.1	NT	Human laminin B1 chain gene, exon 20	
918	6068	11233	0.97	1.0E-126	688735.1	NT	H.sapiens gene for aliphatic-antithrombinoplatin, exon 3	
2325	7433	12698	1.42	1.0E-126	8922958	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA	
2326	7433	12888	1.42	1.0E-126	8923058	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA	
2660	7862	12816	3.07	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA	
3044	8198	13354	7.24	1.0E-126	AA160709.1	EST_HUMAN	2072603.11 Strategene pancreas (#837208) Homo sapiens cDNA clone IMAGE:562420 5'	
3044	8198	13355	7.24	1.0E-126	AA160708.1	EST_HUMAN	2072603.11 Strategene pancreas (#837208) Homo sapiens cDNA clone IMAGE:562420 5'	
3609	8748	13894	1.24	1.0E-126	653941.1	NT	H.sapiens DNA for liver cytochrome b5 pseudogene	

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Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3632	8771	139277	2.35	1.0E-128	7697038	NT	Homo sapiens death receptor 8 (DR8), mRNA
4802	8916	150158	1.67	1.0E-128	NC_0478.1	EST_HUMAN	Homo sapiens melanocyte 21b/Homo sapiens cDNA clone IMAGE:207880 5'
187	5363	105054	9.45	1.0E-127	AB024697.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
187	5363	105054	8.45	1.0E-127	AB024697.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
168	5363	105054	7	1.0E-127	AB024697.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
188	5363	105055	7	1.0E-127	AB024697.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
271	6461	10602	1.52	1.0E-127	D37675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
271	6461	10603	1.52	1.0E-127	D37675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
882	6032	11204	1.34	1.0E-127	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
1705	6833	12034	1.58	1.0E-127	4827093	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2058	7174	12412	1.78	1.0E-127	56903085	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2058	7174	12413	1.78	1.0E-127	56903085	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2184	7297	12545	47.43	1.0E-127	45066220	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2323	7431	12883	3.12	1.0E-127	AF246505.1	NT	Homo sapiens acidic mRNA, complete cds
2573	7673	12828	49.35	1.0E-127	X1/2861.1	NT	Human mRNA for cytokeratin 18
2585	7688	12840	1	1.0E-127	AA450131.1	EST_HUMAN	2042602.1! Soares, total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789088 5'
2585	7688	12841	1	1.0E-127	AA450131.1	EST_HUMAN	2042602.1! Soares, total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789088 6'
							eu9808.1! Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR SII-RELATED PROTEIN :contains element MER22 repetitive element;
3788	8825	14076	1	1.0E-127	AW_161297.1	EST_HUMAN	
4230	8355	14487	19.81	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-embryoid protein (LOC81684), mRNA
4230	8356	14488	19.81	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-embryoid protein (LOC81684), mRNA
4473	9592	14731	0.73	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 reductase P450 reductase P450 reductase P450RA1-2 mRNA, complete cds
4579	9694	14831	4.77	1.0E-127	450584	NT	Homo sapiens RADI (S. pombe) homolog (RAD1) mRNA, and translated products
4601	9718		2.3	1.0E-127	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C058
4844	9162	14807	1.49	1.0E-127	6912839	NT	Homo sapiens Ring 1 and YY1 binding protein (RYBP), mRNA
4359	5827	10767	2.84	1.0E-128	BE385617.1	EST_HUMAN	601278127F_1 NIH_3T3 cells cDNA clone IMAGE:3618822 5'
2083	7179	12417	80.69	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, tri nucleotide repeat regions
2083	7179	12418	80.69	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, tri nucleotide repeat regions
2181	7303	12553	172.11	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2422	7627		6.08	1.0E-128	11437485	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA

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**Table 4**  
**Single Exon Probes Expressed In BT474 Cells**

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3375	8520	13684	1.11	1.0E-128	AB033073.1	NT	Human sepiens mRNA for KIAA1247 protein, partial cds's
4634	9752	14889	5.88	1.0E-128	14268073	NT	Human sepiens prospero-related homeobox 1 (PROX1), mRNA
117	6680	10730	3.07	1.0E-129	S37722.1	NT	Insulin-like growth factor binding protein-2 [Human, placenta, Genomic, 1018 nt, segment 2 of 4]
412	5580	10730	3.48	1.0E-129	S37722.1	NT	Insulin-like growth factor binding protein-2 [Human, placenta, Genomic, 1018 nt, segment 2 of 4]
7733	6680	12063	5.33	1.0E-129	AB086880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1737	6884	12067	1.66	1.0E-129	AF240788.1	NT	Human sepiens glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1737	6884	12068	1.68	1.0E-129	AF240788.1	NT	Human sepiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1857	6977	12199	3.1	1.0E-129	11418522	NT	Human sepiens zinc finger protein 78 (expressed in testis) (ZNF78), mRNA
3105	8258	13409	1.84	1.0E-129	Q14885	SWISSPROT	ZINC FINGER PROTEIN HZF10
3105	8258	13410	1.84	1.0E-129	Q14885	SWISSPROT	ZINC FINGER PROTEIN HZF10
3105	8258	13411	1.84	1.0E-129	Q14885	SWISSPROT	ZINC FINGER PROTEIN HZF10
4135	8283	14402	2.01	1.0E-129	AB040882.1	NT	Human sepiens mRNA for KIAA1459 protein, partial cds
4284	8379	14510	2.21	1.0E-129	AW75254.1	EST_HUMAN	CNAYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151936 similar to CNAYA5 Cardiomyopathy associated gene 5
4254	8379	14511	2.21	1.0E-129	AW75254.1	EST_HUMAN	CNAYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151936 similar to CNAYA5 Cardiomyopathy associated gene 5
76	6284	10423	2.24	1.0E-150	7705630	NT	Human sepiens hypothetical protein (HSP-C242), mRNA
1172	6307	11474	0.97	1.0E-150	AB0317835.1	NT	Human sepiens mRNA for KIAA1414 protein, partial cds's
1680	6809	12007	38.02	1.0E-150	BE2776192.1	EST_HUMAN	601121885F NIH_MGCC_59 Human sepiens cDNA clone IMAGE:3348368 5'
1680	6809	12008	38.02	1.0E-150	BE2776192.1	EST_HUMAN	601121885F NIH_MGCC_20 Human sepiens cDNA clone IMAGE:3348368 5'
1885	7102		2.3	1.0E-150	X040922.1	NT	Human gene for cathepsin (EC 3.4.22.6) exon 8 mapping to chromosome 11, band p13
2733	7827		3.54	1.0E-150	AJ010230.1	NT	Human sepiens RET finger protein-like 1 antisense transcript, partial
2844	7889	13167	1.29	1.0E-150	BE694219.1	EST_HUMAN	601343018F1 NIH_MGCC_53 Human sepiens cDNA clone IMAGE:3385468 5'
2844	7889	13168	1.29	1.0E-150	BE694219.1	EST_HUMAN	601343018F1 NIH_MGCC_53 Human sepiens cDNA clone IMAGE:3385468 5'
3563	8170	13967	0.8	1.0E-150	AF240698.1	NT	Human sepiens retinal dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3748	7989	13157	6.46	1.0E-150	BE694219.1	EST_HUMAN	601343018F1 NIH_MGCC_53 Human sepiens cDNA clone IMAGE:3385468 5'
3748	7989	13158	5.45	1.0E-150	BE694219.1	EST_HUMAN	601343018F1 NIH_MGCC_50 Human sepiens cDNA clone IMAGE:3385468 5'
3809	8046	14204	1.33	1.0E-150	AW5056580.1	EST_HUMAN	U14-9-Biotinyl-glycine-1-U1 NIH_MGCC_5 Human sepiens cDNA clone IMAGE:3385468 5'
4048	9178	14920	1.05	1.0E-150	MB7710.1	NT	Human T-cell receptor (V alpha 22-1, J alpha Rho4/885-varient, C alpha 1)mRNA
4511	9630	14774	6.92	1.0E-150	AW848983.1	EST_HUMAN	CNA-CN0045-180200-511-02 GNO045 Human sepiens cDNA
6082	10188	15320	1.33	1.0E-150	AW363289.1	EST_HUMAN	ROO-CT0318-201188-Q31-a11 CT0318 Human sepiens cDNA
6082	10183	15324	1.33	1.0E-150	AW363289.1	EST_HUMAN	ROO-CT0318-201188-Q31-a11 CT0318 Human sepiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4	6218	10328	1.91	0.0E+00	AA228126.1	EST_HUMAN	Zf580544_r1 Scores_NhHMPU_S1 Homo sapiens cDNA clone IMAGE:687680 6 similar to TR:G222811
4	5218	10329	1.91	0.0E+00	AA228126.1	EST_HUMAN	Zf580544_r1 Scores_NhHMPU_S1 Homo sapiens cDNA clone IMAGE:687680 6 similar to TR:G222811
7	5218	10332	3.36	0.0E+00	4885135	NT	Homo sapiens checkin suppressor 1 (CHES1), mRNA
14	6225	10337	1.38	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
14	5225	10338	1.38	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
21	62322	10345	13.75	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
21	62322	10348	13.75	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
25	62385	10350	51.42	0.0E+00	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
33	62444	10350	1.89	0.0E+00	6802867	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
35	5248	10363	0.77	0.0E+00	MR88601.1	NT	Human hepatitis cofactor II (HCf2) gene, exons 1 through 6
39	6250	10368	8.5	0.0E+00	6857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
68	6297	10395	12.92	0.0E+00	Y17161.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
98	52677	10398	12.92	0.0E+00	Y17161.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
88	52689	10400	6.88	0.0E+00	D78804.1	EST_HUMAN	HUM516108B Human placenta polyA+ (TF4jMara) Homo sapiens cDNA clone GEN:5161085'
68	5269	10401	6.88	0.0E+00	D78804.1	EST_HUMAN	HUM516108B Human placenta polyA+ (TF4jMara) Homo sapiens cDNA clone GEN:5161085'
59	6270	10402	3173	0.0E+00	L16558.1	NT	Human fibosomal protein L7 (RPL7) mRNA, complete cds
81	52722	10403	13.22	0.0E+00	AW089534.1	EST_HUMAN	cr48ed073' x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48ed073'
61	6272	10408	13.22	0.0E+00	AV069534.1	EST_HUMAN	cr48ed073' x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48ed073'
65	5275	10410	1.1	0.0E+00	M60578.1	NT	Human von Willebrand factor pseudogenes corresponding to exons 23 through 34
68	5276	10412	0.79	0.0E+00	M60578.1	NT	Human von Willebrand factor pseudogenes corresponding to exons 23 through 34
74	5283	10421	1.92	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
74	6283	10422	1.82	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
78	6287	10427	0.72	0.0E+00	4501850	NT	Homo sapiens amilioride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene
78	5288	10428	31.31	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
81	6289	10435	84.52	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
90	6289	10438	71.3	0.0E+00	U88277.1	NT	Human polyhomeotic 1 homolog (HPHT) mRNA, partial cds
97	6308	10443	4.27	0.0E+00	AI114743.1	EST_HUMAN	HA347 Human telomeric DNA library Homo sapiens cDNA
98	6307	10448	1.62	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
112	5318	10455	1.5	0.0E+00	AI623701.1	EST_HUMAN	fs88bs_x1 NCI CGAP_UM Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q89551 Q89551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR ;

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113	5318	10455	3.14	0.0E+00	AI823701.1	EST_HUMAN	ts880-x1 NCI CGAP_Ut <sub>4</sub> Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:QR88531 Q88851
114	7880	10458	4.61	0.0E+00	NS8040.1	EST_HUMAN	MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR;
114	7880	10467	4.61	0.0E+00	NS8040.1	EST_HUMAN	ya01h01 Scores melanocyte 2NbH Human sapiens cDNA clone IMAGE:2700176
129	5324	10469	5.01	0.0E+00	4505838	NT	ya01h01 Scores melanocyte 2NbH Human sapiens cDNA clone IMAGE:2700175
129	5324	10470	5.01	0.0E+00	4505838	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (22kD) (POLR2A) mRNA
134	5588	10714	1.62	0.0E+00	4503880	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (22kD) (POLR2A) mRNA
138	5332	10477	1.43	0.0E+00	T66945.1	EST_HUMAN	Homo sapiens IgG Fc binding protein (FCY GAMMA1B2) mRNA
138	5332	10478	1.43	0.0E+00	T66946.1	EST_HUMAN	ya83g04-2 Strategene fetal spleen (#897205) Human sapiens cDNA clone IMAGE:688310 5'
148	6246		24.18	0.0E+00	4504444	NT	ya83g04-2 Strategene fetal spleen (#887205) Human sapiens cDNA clone IMAGE:688310 6'
162	6249	10481	6.08	0.0E+00	BFD36881.1	EST_HUMAN	ya0146207f1 NIH_MGC_66 Human sapiens cDNA clone IMAGE:383803 5'
154	5351		83.55	0.0E+00	4504444	NT	Homo sapiens heterogeneus nuclear ribonucleoprotein A1 (HNRPA1) mRNA
157	5354	10494	0.85	0.0E+00	AF11168.2	NT	Homo sapiens serine palmitoyl transferase, subunit 1 gene, complete cds; and unknown gene
159	6253	10495	4.11	0.0E+00	BE2858973.1	EST_HUMAN	601174270f1 NIH_MGC_17 Human sapiens cDNA clone IMAGE:3528864 5'
160	6253	10495	3.81	0.0E+00	BE2858973.1	EST_HUMAN	601174270f1 NIH_MGC_17 Human sapiens cDNA clone IMAGE:3528864 5'
161	5357	10498	7.12	0.0E+00	W78973.1	EST_HUMAN	zg62b05.11 Scores fetal heart NIH-H19W Human sapiens cDNA clone IMAGE:346201 5' similar to
162	5358	10497	2.87	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-058-d04 HT0457 Human sapiens cDNA
162	5358	10498	2.87	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-058-d04 HT0457 Human sapiens cDNA
163	5359	10489	3.87	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
168	6382	10502	57.01	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
169	6382	10503	57.01	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
178	6370	10510	6.34	0.0E+00	BE018970.1	EST_HUMAN	bb24e12y1 NIH_MGC_14 Human sapiens cDNA clone IMAGE:283884 5' similar to WP:Y5TA10A.2
178	6370	10511	6.34	0.0E+00	BE018970.1	EST_HUMAN	CE22631;
181	6376	10514	7.68	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
181	6376	10516	7.68	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
182	6378	10516	6.19	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
182	6378	10517	6.19	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	6388	10529	309.01	0.0E+00	D50689.1	NT	Human gamma-cytoplasmic actin (ACTGP2) pseudogene
198	6391	10534	13.52	0.0E+00	AF273045.1	NT	Homo sapiens C10L tumor antigen seq14-3 mRNA, complete cds
198	6391	10535	13.52	0.0E+00	AF273045.1	NT	Homo sapiens C10L tumor antigen seq14-3 mRNA, complete cds
198	6393	10537	7.31	0.0E+00	AF187174.1	NT	Homo sapiens chromosome XMS13-2 protein mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Meet Similar BLAST E Value	Top Hit No.	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
188	5393	10538	7.31	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL-3-2 protein mRNA, complete cds	tq1408.X1_NCI_CGAP_U3 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN); tq0408.X1_NCI_CGAP_U3 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN);
207	7895	10544	27.02	0.0E+00	AI887308.1	EST_HUMAN	Homo sapiens ribosomal protein L3 (RPL31) mRNA	tq0408.X1_NCI_CGAP_U3 Homo sapiens ribosomal protein L3 (RPL31) gene, complete cds
209	5403	10545	27.02	0.0E+00	AI887308.1	EST_HUMAN	Homo sapiens ribosomal protein L3 (RPL31) mRNA	tq0408.X1_NCI_CGAP_U3 Homo sapiens ribosomal protein L3 (RPL31) gene, complete cds
212	6406	10547	2.69	0.0E+00	4506532	NT	Homo sapiens TADAF1 protein mRNA, complete cds	Homo sapiens TADAF1 protein mRNA, complete cds
213	6407		53.6	0.0E+00	AF132000.1	NT	Homo sapiens AB018284.1	Homo sapiens AB018284.1
216	5413	10552	4.01	0.0E+00	AB018284.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds	Homo sapiens mRNA for KIAA0721 protein, partial cds
220	6413	10552	2.98	0.0E+00	AB018284.1	NT	Mus musculus testis-specific protein, Y-encoded-like ('spp1), mRNA	Mus musculus testis-specific protein, Y-encoded-like ('spp1), mRNA
221	6414	10553	4.61	0.0E+00	6878444	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
235	8428	10558	22.84	0.0E+00	5453805	NT	Homo sapiens chromosome 21 segment HS21 C001	Homo sapiens chromosome 21 segment HS21 C001
237	5430		14.18	0.0E+00	AL183201.2	NT	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA
244	6435	10574	3.02	0.0E+00	AF231919.1	NT	Homo sapiens mRNA for Interferon alpha/beta receptor (long form)	Homo sapiens mRNA for Interferon alpha/beta receptor (long form)
248	6437	10577	1.02	0.0E+00	X89772.1	NT	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA
254	6445		6.18	0.0E+00	AF231918.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
267	6457	10596	1.46	0.0E+00	4507650	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
287	6457	10597	1.45	0.0E+00	4507500	NT	Homo sapiens hypothetical protein LOC51250, mRNA	Homo sapiens hypothetical protein LOC51250, mRNA
269	5459	10599	2.13	0.0E+00	7708928	NT	Homo sapiens DCR1 1 mRNA, partial cds	Homo sapiens DCR1 1 mRNA, partial cds
280	6458		4.7	0.0E+00	D83327.1	NT	Homo sapiens DCR1 mRNA, partial cds	Homo sapiens DCR1 mRNA, partial cds
281	5470	10612	5.27	0.0E+00	D83327.1-	NT	IL2-CT0031-187188-020-B03 CT0031-Homo sapiens cDNA	IL2-CT0031-187188-020-B03 CT0031-Homo sapiens cDNA
282	6471	10613	6.27	0.0E+00	DB3327.1	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
281	6479	10620	6.27	0.0E+00	4557028	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
281	5478	10621	5.27	0.0E+00	4557028	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens mRNA for KIAA1019 protein, partial cds
302	5480	10631	14.01	0.0E+00	AB028842.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA	Homo sapiens ribosomal protein S5 (RPS5) mRNA
303	6481	10632	7.12	0.0E+00	AB028842.1	NT	Homo sapiens phosphatidylcholine N-methyltransferase, phosphatidylcholine synthetase	Homo sapiens phosphatidylcholine N-methyltransferase, phosphatidylcholine synthetase
304	7888		24.79	0.0E+00	4506728	NT	218686.1 Scaree N1 Homo sapiens clone IMAGE:763894 6	218686.1 Scaree N1 Homo sapiens clone IMAGE:763894 6
305	6492	10633	0.93	0.0E+00	4503914	NT	Home sapiens SON DNA binding protein (SON) mRNA	Home sapiens SON DNA binding protein (SON) mRNA
306	6493		3.88	0.0E+00	AA480602.1	EST_HUMAN	Home sapiens SON DNA binding protein (SON) mRNA	Home sapiens SON DNA binding protein (SON) mRNA
307	5494	10634	17.26	0.0E+00	4507152	NT	Home sapiens intersectin short isoform (ITSN) mRNA, complete cds	Home sapiens intersectin short isoform (ITSN) mRNA, complete cds
308	5494	10634	18.94	0.0E+00	4507162	NT		
312	5498	10638	2.05	0.0E+00	AF114468.1	NT		

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325	5610	10847	1.9	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (H23833)
325	5610	10848	1.9	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (H23833)
326	6511	10848	3.18	0.0E+00	76572/3 NT	Homo sapiens harmonin upregulated new tumor-associated kinase (HUNK), mRNA	
327	5611	10848	2.21	0.0E+00	76572/3 NT	Homo sapiens harmonin upregulated new tumor-associated kinase (HUNK), mRNA	
342	5625	10881	6.87	0.0E+00	51745/4 NT	Homo sapiens myeloid lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to 4 (MLL4) mRNA	
345	6523	10988	43.24	0.0E+00	48270/57 NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA	
348	6531	10570	2.66	0.0E+00	U71600_1 NT	Human zinc finger protein zfp31 (Z31) mRNA, partial cds	
353	6535	10574	2.88	0.0E+00	AF231919_1 NT	Homo sapiens chromosome 21 unknown mRNA	
353	6535	10676	2.88	0.0E+00	AF231919_1 NT	Homo sapiens chromosome 21 unknown mRNA	
354	7889	10576	2.85	0.0E+00	AF231919_1 NT	Homo sapiens chromosome 21 unknown mRNA	
356	6537	10578	1.14	0.0E+00	45076/0 NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAN1) mRNA	
359	6540	10682	1.84	0.0E+00	45038/54 NT	Homo sapiens Gα-h-binding protein transcription factor, alpha subunit (Gα0βγ) (GABPA), mRNA	
360	6541	10683	2.71	0.0E+00	D80006_1 NT	Human mRNA for KIAA0184 gene, partial cds	
361	6541	10583	2.65	0.0E+00	D80006_1 NT	Human mRNA for KIAA0184 gene, partial cds	
363	6543	10685	1.05	0.0E+00	45076/0 NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAN1) mRNA	
374	5652	10598	4.43	0.0E+00	AJ349863_1 EST_HUMAN	AU1349863 PLACE: Homo sapiens cDNA clone P1ACE:1000899 5'	
385	6594	10740	7.76	0.0E+00	AB228942_1 NT	Homo sapiens mRNA for KIAA1019 protein, partial cds	
386	6595	10741	2.53	0.0E+00	AJ363014_1 EST_HUMAN	φ81105_XR_NCL_CGAP_Bm28_Homo sapiens cDNA clone IMAGE:2018457 3 similar to qb:X54188	
391	5650	10703	4.73	0.0E+00	AN754180_1 EST_HUMAN	RC2-CT0320-360100-01B-a09 C70320 Homo sapiens cDNA	
394	6592	10708	2.69	0.0E+00	45036/0 NT	Homo sapiens IgG Fc binding protein (FC GAMMA/BP) mRNA	
395	6593	10707	2.17	0.0E+00	45036/0 NT	Homo sapiens IgG Fc binding protein (FC GAMMA/BP) mRNA	
395	6593	10708	2.17	0.0E+00	45036/0 NT	Homo sapiens IgG Fc binding protein (FC GAMMA/BP) mRNA	
396	6594	10709	1.86	0.0E+00	45036/0 NT	Homo sapiens IgG Fc binding protein (FC GAMMA/BP) mRNA	
397	6595	10710	2.01	0.0E+00	45036/0 NT	Homo sapiens IgG Fc binding protein (FC GAMMA/BP) mRNA	
397	5695	10711	2.01	0.0E+00	45036/0 NT	Homo sapiens IgG Fc binding protein (FC GAMMA/BP) mRNA	
398	5698	10712	2.45	0.0E+00	45036/0 NT	Homo sapiens IgG Fc binding protein (FC GAMMA/BP) mRNA	
399	5697	10713	3.28	0.0E+00	45036/0 NT	Homo sapiens IgG Fc binding protein (FC GAMMA/BP) mRNA	
400	5698	10714	2.6	0.0E+00	45036/0 NT	Homo sapiens IgG Fc binding protein (FC GAMMA/BP) mRNA	
401	6669	10715	3.22	0.0E+00	X74870_1 NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29	
401	6669	10716	3.22	0.0E+00	X74870_1 NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29	
402	5698	10716	3.76	0.0E+00	X74870_1 NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29	
402	5699	10716	3.76	0.0E+00	X74870_1 NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29	

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
408	6673		7629	0.0E+00	45066308	NT	Hom sapiens ribosomal protein L19 (RPL19) mRNA
419	5208	10318	1.15	0.0E+00	R17795.1	EST_HUMAN	NP_000202.1  Soares infant brain NIH Hom sapiens cDNA clone IMAGE:311652 5'
427	5598	10742	1.21	0.0E+00	4503914	NT	Hom sapiens phosphotriesterase/glyceraldehyde-3-phosphate dehydrogenase synthetase, phosphotriesterase/glyceraldehyde-3-phosphate dehydrogenase (GART) mRNA
428	5597		20.02	0.0E+00	4506728	NT	Hom sapiens ribosomal protein S8 (RPS8) mRNA
429	6598	10743	6.43	0.0E+00	AB028594.2	NT	Hom sapiens mRNA for KIAA01018 protein, partial cds
430	5599	10744	15.73	0.0E+00	4507152	NT	Hom sapiens SON DNA binding protein (SON) mRNA
430	6699	10746	16.73	0.0E+00	4607162	NT	Hom sapiens truncated SON protein (Son) mRNA, complete cds
431	5600	10746	6.04	0.0E+00	AF186367.1	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
443	6611		1.6	0.0E+00	AL163201.2	NT	Hom sapiens chromosome 21 segment HS21C001
445	5613	10759	1.85	0.0E+00	4557978	NT	Hom sapiens Interferon gamma receptor 1 (IFNGR1) mRNA
450	6619		1.13	0.0E+00	AA224262.1	EST_HUMAN	EST27054 Cerebellum II Hom sapiens cDNA 5' end
451	6619		1.64	0.0E+00	BE264447.1	EST_HUMAN	6011115201F1 NIH MGCC_16 Hom sapiens cDNA clone IMAGE:332348 5'
467	5636	10773	9.39	0.0E+00	4504532	NT	Hom sapiens 6-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
467	5635	10774	9.39	0.0E+00	4504532	NT	Hom sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
473	5640	10782	65.72	0.0E+00	4557987	NT	Hom sapiens keratin 18 (KRT18) mRNA
473	5640	10783	55.72	0.0E+00	4557987	NT	Hom sapiens keratin 18 (KRT18) mRNA
483	6651	10789	4.42	0.0E+00	AL163246.2	NT	Hom sapiens chromosome 21 segment HS21C048
484	5652	10790	5.19	0.0E+00	AL163246.2	NT	Hom sapiens chromosome 21 segment HS21C048
484	5652	10791	5.18	0.0E+00	AL163246.2	NT	Hom sapiens chromosome 21 segment HS21C048
493	5650	10786	3.49	0.0E+00	AB0333035.1	NT	Hom sapiens mRNA for KIAA1205 protein, partial cds
495	6662	10788	1.68	0.0E+00	AU132289.1	EST_HUMAN	AU132289 NT2RP4 Hom sapiens cDNA clone NT2RP400087 5'
503	5670	10804	3.16	0.0E+00	BE285144.1	EST_HUMAN	6011748561F1 NIH MGCC_20 Hom sapiens cDNA clone IMAGE:3816758 5'
604	7892	10805	1.28	0.0E+00	AW0888825.1	EST_HUMAN	PM0-D7005F-130400-002-c08 DT0065 Hom sapiens cDNA
607	5673	10807	2.7	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
608	6674	10808	1.29	0.0E+00	8923586	NT	Hom sapiens PC238 protein (PC238), mRNA
517	5683	10817	5.2	0.0E+00	AL163210.2	NT	Hom sapiens chromosome 21 segment HS21C010
624	7893	10821	1.98	0.0E+00	BE081627.1	EST_HUMAN	QY2-BT0635-160400-142-h05 BT0635 Hom sapiens cDNA
629	6659	10827	-1.37	0.0E+00	BF028005.1	EST_HUMAN	601784888F1 NIH MGCC_53 Hom sapiens cDNA clone IMAGE:3886938 5'
635	5701	10834	2.3	0.0E+00	AB040809.1	NT	Hom sapiens mRNA for KIAA1478 protein, partial cds
636	5704	10837	19.21	0.0E+00	6006030	NT	Hom sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
639	6705	10838	4.52	0.0E+00	4504038	NT	Hom sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gα11) mRNA
639	6706	10839	4.62	0.0E+00	4504036	NT	Hom sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gα11) mRNA
541	6707	10841	5.08	0.0E+00	8923531	NT	Hom sapiens anillin (LOC54443), mRNA

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
542	6708	10842	2.92	0.0E+00	8923831	NT	Homo sapiens amilin (LOC544443), mRNA	
542	6708	10843	2.92	0.0E+00	8923831	NT	Homo sapiens amilin (LOC544443), mRNA	
547	5712		5.28	0.0E+00	AF003628.1	NT	Homo sapiens X-linked arthrogryposis ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	U1-H-EII-1-acb-h-04-0-U1.s1 NCJ_CGAP_Sub3_Homo sapiens cDNA clone IMAGE:2713951 3'
555	6720	10852	2.09	0.0E+00	AW_135324.1	EST_HUMAN		
565	5730		4.68	0.0E+00	D10083.1	NT	Homo sapiens RGH gene, retrovirus-like element	
584	5747	10876	4.19	0.0E+00	5174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, flavo-iron-sulfur polypeptide 1 (UQCRCFS1), nuclear gene encoding mitochondrial protein, mRNA	
687	6759		3.99	0.0E+00	J04068.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1	
690	5762	10890	2.17	0.0E+00	BF104898.1	EST_HUMAN		601826277F1 NIH MGIC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
696	6768	10894	0.67	0.0E+00	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA	
694	6771	10899	1	0.0E+00	AF221712.1	NT	Homo sapiens SmaD- and Olf-interacting zinc finger protein mRNA, partial cds	
611	5771	10891	1	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds	
621	5761	10891	2.78	0.0E+00	AF148773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	
623	6783	10914	2.3	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds	
625	6785	10915	1.54	0.0E+00	68005918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	
626	5788	10916	1.9	0.0E+00	68005918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	
626	6788	10917	1.9	0.0E+00	68005918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	
627	5787	10918	0.89	0.0E+00	68005918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	
627	5787	10919	0.89	0.0E+00	68005918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	
634	5795	10929	1.18	0.0E+00	AA398488.1	EST_HUMAN	ZB600717.1 Scores testis, NT-Homo sapiens cDNA clone IMAGE:728732 5'	
638	5799	10933	6.88	0.0E+00	D11078.1	NT	Homo sapiens RGT2 gene, retrovirus-like element	
642	5803	10936	0.67	0.0E+00	W78811.1	EST_HUMAN	zhs1b04.1 Scores fetal liver spleen cDNA clone INF1S_S1 Homo sapiens cDNA clone IMAGE:415597 5' similar to gba2-187 ALPH-2-MACROGLOBULIN PRECURSOR (HUMAN);	
642	5803	10937	0.67	0.0E+00	W78811.1	EST_HUMAN	zhs1b04.1 Scores fetal liver spleen INF1S_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gba2-187 ALPH-2-MACROGLOBULIN PRECURSOR (HUMAN);	
645	5806		4.84	0.0E+00	4885528	NT	Homo sapiens novel Sh2-containing protein 3 (NSP3) mRNA	
652	5813	10949	2.56	0.0E+00	60005003	NT	Homo sapiens glutamate receptor, kainotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA	
654	6815	10952	2	0.0E+00	6031824	NT	Homo sapiens CCAT-box-binding transcription factor (CBF2) mRNA	
657	5818	10958	5.7	0.0E+00	U06235.1	NT	Human neutral amino acid transporter (ASC1) gene, exon 8	
661	5822	10959	0.8	0.0E+00	AF1085389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaC83 (NCX1) mRNA, complete cds	
661	5822	10960	0.8	0.0E+00	AF1083389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaC83 (NCX1) mRNA, complete cds	
667	5827	10965	4.68	0.0E+00	4823847	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA	
667	5827	10968	4.66	0.0E+00	4823947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA	

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
673	7888		2.1	0.0E+00	X57147.1	NT	Human endogenous retrovirus RHE-1 (ERV8)
681	5839	10879	18.62	0.0E+00	4504424	NT	Homo sapiens High-mobility group (histone chromosome) protein 1 (HMG1) mRNA
685	6843	10882	15.5	0.0E+00	ABU28012.1	NT	Homo sapiens mRNA for KIAA01689 protein; partial cds
695	5952	10897	9.94	0.0E+00	7857468	NT	Homo sapiens similar to rat integrin membrane glycoprotein POM121 (POM121L1), mRNA NP48011.61 INCL CG4AP_Br1.1 Homo sapiens cDNA clone IMAGE:1128633 3' similar to gb:X57352
707	5884	11011	7.47	0.0E+00	AA614537.1	EST_HUMAN	INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN)
711	5888	11016	6.36	0.0E+00	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
711	5888	11016	5.35	0.0E+00	M60875.1	NT	Human von Willebrand factor gene, exons 28 through 34
721	6878	11025	1.28	0.0E+00	6032182	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
727	5883	11031	4.45	0.0E+00	AF284760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
727	5883	11032	4.45	0.0E+00	AF284760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
729	5885	11034	8.31	0.0E+00	1154530	NT	Homo sapiens hypothetical protein El_121634 (El_121634), mRNA
735	5891	11043	9.29	0.0E+00	BE24157.1	EST_HUMAN	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Bayfer-HGBC project=TCAA Hemo
755	5910	11067	0.87	0.0E+00	AF228590.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
765	5910	11068	0.87	0.0E+00	AF228590.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
768	5913	11071	0.77	0.0E+00	J03784.1	NT	Human plasmogen activator inhibitor-1 gene, exons 2 to 9
788	5913	11072	0.77	0.0E+00	J03784.1	NT	Human plasmogen activator inhibitor-1 gene, exons 2 to 9
761	5918	11073	2.26	0.0E+00	AB0837760.1	NT	Homo sapiens mRNA for KIAA1330 protein, partial cds
762	5917	11074	3.68	0.0E+00	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
764	7800	11076	4.44	0.0E+00	D50612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
765	5918	11077	8.27	0.0E+00	BE2689/35.1	EST_HUMAN	601445847F1 NIH_MGGC_65 Homo sapiens cDNA clone IMAGE:3849803 8'
769	5923	11081	3.55	0.0E+00	RA8915.1	EST_HUMAN	Y589d38.1 Rat breast 2B19Bc1 Homo sapiens cDNA clone IMAGE:154046 6'
770	5924	11082	9.85	0.0E+00	6032088	NT	Homo sapiens splicing factor 9a, subunit 1, 120kD (SF3A1), mRNA
779	6933	11081	2.29	0.0E+00	AB011389.1	NT	Homo sapiens gene for Af-8, complete cds
782	5937	11085	4.83	0.0E+00	7861195	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
783	5947	11107	1.45	0.0E+00	DS00068.1	NT	Human mRNA for KIAA0184 gene, partial cds
783	5947	11108	1.45	0.0E+00	DS00068.1	NT	Human mRNA for KIAA0184 gene, partial cds
783	5952	11112	1.99	0.0E+00	J089772.1	NT	H.sapiens mRNA for interferon alphabeta receptor (long form)
802	5958	11116	2.27	0.0E+00	AB02017.1	NT	Homo sapiens mRNA for KIAA0810 protein, partial cds
807	5960	11123	7.36	0.0E+00	5174478	NT	Homo sapiens perlecanin (PCNT) mRNA
808	5961	11124	7.7	0.0E+00	4807500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
825	5978	11144	1.77	0.0E+00	7857213	NT	Homo sapiens harmonically upregulated neu tumor-associated kinase (HUNK), mRNA

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit No.	Top Hit Database Source	Top Hit Descriptor
828	6978	11145	2.22	0.0E+00	7657213	NT	Human sapiens harmonically upregulated neu tumor-associated kinase (HUNK), mRNA
828	6981	11147	2.39	0.0E+00	4657888	NT	Human sapiens potassium voltage-gated channel, I <sub>K</sub> -related family, member 1 (KCNIE1), mRNA
834	6986	11153	1.75	0.0E+00	AF088830.1	NT	Human sapiens serine-threonine protein kinase (MNKH) mRNA, complete cds
834	6989	11164	1.75	0.0E+00	AF088830.1	NT	Human sapiens serine-threonine protein kinase (MNKH) mRNA, complete cds
835	5987	11165	0.84	0.0E+00	AF088830.1	NT	Human sapiens serine-threonine protein kinase (MNKH) mRNA, complete cds
840	6982	11160	2.02	0.0E+00	4503854	NT	Human sapiens GA-binding protein transcription factor, alpha subunit (GαD) (GαBPα), mRNA
844	5995	11165	1.79	0.0E+00	4507500	NT	Human sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
844	5996	11166	1.79	0.0E+00	4607500	NT	Human sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
851	6002		1.67	0.0E+00	AF027153.1	NT	Human sapiens sodium/myo-inositol cotransporter (SLC6A3) gene, complete cds
855	6003	11177	6.75	0.0E+00	AB028842.1	NT	Human sapiens mRNA for KIAA0119 protein, partial cds
859	6005	11178	6.75	0.0E+00	AB028842.1	NT	Human sapiens mRNA for KIAA0119 protein, partial cds
859	6007	11179	14.37	0.0E+00	4507452	NT	Human sapiens SON DNA binding protein (SDN) mRNA
857	6008	11180	9.8	0.0E+00	AB028842.1	NT	Human sapiens mRNA for KIAA0119 protein, partial cds
859	6009	11181	12.33	0.0E+00	4606728	NT	Human sapiens ribosomal protein S5 (RPS5) mRNA
862	6013	11184	1.11	0.0E+00	AB020717.1	NT	Human sapiens mRNA for KIAA0910 protein, partial cds
862	6013	11185	1.11	0.0E+00	AB020717.1	NT	Human sapiens mRNA for KIAA0910 protein, partial cds
863	6014	11186	1.69	0.0E+00	AA33272.1	EST_HUMAN	Human sapiens cDNA clone [MAGE3:897453]
863	6014	11187	1.69	0.0E+00	AA4833272.1	EST_HUMAN	Human sapiens cDNA clone [MAGE3:897453]
864	6015		5.77	0.0E+00	Bf6777694.1	EST_HUMAN	Human sapiens cDNA clone [MAGE4:249915.5]
858	6019	11188	1.57	0.0E+00	7657213	NT	Human sapiens harmonically upregulated neu tumor-associated kinase (HUNK), mRNA
858	6019	11189	1.57	0.0E+00	7657213	NT	Human sapiens harmonically upregulated neu tumor-associated kinase (HUNK), mRNA
859	6020	11190	1.93	0.0E+00	7657213	NT	Human sapiens harmonically upregulated neu tumor-associated kinase (HUNK), mRNA
859	6020	11191	1.93	0.0E+00	7657213	NT	Human sapiens harmonically upregulated neu tumor-associated kinase (HUNK), mRNA
859	6042	11214	0.89	0.0E+00	AL168203.2	NT	Human sapiens chromosome 21 segment HS21C003
859	6049	11219	1.47	0.0E+00	BE088592.1	EST_HUMAN	QVO-BT0703-28040-211-811 B10703 Homo sapiens cDNA
859	6049	11220	1.47	0.0E+00	BE088592.1	EST_HUMAN	QVO-BT0703-28040-211-811 B10703 Homo sapiens cDNA
860	6059	11229	3.59	0.0E+00	AL168203.2	NT	Human sapiens chromosome 21 segment HS21C003
918	6067		28.71	0.0E+00	4504958	NT	Human sapiens laminin receptor 1 (67/10, fibronectin SA) (LAMR1), mRNA
921	6067		23.9	0.0E+00	4504958	NT	Human sapiens laminin receptor 1 (67/10, fibronectin SA) (LAMR1), mRNA
922	6070	11239	1	0.0E+00	AF089747.1	NT	Human sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds
923	6071	11237	0.75	0.0E+00	SG89384.1	NT	protein C inhibitor human, leukocytes, Genomic, 1216 nt, segment 2 of 5
923	6071	11238	0.75	0.0E+00	SG89384.1	NT	protein C inhibitor human, leukocytes, Genomic, 1216 nt, segment 2 of 5
923	6071	11239	0.75	0.0E+00	SG89384.1	NT	protein C inhibitor human, leukocytes, Genomic, 1216 nt, segment 2 of 5
924	6072	11240	1.68	0.0E+00	L28101.1	NT	Human sapiens killifatin (P4) beta, exon 1-4, complete cds

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Table 4

## Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
827	60765	11243	4.57	0.0E+00	220686.1	NT	Human sapiens of cardiac alpha-myosin heavy chain gene
827	60765	11244	4.57	0.0E+00	220686.1	NT	Human sapiens of cardiac alpha-myosin heavy chain gene
847	60865	11262	2.02	0.0E+00	AB023211.1	NT	Human sapiens mRNA for KIAA0864 protein, partial cds
847	60865	11263	2.02	0.0E+00	AB023211.1	NT	Human sapiens mRNA for KIAA0864 protein, partial cds
952	6100	11268	1.26	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
953	6101	11269	8.7	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
954	6102	11270	0.79	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
955	6103	11271	2.01	0.0E+00	4607430	NT	Human sapiens thyrotrophic embryonic factor (TEF), mRNA
955	6103	11272	2.01	0.0E+00	4507430	NT	Human sapiens thyrotrophic embryonic factor (TEF), mRNA
863	7803	11278	2.13	0.0E+00	AL001948.1	EST_HUMAN	os88e03.s1 NCI_CGAP_GC3 Human sapiens cDNA clone IMAGE:613404 3'
863	7803	11280	2.13	0.0E+00	AL001948.1	EST_HUMAN	os88e03.s1 NCI_CGAP_GC3 Human sapiens cDNA clone IMAGE:613404 3'
985	6112	11282	11.65	0.0E+00	7657286	NT	Human sapiens KIAA0929 protein Mac22 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
978	6122	11282	1.42	0.0E+00	AB030568.1	NT	Human sapiens mRNA for PSP24, complete cds
884	6130	11288	1.57	0.0E+00	BF366974.1	EST_HUMAN	PN2-GN0014-050800-001-02 GN0014 Human sapiens cDNA
884	6130	11289	1.57	0.0E+00	BF366974.1	EST_HUMAN	PN2-GN0014-050800-001-02 GN0014 Human sapiens cDNA
884	6130	11300	1.57	0.0E+00	BF366974.1	EST_HUMAN	PN2-GN0014-050800-001-02 GN0014 Human sapiens cDNA
885	6131	11301	1.52	0.0E+00	632207.1	NT	Human sapiens partial c-fgr gene, exons 2 and 3
885	6131	11302	1.52	0.0E+00	632207.1	NT	Human sapiens partial c-fgr gene, exons 2 and 3
884	6140	11309	6.83	0.0E+00	4757889	NT	Human sapiens chromodomain protein Y chromosome-like (CDY1) mRNA
1005	6150	11317	1.56	0.0E+00	UB3668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1005	6151	11318	37.21	0.0E+00	UB3668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1007	6151	11318	22.91	0.0E+00	UB3668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1010	6154		4.61	0.0E+00	AF188480.1	NT	Human sapiens CBFA2T11 gene, partial cds
1011	6154		9.74	0.0E+00	AF188490.1	NT	Human sapiens CBFA2T11 gene, partial cds
1016	6158	11324	2.06	0.0E+00	AF111170.3	NT	Human sapiens Jagged2 gene, complete cds; and unknown gene
1016	6158	11324	3.94	0.0E+00	AF111170.3	NT	Human sapiens Jagged2 gene, complete cds; and unknown gene
1017	6158	11324	3.21	0.0E+00	AF111170.3	NT	Human sapiens Jagged2 gene, complete cds; and unknown gene
1018	6159	11325	4.91	0.0E+00	AF111170.3	NT	Human sapiens Jagged2 gene, complete cds; and unknown gene
1021	6162	11328	2.38	0.0E+00	7681685	NT	Human sapiens DKK2P563M0122 protein (DKK2P563M0122), mRNA
1025	6165	11332	3.63	0.0E+00	5803114	NT	Human sapiens inner membrane protein, mitochondrial (mifillin) (IMMT), mRNA
1027	6168		4.4	0.0E+00	AA458880.1	EST_HUMAN	SW_PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8;

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**Table 4**  
**Single Exon Probes Expressed in BT474 Cells**

Probe Seq ID No:	Exam Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1030 6171	11337		7.44	0.0E+00	NA3182.1	EST_HUMAN	EST51124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1030 6171	11338		7.44	0.0E+00	NA3182.1	EST_HUMAN	EST51124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1031 6172	11339		1.27	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1031 6172	11340		1.27	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1036 6176			2.42	0.0E+00	8922933	NT	Homo sapiens hypothetical protein FLJ11982 (FLJ11982) mRNA
1049 6180	11365		10.11	0.0E+00	4758590	NT	Homo sapiens heat shock 70kD protein 8B (mortalin-2) (HSP88) mRNA
1068 6208	11368		2.38	0.0E+00	4926672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1068 6208	11369		2.38	0.0E+00	4926672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1070 6210	11373		2.8	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695) mRNA
1070 6210	11374		2.8	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695) mRNA
1071 6211	11375		58.12	0.0E+00	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1073 6213			2.44	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080) mRNA
1075 6215	11378		4.37	0.0E+00	5174384	NT	Homo sapiens eukaryotic initiation factor 4B homolog (eIF4B), mRNA
1083 6222	11389		4.61	0.0E+00	4759117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1087 6235	11398		2.69	0.0E+00	BE005208.1	EST_HUMAN	MFO-BN0116-200300-003-H08 BA0116 Homo sapiens cDNA
1120 6258	11422		5.21	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNKG) mRNA
1120 6258	11423		5.21	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNKG) mRNA
1133 6270	11433		2.98	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1133 6270	11434		2.88	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1134 6271	11435		20.33	0.0E+00	4505712	NT	Homo sapiens thioester protein FLJ20309 (FLJ20309) mRNA
1135 6273	11437		1.6	0.0E+00	8923280	NT	Homo sapiens hypothetical protein P2X4, complete cds
1139 6276	11440		16.73	0.0E+00	AB020269.1	NT	Homo sapiens DNA for Human P2X4, complete cds
1141 6278	11441		52.48	0.0E+00	AB020269.1	NT	Homo sapiens protein POM121 (POM121L) mRNA
1142 6278	11442		6.53	0.0E+00	7687488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L) mRNA
1142 6278	11443		6.63	0.0E+00	7687488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L) mRNA
1148 6282	11446		2.67	0.0E+00	7706500	NT	Homo sapiens Np48-binding protein Np48BP (LOC51729) mRNA
1147 6283	11447		0.7	0.0E+00	X88828.1	NT	H.sapiens AR74 gene
1147 6283	11448		0.7	0.0E+00	X88828.1	NT	H.sapiens AR74 gene
1148 6284	11449		1.44	0.0E+00	AI147650.1	EST_HUMAN	gb2201011 Scores, pregnant uterus, Ni3PdU Homo sapiens cDNA clone IMAGE_16970113'
1150 6286	11451		1.69	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
1157 6283	11457		1.11	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) CSPG32 mRNA
1157 6283	11458		1.11	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) CSPG32 mRNA

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 Table 4  
 Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Most Similar (Top) Hit BLAST E Value	Expression Signal	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11638	6224	11459	0.9	0.0E+00	8888844	NT	Human sapiens chromosomes 12 open reading frame 3 (C12orf3), mRNA
1170	6305	11471	3.47	0.0E+00	7305078	NT	Human sapiens glutamate decarboxylase 1 (brn3, GAD67) (GAD1), transcript variant GAD25, mRNA
1170	6305	11472	3.47	0.0E+00	7305078	NT	Human sapiens glutamate decarboxylase 1 (brn3, GAD67) (GAD1), transcript variant GAD25, mRNA
1173	6308	11476	1.64	0.0E+00	AB037826.1	NT	Human sapiens mRNA for KIAA1414 protein, partial cds
1180	6315	11484	51.8	0.0E+00	4557887	NT	Human sapiens keratin 18 (KRT18) mRNA
1184	6328	11495	2.36	0.0E+00	AF073289.1	NT	Human sapiens Na+/H+ exchanger isoform 2 (NHE2) mRNA, complete cds
1212	6344		1.73	0.0E+00	7587338	NT	Human sapiens mutL (E. coli) homolog 3 (MLH3), mRNA
1225	6357	11527	1.28	0.0E+00	8922583	NT	Human sapiens hypochlorotidal protein FLJ10697 (FLJ10697), mRNA
1229	6381	11531	3.23	0.0E+00	AF284750.1	NT	Human sapiens ALR-like protein mRNA, partial cds
1229	6381	11532	3.23	0.0E+00	AF284750.1	NT	Human sapiens ALR-like protein mRNA, partial cds
1230	6362	11533	5.19	0.0E+00	AF284750.1	NT	Human sapiens ALR-like protein mRNA, partial cds
1231	7811	11534	4.17	0.0E+00	AF284750.1	NT	Human sapiens ALR-like protein mRNA, partial cds
1250	6380	11559	8.44	0.0E+00	AF109718.1	NT	Human sapiens chromosomal 3 subtelomeric region
1261	6381	11560	1.11	0.0E+00	4563098	NT	Human sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1281	6390	11568	10.12	0.0E+00	4505740	NT	Human sapiens prefoldin 4 (PFDN4) mRNA
1270	6399		2.69	0.0E+00	Y18000.1	NT	Human sapiens NF2 gene
1278	6407	11581	191.34	0.0E+00	4608718	NT	Human sapiens fibrosin protein S2 (RPS2) mRNA
1285	6414	11590	5.41	0.0E+00	AF084478.1	NT	Human sapiens Williams-Bailey syndrome deletion transcript 9 (WBSC9), mRNA, complete cds
1291	6420	11594	2.8	0.0E+00	AB040840.1	NT	Human sapiens mRNA for KIAA1607 protein, partial cds
1291	6420	11595	2.8	0.0E+00	AB040840.1	NT	Human sapiens mRNA for KIAA1607 protein, partial cds
1304	6434	11608	2.48	0.0E+00	5174748	NT	Human sapiens Wolfram syndrome (WFS) mRNA
1304	6434	11609	2.48	0.0E+00	5174748	NT	Human sapiens Wolfram syndrome (WFS) mRNA
1304	6434	11610	2.48	0.0E+00	5174748	NT	Human sapiens Wolfram syndrome (WFS) mRNA
1305	6435		2.72	0.0E+00	AF086156.1	NT	Human sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1316	7913	11622	1.16	0.0E+00	7857628	NT	Human sapiens fibroblast tumor deletion region protein 1 (RTDR1), mRNA
1316	7913	11623	1.16	0.0E+00	7857629	NT	Human sapiens fibroblast tumor deletion region protein 1 (RTDR1), mRNA
1321	8480	11628	1.18	0.0E+00	5803146	NT	Human sapiens ring finger protein 9 (RNFP9), mRNA
1322	8481	11630	3.28	0.0E+00	4508004	NT	Human sapiens zinc finger protein 173 (ZNF173) mRNA
1324	8483	11631	1.01	0.0E+00	5803148	NT	Human sapiens ring finger protein 9 (RNFP9), mRNA
1325	8484	11632	2.76	0.0E+00	4508004	NT	Human sapiens zinc finger protein 173 (ZNF173) mRNA
1327	8486	11654	4.1	0.0E+00	AB011149.1	NT	Human sapiens mRNA for KIAA0577 protein, complete cds
1328	8487	11655	7.17	0.0E+00	7661868	NT	Human sapiens KIAA070 gene product (KIAA070), mRNA
1329	8488	11656	4.33	0.0E+00	7661868	NT	Human sapiens KIAA070 gene product (KIAA070), mRNA
1330	8489	11657	4.08	0.0E+00	8567337	NT	Human sapiens period (Drosophila) homolog 3 (PER3), mRNA

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T <sub>cap</sub> ) Hit BLAST E Value	Top Hit No.	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1330	6459	11638	4.08	0.0E+00	8567387	NT	Homo sapiens peroxisome proliferator-activated receptor gamma 3 (PPAR3), mRNA	
1342	6470	11681	2.07	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10	
1418	6548	11722	0.98	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Ciliadromatosis syndromic gene	
1422	6549	11730	5.33	0.0E+00	AJ277692.1	NT	Homo sapiens partial TTN gene for titin	
1426	6552	11734	1.43	0.0E+00	AJ208758.1	EST_HUMAN	q938bq8_x1 Scores_1600 Homo sapiens cDNA clone IMAGE:1837427's similar to WP:T27A1.5 CE14213;	
1428	6553	11735	22.77	0.0E+00	6042209	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA	
1435	6562	11745	2.3	0.0E+00	4505648	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA	
1436	6562	11746	2.3	0.0E+00	4505648	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA	
1437	6564	11749	4.16	0.0E+00	7705568	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA	
1437	6564	11750	4.16	0.0E+00	7705568	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA	
1440	6567	11762	4.87	0.0E+00	AJ238693.1	NT	Homo sapiens alpha 1'-fucosidase (alpha-L-fucosidase) gene, exon 7	
1450	6578	11765	4.23	0.0E+00	AF038280.1	NT	Homo sapiens alpha 1'-fucosidase (alpha-L-fucosidase) gene, exon 7	
1451	6588	11776	2.18	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA	
1461	6588	11777	2.18	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA	
1468	6593	11781	4.88	0.0E+00	U36837.1	NT	Human nebulin mRNA, partial cds	
1468	6593	11782	4.88	0.0E+00	U36837.1	NT	Human nebulin mRNA, partial cds	
1474	6601	11786	2.57	0.0E+00	AL132898.1	NT	Novel human gene mapping to chromosome 20	
1476	6602	11787	1.36	0.0E+00	AL137784.1	NT	Novel human gene mapping to chromosome 1	
1479	6606	11782	1.8	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds	
1482	6609	11785	8.7	0.0E+00	6912467	NT	Homo sapiens cathepsin binding protein 1 (KIAA0330), mRNA	
1484	6611	11787	1.25	0.0E+00	7681685	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA	
1484	6611	11788	1.25	0.0E+00	7681685	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA	
1625	6652	11838	1.36	0.0E+00	7708434	NT	Homo sapiens hHDC for homolog of Drosophila hedgehog (LOC51686), mRNA	
1639	6687	11853	1.51	0.0E+00	AW958687.1	EST_HUMAN	EST377757 MAGE resequences, MAGF Homo sapiens cDNA	
1540	6688	11854	2.48	0.0E+00	AA481172.1	EST_HUMAN	aa346334 NC_0281 Homo sapiens cDNA clone IMAGE:815118	
1646	6674	11858	130.24	0.0E+00	AF0223860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds	
1648	6674	11859	130.24	0.0E+00	AF0223860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds	
1548	6676	11862	1.27	0.0E+00	AW976097.1	EST_HUMAN	EST386205 MAGE resequences, MAGN Homo sapiens cDNA	
1548	6676	11863	1.27	0.0E+00	AW976097.1	EST_HUMAN	EST386205 MAGE resequences, MAGN Homo sapiens cDNA	
1549	6677	11864	2.41	0.0E+00	D10884.1	NT	Bovine mRNA for neurotrophin (NT-44L) and FTR3 (FTR3) genes, complete cds	
1551	6678		2.42	0.0E+00	U78027.1	NT		

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 Table 4  
 Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Meet Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1552	6881	118688	8.69	0.0E+00	4605404	NT	Human sepiens transmembrane glycoprotein (GPNM) mRNA
1552	6881	11889	5.69	0.0E+00	4505404	NT	Human sepiens transmembrane glycoprotein (GPNM) mRNA
1553	6882	11870	2.73	0.0E+00	7682405	NT	Human sepiens KIAA0857 protein (KIAA0857) mRNA
1554	6883		7.14	0.0E+00	7686972	NT	Human sepiens TNF-inducible protein CG12-1 (CG12-1) mRNA
1560	6889	11876	3.37	0.0E+00	MB8478.1	NT	Human transglutaminase mRNA, complete cds
1563	6892	11878	2.36	0.0E+00	4507720	NT	Human sepiens titin (TTN) mRNA
1563	6892	11878	2.36	0.0E+00	4507720	NT	Human sepiens titin (TTN) mRNA
1584	7820		48.38	0.0E+00	4506854	NT	Human sepiens ribosomal protein L5 (RPL5) mRNA
1665	8883	11880	42.77	0.0E+00	M14189.1	NT	Human laminin receptor (2B16 epitope) mRNA, 6' end
1678	6705	11895	2.22	0.0E+00	4507720	NT	Human sepiens titin (TTN) mRNA
1678	6705	11896	2.22	0.0E+00	4507720	NT	Human sepiens titin (TTN) mRNA
1578	8707	11897	6.89	0.0E+00	4503098	NT	Human sepiens chondroitin sulfatase proteoglycan 4 (melanoma-associated) (CSPG4) mRNA
1584	8713		3.70	0.0E+00	D00333.1	NT	Human c-type-2 gene
1583	8722	11812	11.87	0.0E+00	288738.1	NT	Human sepiens HIF2B/e gene
1594	8723	11813	1.35	0.0E+00	5921460	NT	Human sepiens butyrophilin, subfamily 2, member A1 (BTN2A1) mRNA
1594	8723	11814	1.35	0.0E+00	6921460	NT	Human sepiens butyrophilin, subfamily 2, member A1 (BTN2A1) mRNA
1695	8724	11816	7.46	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Human sepiens cDNA clone GKCB0F02 6'
1695	8724	11818	7.45	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Human sepiens cDNA clone GKCB0F02 5'
1689	7821	11819	6.37	0.0E+00	AB040505.1	NT	Human sepiens mRNA for KIAA1472 protein, partial cds
1601	8729	11820	1.84	0.0E+00	AF167476.1	NT	Human sepiens DNA polymerase zeta catalytic subunit (PZEV3) mRNA, complete cds
1603	8731	11823	6.11	0.0E+00	7882183	NT	Human sepiens KIAA0569 gene product (KIAA0569) mRNA
1603	8731	11824	6.11	0.0E+00	7882183	NT	Human sepiens KIAA0569 gene product (KIAA0569) mRNA
1605	8733	11825	108.24	0.0E+00	5728876	NT	Human sepiens heat shock 70kD protein 10 (HSC71) (HSP71) mRNA
1605	8733	11828	108.24	0.0E+00	5728876	NT	Human sepiens heat shock 70kD protein 10 (HSC71) (HSP71) mRNA
1607	8736	11828	2.08	0.0E+00	M81803.1	NT	Human sodium channel mRNA
1622	8750	11824	8.74	0.0E+00	H28973.1	EST_HUMAN	Y578c5.41 Scores adult brain N244H855Y Homo sapiens cDNA clone IMAGE:1838483
1630	8759	11854	2.1	0.0E+00	AB046829.1	NT	Human sepiens mRNA for KIAA1609 protein, partial cds
1630	8759	11855	2.1	0.0E+00	AB046829.1	NT	Human sepiens mRNA for KIAA1609 protein, partial cds
1648	8777	11869	1.59	0.0E+00	AW444837.1	EST_HUMAN	UH+83-4W~0-0-LJ.81 NC_ CGAP_SubS Human sepiens cDNA clone IMAGE:2733284 3'
1678	8807	12004	1.53	0.0E+00	BE144284.1	EST_HUMAN	MRD-HT0168-181189-004-B11 HT0168 Homo sapiens cDNA
1678	8807	12005	1.53	0.0E+00	BE144284.1	EST_HUMAN	MRD-HT0168-181189-004-B11 HT0168 Homo sapiens cDNA
1682	8811	12009	2.57	0.0E+00	A1768104.1	EST_HUMAN	w891067-x1 Scores JMS_F78_3W_OI_PA_P SI Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR-Q62788 Q62788 CY52HIS2 ZINC FINGER PROTEIN;
1683	8812	12010	1.99	0.0E+00	4758513	NT	Human sepiens hemophiloplatinio-derived zho finger protein (HD-ZNF1) mRNA

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1684	6813	120111	2.16	0.0E+00	AF057177.1	NT	Human sapiens T-cell receptor gamma V1 gene region
1687	6816	12014	3.33	0.0E+00	W28580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1687	6816	12015	3.33	0.0E+00	W28580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1689	6818	12017	46.19	0.0E+00	4857887	NT	Human sapiens keratin 18 (KRT18) mRNA
1690	6819	12018	1	0.0E+00	7657085	NT	Human sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG) mRNA
1694	6823	12021	1.5	0.0E+00	BE222374.1	EST_HUMAN	MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE : hu11d05.51 NCI CGAP_Lu2a Homo sapiens cDNA clone IMAGE-31166281 3' similar to TR:085147 085147
1694	6823	12022	1.5	0.0E+00	BE222374.1	EST_HUMAN	MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE :
1698	6824	12024	1.76	0.0E+00	4557810	NT	Human sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1699	6827	12027	6.05	0.0E+00	HS0132.1	EST_HUMAN	Y569e08.11 Scores breast 3NBH-Bst Homo sapiens cDNA clone IMAGE-182248 5' similar to gbaMR4089 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN); y569e08.11 Scores breast 3NBH-Bst Homo sapiens cDNA clone IMAGE-182248 5' similar to gbaMR4089
1699	6827	12028	5.05	0.0E+00	HS0132.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1701	6829	12030	10.76	0.0E+00	280780.1	NT	H. sapiens H2B/h gene
1701	6829	12031	10.76	0.0E+00	280780.1	NT	H. sapiens H2B/h gene
1704	6832	37.83	0.0E+00	5031748	NT	Human sapiens high-mobility group (nucleosome chaperone) protein 17 (HMGB17) mRNA	
1712	6840	12041	1.57	0.0E+00	AF168683.1	NT	Human sapiens WNT1/B proto-oncogene (WNT16) mRNA, complete cds
1714	6841	12044	4.76	0.0E+00	89223841	NT	Human sapiens FOXJ2 forkhead factor (LOC55810) mRNA
1717	6844	12047	1.8	0.0E+00	8453855	NT	Human sapiens pericentriolar material 1 (PCM1) mRNA
1722	6849	12054	1.39	0.0E+00	4826873	NT	Human sapiens RNA binding motif protein, Y chromosomal, family 1, member A1 (RBMY1A1) mRNA
1728	6855	12061	6.89	0.0E+00	AB029542.1	NT	Human sapiens WAVE2 mRNA for WASP-family protein, complete cds
1730	6857	1.94	0.0E+00	SB94400.1	NT	TCR zeta (human, Germline)mRNA, 385 nt, segment 1 of 8]	
1744	7824	12075	1.21	0.0E+00	1182468H1	NT	Human sapiens NOD2 (NOD2) mRNA
1757	6883	12090	2.78	0.0E+00	AF273841.1	NT	Human sapiens SMCY (SMCY) gene, complete cds
1785	7925	97	0.0E+00	4805718	NT	Human sapiens ribosomal protein S2 (RPS2) mRNA	
1800	6925	12138	2.58	0.0E+00	48577559	NT	Human sapiens E1A binding protein p300 (EP300) mRNA
1800	6925	12137	2.68	0.0E+00	48577558	NT	Human sapiens E1A binding protein p300 (EP300) mRNA
1803	6927	12141	2.04	0.0E+00	U63863.1	NT	Human CSF-1 receptor (FMS) gene, complete cds. and (SMF) gene, partial cds
1807	6931		1.14	0.0E+00	W78571.1	EST_HUMAN	Zd865g08.11 Scores fetal heart Nhlh19W Homo sapiens cDNA clone IMAGE-3456864 5'
1808	7828	12143	6.87	0.0E+00	48056332	NT	Human sapiens nuclear antigenic sperm protein (nuclear-binding) (NASP) mRNA
1819	6942	12160	21.46	0.0E+00	U14987.1	NT	Human ribosomal protein L21 mRNA, complete cds
1821	6944	12163	18.15	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds

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 Table 4  
 Single Exon Probes Expressed In BT474

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1822	6945	12164	23.6	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1822	6945	12165	25.6	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1822	6945	12166	25.6	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1836	6958	12181	2.33	0.0E+00	4504628	NT	Homo sapiens Immunogloblin superfamily, member 3 (IGSF3) mRNA, and translated products
1836	6958	12182	2.33	0.0E+00	4504628	NT	Homo sapiens Immunogloblin superfamily, member 3 (IGSF3) mRNA, and translated products
1848	6969	12189	4.08	0.0E+00	60016855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1848	6969	12190	4.05	0.0E+00	60016855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1855	6976	12197	2.57	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1162 protein, partial cds
1855	6976	12198	2.57	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1859	6979	12200	3.45	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1859	6979	12201	3.45	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1860	6980	12202	0.38	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1860	6980	12203	0.38	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1863	6983	12206	4.21	0.0E+00	AW207280.1	EST HUMAN	UH-B11-arr-f-07-0-U_1.1 NCI CGAP_Subs3 Homo sapiens cDNA clone IMAGE2722333 3'
1863	6983	12207	4.21	0.0E+00	AW207280.1	EST HUMAN	UH-B11-arr-f-07-0-U_1.1 NCI CGAP_Subs3 Homo sapiens cDNA clone IMAGE2722333 3'
1885	7005	12224	3.11	0.0E+00	BE27485.1	EST HUMAN	601178164F1 NIH MGCC_20 Homo sapiens cDNA clone IMAGE3547239 5'
1885	7005	12225	3.11	0.0E+00	BE27485.1	EST HUMAN	601178164F1 NIH MGCC_20 Homo sapiens cDNA clone IMAGE3547239 5'
1901	7020	12240	1.41	0.0E+00	BE006292.1	EST HUMAN	RC2-BN0128-200300-012-004 BN0128 Homo sapiens cDNA
1925	7044	12284	1.89	0.0E+00	7687390	NT	Homo sapiens nuclear protein (NP220), mRNA
1925	7044	12285	1.89	0.0E+00	7687390	NT	Homo sapiens nuclear protein (NP220), mRNA
1925	7044	12286	1.89	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1)mRNA, and translated products
1925	7047	12287	3.05	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1)mRNA, and translated products
1833	7052	12274	2.16	0.0E+00	AB037788.1	NT	Homo sapiens mRNA for KIAA1367 protein, partial cds
1838	7055		1.48	0.0E+00	AF157478.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1841	7060	12283	3.37	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1841	7060	12284	3.37	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGF3), mRNA
1844	7062	12285	1.03	0.0E+00	7687398	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1846	7084		6.43	0.0E+00	AF240788.1	NT	

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 Table 4  
 Single Exon Probes Expressed in BT474

Probe SEQ ID NO:	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit No.	Top Hit Database Source	Top Hit Descriptor
1851	7089		2.25	0.0E+00	M56632.1	NT	Human topoisomerase I pseudogene 1
1852	7830	12283	1.2	0.0E+00	6801605	NT	Human topoisomerase I pseudogene 1
1854	7071	12285	1.08	0.0E+00	BE016068.1	EST_HUMAN	657311.1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048046 6'
1860	7077	12300	1.49	0.0E+00	4809282	NT	Human sapiens histidine ammonia-lyase (HAL) mRNA
1860	7077	12301	1.49	0.0E+00	4809282	NT	Human sapiens histidine ammonia-lyase (HAL) mRNA
1871	7088	12315	2.57	0.0E+00	8401716	NT	Human sapiens nebulin (NEB) mRNA
1871	7088	12316	2.67	0.0E+00	8401716	NT	Human sapiens nebulin (NEB) mRNA
1872	7089	12317	10.13	0.0E+00	4828638	NT	Human sapiens actinin, alpha 4 (ACTN4) mRNA
1872	7089	12318	10.13	0.0E+00	4828638	NT	Human sapiens actinin, alpha 4 (ACTN4) mRNA
1882	7099	12330	1.63	0.0E+00	AB016833.1	NT	Human sapiens mRNA for KIAA0780 protein, partial cds
1882	7099	12331	1.53	0.0E+00	AB016833.1	NT	Human sapiens mRNA for KIAA0780 protein, partial cds
1887	7104	12335	1.18	0.0E+00	M32782.1	NT	Human TFEB protein mRNA, partial cds
1887	7104	12338	1.18	0.0E+00	M32782.1	NT	Human TFEB protein mRNA, partial cds
1889	7108	12337	3.18	0.0E+00	AW168024.1	EST_HUMAN	658560.1 NC_ CGAP_Parti Homo sapiens cDNA clone IMAGE:2878913 3'
1889	7108	12338	3.18	0.0E+00	AW168024.1	EST_HUMAN	658560.1 NC_ CGAP_Parti Homo sapiens cDNA clone IMAGE:2878913 3'
1890	7107	12339	6.81	0.0E+00	6912467	NT	Human sapiens cadherin binding protein 1 (KIAA0330) mRNA
1890	7107	12340	6.81	0.0E+00	6912467	NT	Human sapiens cadherin binding protein 1 (KIAA0330) mRNA
1892	7109	12342	1.01	0.0E+00	AB011149.1	NT	Human sapiens mRNA for KIAA0577 protein, complete cds
1893	7110	12343	1.9	0.0E+00	AB011149.1	NT	Human sapiens genes for semenogelin I and semenogelin II
1894	7111	12344	1.53	0.0E+00	Z47559.1	NT	Human sapiens genes for semenogelin I and semenogelin II
1894	7111	12345	1.53	0.0E+00	Z47558.1	NT	Human sapiens genes for semenogelin I and semenogelin II
2001	7118	12354	5.38	0.0E+00	AB0140546.1	NT	Human sapiens mRNA for KIAA1513 protein, partial cds
2019	7133	12370	1.76	0.0E+00	AF273841.1	NT	Human sapiens SMCY (SMCY) gene, complete cds
2016	7133	12371	1.76	0.0E+00	AF273841.1	NT	Human sapiens SMCY (SMCY) gene, complete cds
2043	7161	12400	1.13	0.0E+00	7708742	NT	Human sapiens TP53TG3 (TP53TG3), mRNA
2049	7166	12404	23.48	0.0E+00	BE145215.1	EST_HUMAN	60167388651 NIH_IMGC_9 Homo sapiens cDNA clone IMAGE:3836198 6'
2049	7166	12405	23.48	0.0E+00	BE145215.1	EST_HUMAN	60157388651 NIH_IMGC_9 Homo sapiens cDNA clone IMAGE:3835198 6'
2061	7167	12408	1.37	0.0E+00	469348	NT	Human sapiens coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B) (FB) mRNA
2052	7168	12407	2.18	0.0E+00	BF20788.1	EST_HUMAN	601861974F1 NIH_IMGC_53 Homo sapiens cDNA clone IMAGE:4081483 6'
2053	7168	12408	3.83	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE:4 Homo sapiens cDNA clone PLACE:4000321 6'
2055	7171	12410	1.58	0.0E+00	AA077689.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2055	7171	12411	1.68	0.0E+00	AA077689.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2057	7173		1.8	0.0E+00	7687488	NT	Human sapiens similar to rat integral membrane glycoprotein POM121 (POM121), mRNA

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 Table 4  
 Single Exon Probes Expressed In BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar ('top' Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2059	7175			1.25	0.0E+00	4585683 NT	Human sepiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE8A), mRNA
2060	7176	12414		1.76	0.0E+00	242359.1 EST HUMAN	HSC01021 NCI_NCI_CGAP_U2 Homo sepiens cDNA clone IMAGE:1888871 3' similar to contains Alt repetitive element
2062	7178			1.1	0.0E+00	A1244247.1 EST HUMAN	q96Q8Bx1 NCI_NCI_CGAP_U2 Homo sepiens cDNA clone IMAGE:1888871 3' similar to contains Alt repetitive element
2066	7182	12422		2.39	0.0E+00	BE877225.1 EST HUMAN	Q01485146F1 NIH_M3C_69 Homo sepiens cDNA clone IMAGE:3887747 5'
2083	7184	12424		2.08	0.0E+00	BF315325.1 EST HUMAN	60190264F1 NIH_M3C_19 Homo sepiens cDNA clone IMAGE:4195320 5'
2088	7184	12425		2.08	0.0E+00	BF315325.1 EST HUMAN	60190264F1 NIH_M3C_19 Homo sepiens cDNA clone IMAGE:4195320 5'
2073	7189	12431		2.68	0.0E+00	BE897125.1 EST HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sepiens cDNA
2073	7189	12432		2.68	0.0E+00	BE897125.1 EST HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sepiens cDNA
2079	7186	12439		2.02	0.0E+00	L00820.1 NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2079	7185	12440		2.02	0.0E+00	L00820.1 NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2080	7198	12441		1.02	0.0E+00	A1287709.1 NT	Human sepiens mRNA for CDCC2A protein kinase (CDCC2L5 gene), isoform 1
2083	7189	12444		1.6	0.0E+00	4768489 NT	Human sepiens GTP binding protein 1 (GTPBP1) mRNA
2103	7218			3.19	0.0E+00	BE767884.1 EST HUMAN	Q11-GN0065-74080-0-18-010 GN0065 Homo sepiens cDNA
2104	7219			1.48	0.0E+00	AF019863.1 NT	Human sepiens X-linked juvenile reticularis protein (XLR5) gene, exon 6 and complete cds
2106	7221	12485		6.48	0.0E+00	BF027562.1 EST HUMAN	6011672068F1 NIH_M3C_20 Homo sepiens cDNA clone IMAGE:3884785 5'
2107	7222	12468		1.85	0.0E+00	BE072824.1 EST HUMAN	PM0-BT0547-210300-004-F04 BT0547 Homo sepiens cDNA
2109	7224	12467		2.8	0.0E+00	AF2240788.1 NT	Human sepiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
2112	7227	12469		6.06	0.0E+00	AW752708.1 EST HUMAN	IL3-CT0218-271089-0-22-G10 CT0218 Homo sepiens cDNA
2113	7228	12470		1.02	0.0E+00	L76827.1 NT	Human sepiens metabotropic glutamate receptor 1 alpha (mGluR1alpha) mRNA, complete cds
2115	7230	12472		10.62	0.0E+00	AI804680.1 EST HUMAN	Q1Y-BT05-020389-0-22-B105 Homo sepiens cDNA
2118	7230	12473		10.62	0.0E+00	AI804680.1 EST HUMAN	Q1V-BT065-020389-0-02-B105 Homo sepiens cDNA
2161	7274			2.02	0.0E+00	L14787.1 NT	Human DNA-binding protein mRNA, 3' end
2168	7281	12527		1.29	0.0E+00	BE274898.1 EST HUMAN	601122338F1 NIH_M3C_20 Homo sepiens cDNA clone IMAGE:3348888 5'
2170	7283	12530		1.18	0.0E+00	D87885.1 NT	Human mRNA for KIAA0244 genes, partial cds
2171	7284	12531		47.78	0.0E+00	AV738288.1 EST HUMAN	AV738288 CB Homo sepiens cDNA clone CBNBD0D8 5'
2171	7284	12532		47.78	0.0E+00	AV738288.1 EST HUMAN	AV738288 CB Homo sepiens cDNA clone CBNBD0D8 5'
2173	7288	12534		20.27	0.0E+00	AA831691.1 EST HUMAN	Q32401.s1.NCI_CGAP_L15 Homo sepiens cDNA clone IMAGE:1667888 3'
2176	7288			1.32	0.0E+00	M19828.1 NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 26
2178	7281	12538		8.02	0.0E+00	BF344434.1 EST HUMAN	602014828F1 NCI_CGAP_Bm84 Homo sepiens cDNA clone IMAGE:4150734 5'
2179	7282	12539		143.71	0.0E+00	BE748898.1 EST HUMAN	60157218071 NIH_M3C_55 Homo sepiens cDNA clone IMAGE:3889012 3'
2183	7288	12543		2.92	0.0E+00	BF377897.1 EST HUMAN	CMI-TR0141-250800-439-508 TN0141 Homo sepiens cDNA
2183	7288	12544		2.92	0.0E+00	BF377897.1 EST HUMAN	CMI-TR0141-250800-439-508 TN0141 Homo sepiens cDNA

Table 4.  
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2188	7836	12547	7.23	0.0E+00	BF313817.1	EST_HUMAN	601600261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126822 5'
2189	7901	12550	2.24	0.0E+00	BED18760.1	EST_HUMAN	6594602Y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170
2190	7302	12551	2.88	0.0E+00	AA042813.1	EST_HUMAN	2K53c07.81 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN (HUMAN);
2190	7302	12552	2.98	0.0E+00	AA042813.1	EST_HUMAN	2K53c07.81 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN (HUMAN);
2197	7309	12559	3.51	0.0E+00	AL168204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2197	7309	12560	3.61	0.0E+00	AL168204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2198	7310	12561	3.77	0.0E+00	7682401	NT	Homo sapiens KIAA0962 protein (KIAA0962), mRNA
2198	7310	12562	3.77	0.0E+00	7682401	NT	Homo sapiens KIAA0962 protein (KIAA0962), mRNA
2203	7315		2.39	0.0E+00	US8264.1	NT	Human beta-prime-adaptin (BAM22), gene, exon 10
2210	7322	12572	6.18	0.0E+00	BB897487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3971453 5'
2222	7334	12588	8.73	0.0E+00	4657568	NT	Homo sapiens ET-1 binding protein P300 (EP300), mRNA
2227	7339	12593	1.81	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2233	7345	12600	4.45	0.0E+00	BB895281.1	EST_HUMAN	6014331523F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:39718607 5'
2237	7349		2.4	0.0E+00	BB895663.1	EST_HUMAN	601438208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3971457 5'
2237	7349	12605	2.4	0.0E+00	BB895663.1	EST_HUMAN	601438208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3971457 5'
2239	7350	12607	2.92	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2274	7384	12632	3.79	0.0E+00	BF344766.1	EST_HUMAN	602014008F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149770 5'
2274	7384	12633	3.79	0.0E+00	BF344766.1	EST_HUMAN	602014008F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149770 5'
2276	7385	12635	3.08	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP_(mouse heart), mRNA
2278	7386	12636	3.08	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP_(mouse heart), mRNA
2277	7387	12637	2.3	0.0E+00	AL076404.1	EST_HUMAN	6020507_X1 Soares_fetal liver_spleen_cDNA clone IMAGE:767428 3'
2280	7390	12640	3.68	0.0E+00	AA428601.1	EST_HUMAN	2K78a11.11 Soares_fetal_fetus_Nb2H_F8_9w Homo sapiens cDNA clone IMAGE:769740 5'
2280	7390	12641	3.59	0.0E+00	AA428601.1	EST_HUMAN	2K78a11.11 Soares_fetal_fetus_Nb2H_F8_9w Homo sapiens cDNA clone IMAGE:769740 5'
2282	7392	12643	2.88	0.0E+00	BF3347038.1	EST_HUMAN	602021846F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4167339 5'
2283	6880	11867	1.1	0.0E+00	M18768.1	NT	Human T-cell receptor gamma chain V1-C1-CII region mRNA, complete cds
2288	7397	12649	1.03	0.0E+00	L02840.1	NT	Homo sapiens potassium channel K2.1 mRNA, complete cds
2289	7398	12650	1.01	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2289	7398	12651	1.01	0.0E+00	AB020717.1	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2290	7399	12652	1.23	0.0E+00	63254661	NT	7022a02X1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3285370 3' similar to TR:Q84839 Q84839
2297	7406	12659	2.88	0.0E+00	BE876095.1	EST_HUMAN	KIAA0857 PROTEIN;

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Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No.	Exon Seq ID No.	ORF SEQ ID NO:	Expression Signal	Most Similar ("Top") Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2300 7409	126860		11.14	0.0E+00	AF044571.1	NT	Homo sapiens phosphotyrosine kinase alpha subunit (PTK2) gene, exon 32
2301 7410	126861		1.94	0.0E+00	AB25542.1	EST_HUMAN	Y57508_x1 NCI_CGAP U2 Homo sapiens cDNA clone IMAGE:2283182 3'
2303 7412	126862		1.89	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
2306 7415	126864		3.71	0.0E+00	7002401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2306 7415	126865		3.71	0.0E+00	7002401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2309 7418	126888		2.32	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2309 7418	126869		2.32	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2318 7424	126774		1.92	0.0E+00	7002407	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2318 7424	126776		1.92	0.0E+00	7002407	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2320 7423	126889		1.25	0.0E+00	DB3778.1	NT	Human mRNA for KIAA0184 gene, partial cds
2320 7423	126861		1.25	0.0E+00	DB3778.1	NT	Human mRNA for KIAA0184 gene, partial cds
2326 7439	126888		1.8	0.0E+00	5174578	NT	Homo sapiens signal regulatory protein, beta 1 (SRP-BETA-1), mRNA
2332 7439	126892		2.97	0.0E+00	AU131142	NT2R3P3 Homo sapiens cDNA clone NT2R3P30022064 6'	
2333 7440			70.49	0.0E+00	BET70426.1	EST_HUMAN	60168843F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:3941003 6'
2334 7441	126893		1	0.0E+00	AW867076.1	EST_HUMAN	MRI-ST0033-12040-002-e04 SIN0033 Homo sapiens cDNA
2335 7442	126894		6.53	0.0E+00	7002417	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2338 7449	126895		1.52	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2338 7443	126895		1.52	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2337 7444			2.39	0.0E+00	AF280107.1	NT	(CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2339 7446	126888		19.43	0.0E+00	AU116082	HEMBA1 Homo sapiens cDNA clone HEMBA1002839 6'	
2339 7446	126889		19.43	0.0E+00	AU116082	HEMBA1 Homo sapiens cDNA clone HEMBA1002839 6'	
2339 7446	127700		19.43	0.0E+00	AU116082	HEMBA1 Homo sapiens cDNA clone HEMBA1002839 6'	
2340 7447	12701		1.58	0.0E+00	8923089	NT	Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA
2353 7465			4.27	0.0E+00	BE814424.1	EST_HUMAN	MRI-BN0070-080680-028-412 BN0070 Homo sapiens cDNA
2392 7498			3.25	0.0E+00	AI042035.1	EST_HUMAN	0x60b022_x1 Scores_NHMPU_S1 Homo sapiens cDNA clone IMAGE:18600883 3' similar to TR008862
2394 7600	12761		4.38	0.0E+00	89223820	NT	Homo sapiens hypothetical protein FLJ20683 (FLJ20683), mRNA
2396 7602	12752		1	0.0E+00	AW303888.1	EST_HUMAN	X01607_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813221 3' similar to TR084924
2398 7604			3.28	0.0E+00	BE5895605.1	EST_HUMAN	601632058F1 NIH MGC 72 Homo sapiens cDNA clone IMAGE:3918168 5'
2410 7616			4.98	0.0E+00	AB005622	EST_HUMAN	AB005622 HeLa cDNA (T-Name) Homo sapiens cDNA similar to adenylyl kinase isoform 2
2413 7619	12769		5.88	0.0E+00	6005002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA

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Table 4  
Single Exon Probes Expressed in BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2417	7622	12773	1.61	0.0E+00	DB5608.1	NT	Human sapiens gene for cholecystokinin type-A receptor, complete cds
2417	7622	12774	1.61	0.0E+00	DB5608.1	NT	Human sapiens gene for cholecystokinin type-A receptor, complete cds
2425	7630	12783	1.04	0.0E+00	AF105276.1	NT	Human sapiens gene for cholecystokinin-like transcript 4 (LTC) beta, exon 6
2429	7633	12788	1.51	0.0E+00	BF7349274.1	EST_HUMAN	Human sapiens immunoglobulin-like transcript 10 variant 4 (LTC) beta, exon 6
2436	7640	12794	2.44	0.0E+00	5129777	NT	Human sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2439	7643	12796	1.13	0.0E+00	BE831003.1	EST_HUMAN	CMD-MT033-150804-428-411 MTF033 Human sapiens cDNA
2439	7643	12797	1.13	0.0E+00	BE831003.1	EST_HUMAN	CMD-MT033-160804-428-411 MT033 Human sapiens cDNA
2444	7648	12801	37.91	0.0E+00	BF756144.1	EST_HUMAN	6021846587 NIH_MGC_42 Human sapiens cDNA clone IMAGE:4300353 3'
2461	7656	12807	4.45	0.0E+00	AW468922.1	EST_HUMAN	6024044.1 NCI_CGAP_K1612 Human sapiens cDNA clone IMAGE:2872768 3'
2453	7657	12808	2.12	0.0E+00	AW501010.1	EST_HUMAN	U1HF-E8P0p-8t8-o-07-0-U..7 NIH_MGC_51 Human sapiens cDNA clone IMAGE:2872768 5'
2473	7680		1.9	0.0E+00	AW813883.1	EST_HUMAN	RC3-ST0197-300300-018-004 ST0197 Human sapiens cDNA
2480	7685	12835	55.02	0.0E+00	BF785542.1	EST_HUMAN	60116233051 NIH_MGC_7 Human sapiens cDNA clone IMAGE:3949518 5'
2481	7682	12838	1.19	0.0E+00	7657038	NT	Human sapiens death receptor 6 (DR6), mRNA
2482	7688	12836	2.07	0.0E+00	BF509482.1	EST_HUMAN	U1H-B14-eaz-b-08-0-U..61 NCI_CGAP_Sub8 Human sapiens cDNA clone IMAGE:3086536 3'
2485	7689	12838	1.23	0.0E+00	ZS2684.2	NT	Human sapiens mRNA for membrane transport protein (XK gene)
2487	7691		2.23	0.0E+00	5453971	NT	Human sapiens platelet-derived growth factor receptor-like (PDGFR $\gamma$ ) mRNA
2490	7694	12842	1.61	0.0E+00	BF8110378.1	EST_HUMAN	601503365F1 NIH_MGC_70 Human sapiens cDNA clone IMAGE:38015148 6'
2491	7686	12843	1.54	0.0E+00	7657468	NT	Human sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2492	7688	12844	6.61	0.0E+00	BE168865.1	EST_HUMAN	RC4H776-160200-013-405 HTCT276 Human sapiens cDNA
2493	7697	12845	3.17	0.0E+00	88223340	NT	Human sapiens hypothetical protein FLJ20368 (FLJ20368), mRNA
2494	7698	12846	10.75	0.0E+00	IS83299.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2499	7603	12851	10.62	0.0E+00	BE888490.1	EST_HUMAN	601508211F1 NIH_MGC_71 Human sapiens cDNA clone IMAGE:3809865 5'
2504	7607	12857	3.04	0.0E+00	BE976611.1	EST_HUMAN	601489241F1 NIH_MGC_69 Human sapiens cDNA clone IMAGE:3891371 5'
2504	7607	12858	3.04	0.0E+00	BE975511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Human sapiens cDNA clone IMAGE:3891371 5'
2505	7608	12859	1.27	0.0E+00	AF114027.1	EST_HUMAN	AF114027 Human sapiens lung fetus Human sapiens cDNA clone ESF6
2507	7610	12862	1.44	0.0E+00	AF245505.1	NT	Human sapiens adican mRNA, complete cds
2522	7628	12870	1.17	0.0E+00	BE836921.1	EST_HUMAN	6010584738F1 NIH_MGC_10 Human sapiens cDNA clone IMAGE:3451161 5'
2528	7629	12876	11.25	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y78AA1 Human sapiens cDNA clone Y78AA1001673 5'
2528	7629	12877	11.25	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y78AA1 Human sapiens cDNA clone Y78AA1001673 5'
2527	7630	12878	1.86	0.0E+00	BE292986.1	EST_HUMAN	601105312F1 NIH_MGC_16 Human sapiens cDNA clone IMAGE:2887955 5'
2527	7630	12879	1.88	0.0E+00	BE292986.1	EST_HUMAN	601105312F1 NIH_MGC_15 Human sapiens cDNA clone IMAGE:2887955 5'
2530	7633	12881	4.83	0.0E+00	AF245505.1	NT	Human sapiens adican mRNA, complete cds
2581	7878	12817	3.58	0.0E+00	AB037886.1	NT	Human sapiens mRNA for KIAA1415 protein, partial cds
2581	7878	12818	3.58	0.0E+00	AB037886.1	NT	Human sapiens mRNA for KIAA1415 protein, partial cds

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2662	7683			1.77	0.0E+00	BF513835.1	EST HUMAN U/H-BW1-amp-F-12-O-U/J_1 NCI CGAP Sub1 Homo sapiens cDNA clone IMAGE:3070831 3'
2668	7689	12824		1.84	0.0E+00	BF72818.1	EST HUMAN G0215633F_1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283612 5
2570	7671			1.23	0.0E+00	BF516895.1	EST HUMAN G01279873F_1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621788 5
2678	7678	12830		4.12	0.0E+00	AB037742.1	NT Homo sapiens mRNA for KIAA1321 protein, partial cds
2577	7677	12831		0.85	0.0E+00	AB571737.1	EST HUMAN tnt1808x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:2168055 3' similar to gb:120377 CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN)
2678	7678	12832		2.82	0.0E+00	5032150 NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF2)
2550	7681	12833		3.53	0.0E+00	AB037859.1	NT Homo sapiens mRNA for KIAA1438 protein, partial cds
2681	7682	12837		1.36	0.0E+00	BF785446.1	EST HUMAN G01580108F_1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 6'
2581	7682	12838		1.35	0.0E+00	BF795448.1	EST HUMAN G01580108F_1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 6'
2691	7692			13.31	0.0E+00	BF782472.1	EST HUMAN G01584830F_1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'
2593	7694	12843		1.19	0.0E+00	AB020710.1	NT Homo sapiens mRNA for KIAA0803 protein, partial cds
2600	7700	12955		3.59	0.0E+00	4504688 NT	Human mRNA (positive map/ncosphate) dystroglycanase 1 (MPDH1) mRNA
2602	7948	12858		0.89	0.0E+00	4507720 NT	Homo sapiens titin (TTN) mRNA
2608	7707	12862		3.82	0.0E+00	AF173227.1	NT Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2611	7711	12863		1.84	0.0E+00	AB011108.1	EST HUMAN G0140558 protein, partial cds
2613	7712	12865		1.12	0.0E+00	AL133385.1	EST HUMAN AU133385 NT2RP4 Human sepius cDNA clone NT2RP4001684 6'
2614	7713	12866		1.11	0.0E+00	MG9225.1	NT Human bulbous penile/gold antigen (EPAG1) mRNA, complete cds
2616	7715	12868		3.79	0.0E+00	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000778 6'	EST HUMAN AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000778 6'
2618	7715	12869		3.79	0.0E+00	AU130403.1	EST HUMAN AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000778 6'
2619	7718	12872		1.49	0.0E+00	AW587015.1	EST HUMAN RG1-OT056-22B2300-011-017 OT0089 Homo sapiens cDNA clone IMAGE:3316088 3'
2622	7721	12875		1.85	0.0E+00	BFO00018.1	EST HUMAN Th1510B1X1 NCI CGAP Co16 Homo sapiens cDNA clone IMAGE:3316088 3'
2623	7722	12878		4.15	0.0E+00	BF5388185.1	EST HUMAN G01298714F_19 Homo sapiens cDNA clone IMAGE:36228523 5'
2624	7723			2.17	0.0E+00	BF531283.1	EST HUMAN G01278373F_1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610287 5'
2649	7747	12898		1.39	0.0E+00	88222643 NT	Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA
2659	7755	13003		1.25	0.0E+00	AB037732.1	NT Homo sapiens mRNA for KIAA1311 protein, partial cds
2684	7761			24.69	0.0E+00	AA316723.1	EST HUMAN EST168414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L12
2685	7782	13030		43.83	0.0E+00	BF784884.1	EST HUMAN G01585926F_1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2690	7787	13037		4.97	0.0E+00	U36263.1	Human beta-prime-adaptin (BAM22) gene, exon 5
2692	7789	13039		1.68	0.0E+00	7688617 NT	Homo sapiens neutrophil 1 (NRG1), transcript variant SWDF, mRNA
2693	7790	13040		1.85	0.0E+00	AF110763.1	Homo sapiens skeletal muscle LIM-protien 1 (FHL1) gene, complete cds
2694	7791	13041		2.6	0.0E+00	AB051828.1	Homo sapiens hCG28K mRNA for GTP-binding protein like 1, complete cds

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon seq ID NO:	Off seq ID NO:	Expression Signal	Most Similar BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2700	7788	13047	80.08	0.0E+00	BE78376.1	EST_HUMAN	601681891F1 NIH MG3C_7 Homo sapiens cDNA clone IMAGE:3845833 5'
2701	7789	13048	1.94	0.0E+00	BP680932.1	EST_HUMAN	602155923F1 NIH MG3C_83 Homo sapiens cDNA clone IMAGE:4287132 5'
2704	7849	13052	75.91	0.0E+00	BE683433.1	EST_HUMAN	601385495F1 NIH MG3C_39 Homo sapiens cDNA clone IMAGE:3685564 5'
2705	7800		2.71	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBVE08 5'
2707	7802	13055	1.9	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated protein PDI (KIAA0757) mRNA
2707	7802	13056	1.9	0.0E+00	6174488	NT	Homo sapiens spermatogenesis associated protein PDI (KIAA0757) mRNA
2708	7803	13057	1.94	0.0E+00	8922341	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477) mRNA
2708	7803	13058	1.94	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477) mRNA
2709	7804	13059	9.14	0.0E+00	AF280185.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2710	7805		61.45	0.0E+00	AV651068	EST_HUMAN	AV651068 GLC Homo sapiens cDNA clone IMAGE:GLCCDD7 3'
2711	7806	13060	2.74	0.0E+00	BF377897.1	EST_HUMAN	CMI-TN0141-250500-438+D08 TN0141 Homo sapiens cDNA
2711	7806	13061	2.74	0.0E+00	BF377897.1	EST_HUMAN	CMI-TN0141-250500-438+D08 TN0141 Homo sapiens cDNA
2716	7810	13064	6.04	0.0E+00	4757883	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2716	7810	13065	6.04	0.0E+00	4757883	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2718	7814	13070	37.71	0.0E+00	BE747193.1	EST_HUMAN	60158063F1 NIH MG3C_9 Homo sapiens cDNA clone IMAGE:3928472 5'
2730	7825		1.28	0.0E+00	AL168201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2731	7826	13081	2.6	0.0E+00	BF561410.1	EST_HUMAN	UH-BW1-armw-e-074-U1.61 NCI_OGAP_Sub/Homo sapiens cDNA clone IMAGE:3071340 3'
2742	7836	13089	1.66	0.0E+00	7705275	NT	Homo sapiens angiopoietin-3 (ANG-3) mRNA
2742	7838	13090	1.66	0.0E+00	7705276	NT	Homo sapiens angiopoietin-3 (ANG-3) mRNA
2743	7837	13091	2.45	0.0E+00	BF677694.1	EST_HUMAN	602085679F1 NIH MG3C_83 Homo sapiens cDNA clone IMAGE:4248916 5'
2749	7843	13089	1.66	0.0E+00	7427322	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT) mRNA
2752	7846	13101	37.83	0.0E+00	AV725334.1	EST_HUMAN	AV725334 HTG Homo sapiens cDNA clone HTGCCA03 5'
2762	7848	13102	37.83	0.0E+00	AV725334.1	EST_HUMAN	AV725334 HTG Homo sapiens cDNA clone HTGCCA03 5'
2764	7848		14.98	0.0E+00	AI878163.1	EST_HUMAN	AI878163.1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518683 5' similar to SW.R13A_HUMAN P40422 GOS RIBOSOMAL PROTEIN L19A ;
2765	7851	13107	2.14	0.0E+00	BF5206681.1	EST_HUMAN	eu65604.1 NCI_OGAP_Bm87 Homo sapiens cDNA clone IMAGE:4214879 5'
2768	7852	13108	147.71	0.0E+00	BE872768.1	EST_HUMAN	601459812F1 NIH MG3C_85 Homo sapiens cDNA clone IMAGE:3884642 5'
2769	7854	13109	3.85	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2769	7854	13110	3.85	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2761	7855	13111	128.52	0.0E+00	BE309844.1	EST_HUMAN	600944784F1 NIH MG3C_17 Homo sapiens cDNA clone IMAGE:2860808 5'
2761	7855	13112	128.62	0.0E+00	BE309844.1	EST_HUMAN	600944784F1 NIH MG3C_17 Homo sapiens cDNA clone IMAGE:2860808 5'
2767	6378	10519	3.63	0.0E+00	S76830.1	NT	glycoprotein D-Duffy group antigen [Human, blood - Genomic DNA, 3038 nt]
2770	7882		2.78	0.0E+00	AB033281.1	NT	Homo sapiens BTRCP2 mRNA for F-box and WD-40 repeats protein isoform C, complete cds
2770	6388	11040	3.94	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe Seq ID No:	Exon seq ID No:	ORF seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Score	Top Hit Descriptor
2778	5888	11041	3.84	0.0E+00	AF264760.1	NT	Human sapiens ALR-like protein mRNA, partial cds
2780	6182	11347	2.85	0.0E+00	4503202	NT	Human sapiens cytochrome P450, subfamily 1 (cliochrome), polypeptide 1 (glutucone 3, primary infantile)
2780	6182	11348	2.85	0.0E+00	4503202	NT	Human sapiens cytochrome P450, subfamily 1 (cliochrome), polypeptide 1 (glutucone 3, primary infantile)
2797	7854	13120	2.93	0.0E+00	JX85880.1	NT	Human sapiens serine hydroxymethyltransferase pseudogene
2798	7855		1.43	0.0E+00	AFU88624.1	NT	Human sapiens 5'-aminoimidazole carboxamide synthase 2 (ALAS2) gene, complete cds
2800	7957		1.28	0.0E+00	AB0540960.1	NT	Human sapiens mRNA for KIAA1527 protein, partial cds
2807	7883		1.07	0.0E+00	AJ238852.1	NT	Human sapiens partial rp3 gene for ribosomal protein L3, U82 snRNA, U83a snRNA and U83b snRNA genes
2808	7894	13125	2.44	0.0E+00	AL163201.2	NT	Human sapiens chromosome 21 segment HS21C001
2812	7858	13128	5.27	0.0E+00	ME80902.1	NT	Human ANNAK nucleoprotein mRNA, 5' end
2816	7971	13130	1.01	0.0E+00	BE154504.1	EST HUMAN	PM00-H10343-281289-003-802 H10343 Human sapiens cDNA
2816	7971	13131	1.01	0.0E+00	BE154504.1	EST HUMAN	PM00-H10343-281289-003-802 H10343 Human sapiens cDNA
2817	7973		1.91	0.0E+00	XK73428.1	NT	Human sapiens lsd3 gene for HLH type transcription factor
2819	7975		2.62	0.0E+00	AL163208.2	NT	Human sapiens chromosome 21 segment HS21C008
2820	7976	13134	1.39	0.0E+00	7018584	NT	Human sapiens zinc finger protein 221 (ZNF221), mRNA
2820	7978	13135	1.39	0.0E+00	7018584	NT	Human sapiens zinc finger protein 221 (ZNF221), mRNA
2820	7978	13136	1.39	0.0E+00	7018584	NT	Human sapiens zinc finger protein 221 (ZNF221), mRNA
2826	7881	13142	46.48	0.0E+00	DS0657.1	NT	Human sapiens Gamma-cytoplasmic actin (ACTGP3) pseudogene
2829	7881	13143	45.48	0.0E+00	DS0657.1	NT	Human sapiens Gamma-cytoplasmic actin (ACTGP3) pseudogene
2830	7885	13146	3.23	0.0E+00	ALD968857.1	NT	None human mRNA from chromosome 1, which has similarities to BA12 genes
2831	7888		5.71	0.0E+00	Y10858.1	NT	Human sapiens mRNA for nuclear DNA helicase II
2832	7887		1.11	0.0E+00	AF152303.1	NT	Human sapiens proto-oncogene alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2833	7888	13147	89.88	0.0E+00	4503470	NT	Human sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1A1) mRNA
2833	7888	13148	89.88	0.0E+00	4503470	NT	Human sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1A1) mRNA
2848	8001	13161	2.44	0.0E+00	4507280	NT	Human sapiens serine/threonine kinase 9 (STK9) mRNA
2849	8004	13165	1.2	0.0E+00	AL047689.1	EST HUMAN	DKFZp588G0821-17 986 (synonym: hub1) Human sapiens cDNA clone DKFZp588G0821
2850	8005	13168	0.93	0.0E+00	7881983	NT	Human sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA
2850	8016	13167	0.93	0.0E+00	7881983	NT	Human sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA
2851	8019		1.65	0.0E+00	4503098	NT	Human sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2854	8019	13169	6.69	0.0E+00	BE081896.1	EST HUMAN	Q12-B10636-130400-138-h03 B10636 Human sapiens cDNA
2854	8019	13170	6.69	0.0E+00	BE081896.1	EST HUMAN	Q12-B10636-130400-138-h03 B10636 Human sapiens cDNA
2859	8014	13178	0.82	0.0E+00	6806318	NT	Human sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2859	8014	13179	0.82	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2860	8017	13183	2	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2862	8017	13184	2	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2865	8023		3.71	0.0E+00	Y18210.1	NT	Homo sapiens <i>hhb5</i> gene for hair keratin, exon 1 to 8
2872	8028	13183	1.05	0.0E+00	4768278	NT	Homo sapiens EphA4 (EPHA4) mRNA
2874	8028	13185	42.84	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1A1) mRNA
2875	8029	13197	0.98	0.0E+00	AI561002.1	EST_HUMAN	In 18d07_X1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE2167881 3' similar to TR:O16247
2876	8029	13198	0.98	0.0E+00	AI561002.1	EST_HUMAN	In 18d07_X1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE2167881 3' similar to TR:O16247
2878	8030	13189	1.47	0.0E+00	P32740	SWISSPROT	ZINC FINGER PROTEIN_132
2877	8031	13200	0.95	0.0E+00	AF152338.1	NT	Homo sapiens proteobetaein gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2883	8047	13212	1.7	0.0E+00	AB033098.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2883	8047	13213	1.7	0.0E+00	AB033098.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2884	8049	13214	5.83	0.0E+00	ABD40944.1	NT	Homo sapiens mRNA for KIAA1608 protein, partial cds
2884	8049	13215	5.83	0.0E+00	ABD40944.1	NT	Homo sapiens mRNA for KIAA1608 protein, partial cds
2887	8051	13218	3.65	0.0E+00	7681803	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2887	8051	13219	3.55	0.0E+00	7681803	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2888	8052	13220	3.81	0.0E+00	6174574	NT	Homo sapiens myeloid lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to 4q13 (MLLT4) mRNA
2888	8052	13221	3.61	0.0E+00	6174574	NT	Homo sapiens myeloid lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to 4q13 (MLLT4) mRNA
2893	8053	13225	1.18	0.0E+00	BF110702.1	EST_HUMAN	7n40d03_X1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE3387028 3' similar to TR:Q8VLN1
2893	8053	13226	1.18	0.0E+00	BF110702.1	EST_HUMAN	7n40d03_X1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE3387028 3' similar to TR:Q8VLN1
2903	8065	13237	2.63	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2911	8065	13238	2.63	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2920	8074	13244	1.53	0.0E+00	4768237	NT	Homo sapiens neurotrophin III (NFON3) mRNA
2921	8075		0.89	0.0E+00	XKB484.1	NT	H. sapiens mRNA for M phase phosphoprotein 10
2924	8078	13247	1.5	0.0E+00	AB033094.1	NT	Homo sapiens mRNA for KIAA1288 protein, partial cds
2927	8081	13249	8.58	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 4 (ILT4c) gene, exon 6
2943	8097		0.88	0.0E+00	AI149889.1	EST_HUMAN	Q43699_X1 Scores_tests_NH-T Homo sapiens cDNA clone IMAGE1762889 3'
2951	8105	13270	2.42	0.0E+00	AB044884.1	NT	Homo sapiens mRNA for PRU-alpha, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar ('Top') BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2882	8116	13278	1.8	0.0E+00	7682273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
2883	8117	13279	2.04	0.0E+00	5729735	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2885	8117	13286	2.04	0.0E+00	6729765	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2887	8121	13286	1.1	0.0E+00	AB037852.1	NT	Homo sapiens mRNA for KIAA1481 protein, partial cds
2897	8126	13282	0.78	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2975	8128	13283	0.78	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2888	8153		0.67	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21 CO48, Human displacement protein (CCAAAT) mRNA
2899	8154	13319	1.15	0.0E+00	M74098.1	NT	Human displacement protein (CCAAAT) mRNA
3009	8163	13320	0.85	0.0E+00	4506882	NT	Homo sapiens semenogelin I (SEMG1) mRNA
3011	8165	13322	1.09	0.0E+00	AW976288.1	EST_HUMAN	EST388176 MAGE resequencing, MAGN Homo sapiens cDNA
3016	8170		3.92	0.0E+00	AF189553.1	NT	Homo sapiens membrane-bound antimopeptides P (XNPFP2) gene, complete cds
3019	8173	13330	6.99	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3019	8173	13331	6.99	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3021	8175		6.28	0.0E+00	AL369403.1	NT	Isoform 2 of a novel human mRNA from chromosome 22
3025	8179	13335	2.77	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CTF53 (CFT53) mRNA, partial cds
							Homo sapiens transmembrane protein JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha 2$
3028	8182		1.92	0.0E+00	AF188779.1	NT	Human $\beta$ -myosin heavy chain mRNA, complete cds
3048	8202	13358	3.16	0.0E+00	203628.1	NT	Human $\gamma$ -myosin heavy chain C region (Ig-L-C16.1)
3054	8207		1.54	0.0E+00	AF188365.1	NT	Homo sapiens F-box protein FB15 (FB15) mRNA, complete cds
3058	8211	13365	1.43	0.0E+00	AF046589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-E-C1) gene, complete cds
3082	8235	13385	4.26	0.0E+00	AF2265203.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3083	8236	13386	5.02	0.0E+00	AF148773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3088	8241	13390	3.23	0.0E+00	7682139	NT	Homo sapiens KIAA0468 gene product (KIAA0468), mRNA
3089	8242	13391	1.32	0.0E+00	AF042076.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-0110 allele, partial cds
3119	8271	13427	3.27	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3128	8280	13436	50.69	0.0E+00	L20841.1	NT	Human ferritin heavy chain mRNA, complete cds
3132	8283	13439	1.16	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3132	8283	13440	1.16	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3139	8290	13447	22.17	0.0E+00	T84870.1	EST_HUMAN	y632fb3 5' Strategene lung #867210 Homo sapiens cDNA clone IMAGE:118453 5' similar to SP:S:28539
3155	8306	13468	1.16	0.0E+00	BF242336.1	EST_HUMAN	S28539 BASIC PROTEIN_23K -;
3157	8309	13467	1.08	0.0E+00	AB958086.1	EST_HUMAN	wu112n10_x1 NCI_OGAP_GCB_Homo sapiens cDNA clone IMAGE:2516803 3'

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Probe SEQ ID NO:	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3162	8313	13474	4.29	0.0E+00	X088922.1	NT	Homo sapiens mRNA for gamma-glutamyltransferase
3162	8313	13473	4.29	0.0E+00	X088922.1	NT	Homo sapiens mRNA for gamma-glutamyltransferase
3184	8318	13477	1.37	0.0E+00	AI685850.1	EST_HUMAN	It38903_X NC_ CGAP_P728 Homo sapiens cDNA clone IMAGE:2253376 3' similar to SW:RASD_DICDI
3176	8327	13480	1.73	0.0E+00	475827	NT	Homo sapiens neutrophil III (NFXN3) mRNA
3176	8327	13491	1.73	0.0E+00	475827	NT	Homo sapiens neutrophil III (NFXN3) mRNA
3183	8334	13497	8.18	0.0E+00	4504658	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3202	8353	13515	6.29	0.0E+00	M22669.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NP23) mRNA, complete cds
3205	8358	13517	2.68	0.0E+00	4802988	NT	Homo sapiens solute carrier family 28 (mitochondrial carrier, adenine nucleotide translocator), member 6 (SLC28A5), nuclear gene encoding mitochondrial protein, mRNA
9211	8362	13525	0.79	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rabbitstein-Taylor syndrome) (CREBBP) mRNA
9211	8362	13526	0.79	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rabbitstein-Taylor syndrome) (CREBBP) mRNA
3213	8384	13527	34.87	0.0E+00	AA774783.1	EST_HUMAN	aa87b11_61 Stratagene ochzo brain S111 Homo sapiens cDNA clone IMAGE:971133 3'
3221	8372	13535	6.57	0.0E+00	AF286588.1	NT	Homo sapiens angiostatin binding protein 1 mRNA, complete cds
3221	8372	13536	6.57	0.0E+00	AF286588.1	NT	Homo sapiens angiostatin binding protein 1 mRNA, complete cds
3231	8381	13541	1.18	0.0E+00	4557580	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3238	8393	13548	0.92	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3244	8394	13658	1.1	0.0E+00	AF018413.1	NT	Homo sapiens HLA class II region containing tenascin-X (tenascin-X) gene, partial cds; orthochromosome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W1), RD, complement factor B (B), and complement component C2 (C2) genes?
3247	8397	13559	4.03	0.0E+00	AF055084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3250	8400	13561	1.25	0.0E+00	7682126	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3250	8400	13562	1.25	0.0E+00	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3258	10304	13569	2.51	0.0E+00	4602014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3268	10304	13570	2.61	0.0E+00	4602014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3274	8423	13584	3.1	0.0E+00	AF265203.1	NT	Homo sapiens SWI-SNF complex p270 mRNA, partial cds
3276	8424	13585	1.83	0.0E+00	8922624	NT	Homo sapiens hypothetical protein FLJ202695 (FLJ202695), mRNA
3285	8442	13604	0.67	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3305	8452	13614	4.47	0.0E+00	AI689294.1	EST_HUMAN	tr68103_42_X NC_ CGAP_Pant Homo sapiens cDNA clone IMAGE:2222535 3' similar to SW:RL11_RAT_P25121_60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element
3313	8460	13622	2.76	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
3313	8460	13623	2.76	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
3314	8461	13624	1.06	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA
3314	8461	13625	1.06	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit No.	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3317	8484	136277	2.12	0.0E+00	4502582	NT	Homo sapiens caspase-8, apoptosis-related cysteine protease (CASP8) mRNA	
3317	8484	136283	2.12	0.0E+00	4602582	NT	Homo sapiens caspase-8, apoptosis-related cysteine protease (CASP8) mRNA	
3320	8467	13630	10.6	0.0E+00	AF111633.1	NT	Homo sapiens pyruvate/MEFV genes, complete cds	
3322	8468	13632	1.76	0.0E+00	AB049940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds	
3326	8475	13638	0.62	0.0E+00	BE7780339.1	EST_HUMAN	CD146485FI_NIH_MSC_07 Homo sapiens cDNA clone IMAGE:3682465	
3338	8485	13651	0.74	0.0E+00	AB32569.1	EST_HUMAN	WB10104_X1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR-C081928 Q91929	ZINC FINGER PROTEIN_;
3377	8522	13688	6.65	0.0E+00	AL122684 NT2RM2Homo sapiens cDNA clone NT2RM2000735 5'	EST_HUMAN	AL122684 NT2RM2Homo sapiens cDNA clone NT2RM2000735 5'	
3384	8528	13689	0.88	0.0E+00	7363438	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1) mRNA	
3384	8528	13690	0.88	0.0E+00	7363438	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1) mRNA	
3387	8531	13692	1.89	0.0E+00	7706239	NT	Homo sapiens neurofibromatosis-1 amplified protein (LOC51584), mRNA	
3388	8532	13693	1.14	0.0E+00	AF211188.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1a isoform (CACNA1I) mRNA, complete cds	
3389	8537	13701	1.12	0.0E+00	AW887015.1	EST_HUMAN	MR1-SN033-10040-001-008 SN033 Homo sapiens cDNA	
3408	8549	13707	1.44	0.0E+00	7682401	NT	Homo sapiens KIAA0852 protein (KIAA0852) mRNA	
3408	8549	13708	1.44	0.0E+00	7682401	NT	Homo sapiens KIAA0852 protein (KIAA0852) mRNA	
3407	8550	13709	1.16	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filenin (BFSP1) mRNA	
3409	8552	13710	1.95	0.0E+00	6803067	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHIL1) gene, complete cds	
3418	7790	13940	1.48	0.0E+00	AF110763.1	NT	Homo sapiens death receptor 8 (DR8), mRNA	
3423	8563	13723	1.85	0.0E+00	7857038	NT	Homo sapiens mRNA for rapa-2 (rapa gene)	
3426	8563	13728	1.19	0.0E+00	AF277278.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)	
3427	8568	13729	4.88	0.0E+00	IC02380.1	NT	Bacteriophage PI replication region including rapA, rapB genes and IncC, IncB, and IncC incompatibility determinants	
3428	8571	13731	1.17	0.0E+00	7427622	NT	Homo sapiens protein tyrosine phosphatase, receptor type T (PTPRT), mRNA	
3437	8579	13738	4.18	0.0E+00	AB325159.1	EST_HUMAN	WP14610_X1 NCI CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR-O73634 073634 NEURAL CELL ADHESION MOLECULE_;	
3437	8579	13739	4.18	0.0E+00	AB325159.1	EST_HUMAN	WP14610_X1 NCI CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR-O73634 073634 NEURAL CELL ADHESION MOLECULE_;	
9441	8583	13744	2.5	0.0E+00	AF278120.1	NT	Homo sapiens protein tyrosine-phosphatase containing protein (ORF1)	
3447	8589	13752	4.5	0.0E+00	6852332	NT	Homo sapiens Mu-tos_FEU murine osteosarcoma viral oncogene homolog (FOS), mRNA	
3447	8589	13763	4.5	0.0E+00	6852332	NT	Homo sapiens Mu-tos_FEU murine osteosarcoma viral oncogene homolog (FOS), mRNA	
9453	8595	13769	1.7	0.0E+00	MN14123.1	NT	Human endogenous retrovirus HERV-K10	

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Probe SEQ ID NO:	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar BLASTE Value	Top Hit No.	Top Hit Database Source	Top Hit Descriptor
3468	8600	13764	5.67	0.0E+00	U43268.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3463	8605	13768	0.88	0.0E+00	8558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3463	8605	13769	0.86	0.0E+00	8558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3467	8609	13774	2.45	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3467	8609	13775	2.45	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3474	8616	13783	0.97	0.0E+00	AF231822.1	NT	Homo sapiens chromosome 21 unknown mRNA
3479	8620	13785	1.12	0.0E+00	AJ01070.1	NT	Homo sapiens hydron gene, exons 1-50
3481	8622	13787	1.1	0.0E+00	AA628687.1	EST_HUMAN	ab51112.1 Strategene lung carcinoma S37218 Homo sapiens cDNA clone IMAGE:844387 6'
3481	8622	13788	1.1	0.0E+00	AA628687.1	EST_HUMAN	ab51112.1 Strategene lung carcinoma S37218 Homo sapiens cDNA clone IMAGE:844387 6'
3481	8622	13789	1.1	0.0E+00	AA628687.1	EST_HUMAN	ab51112.1 Strategene lung carcinoma S37218 Homo sapiens cDNA clone IMAGE:844387 6'
3485	8626	13783	1.02	0.0E+00	450828	NT	Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRA8) domain polypeptide) (ZNF45) mRNA
3488	8629	13785	2.4	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_3T3
3488	8629	13786	2.4	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_3T3
3492	8633	13800	0.89	0.0E+00	4826785	NT	Homo sapiens potassium voltage-gated channel, Iso-related family, member 2 (KCNE2) mRNA
3495	8636	13803	1.52	0.0E+00	DT4887	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HAC2303)
3499	8640	13808	0.82	0.0E+00	AJ384007.1	EST_HUMAN	1835q12.1 Scores_NHMMPU_S1 Homo sapiens cDNA clone IMAGE:2088742 3 similar to TR-C08498
3502	8643	13809	1.25	0.0E+00	AB09785.1	NT	Homo sapiens endogenous retroviral DNA (ER) 1, complete retroviral segment
3619	8660	13827	0.77	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3519	8670	13828	0.77	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3625	8678	13834	1.13	0.0E+00	AB028619.1	NT	Homo sapiens mRNA for KIAA0589 protein, partial cds
3528	8670	13835	1.20	0.0E+00	AV701869.1	EST_HUMAN	AV701869 ADB_Homo sapiens cDNA clone AD05DAH03 6'
3629	8671	13836	0.87	0.0E+00	4806884	NT	Homo sapiens semenogelin II (SEMG2) mRNA
3631	8673		2.24	0.0E+00	AF078888.1	NT	Homo sapiens homologous yeast 44.2 protein mRNA, complete cds
3639	8681	13844	0.98	0.0E+00	AL38204.1	NT	Novel human gene mapping to chromosome X
3541	8682	13845	1.16	0.0E+00	AB0540609.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
3551	8682	13854	2.08	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
3561	8702	13862	1.08	0.0E+00	6397248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
9561	8702	13863	1.09	0.0E+00	6397249	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3562	8703		1.39	0.0E+00	AJ081807.1	EST_HUMAN	cX77c11.1 Scores_NHMMPU_S1 Homo sapiens cDNA clone IMAGE:1662356 3 similar to WPT18B4.4 CE:13742;
3664	8705	13866	1.09	0.0E+00	6325483	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTNSA3), mRNA
3569	8710		4.53	0.0E+00	AW852217.1	EST_HUMAN	QVO-C70226-230300-168-e01 C70226 Homo sapiens cDNA

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 Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3576	8717			0.82	0.0E+00 AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GCLC) gene, partial cds
3577	8718	13875		0.8	0.0E+00 BF676393.1	EST_HUMAN	60208583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:2246538 5'
3588	8728	13985		1.05	0.0E+00 AW831977.1	EST_HUMAN	QVD-DT0047-170201-12-0-U1 DT0047 Homo sapiens cDNA
3588	8727	13989		1.23	0.0E+00 BF672054.1	EST_HUMAN	602162488F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:1283645 5'
3588	8737	13981		1.23	0.0E+00 BF672054.1	EST_HUMAN	602162488F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:1283645 5'
3589	8738			1.31	0.0E+00 48263957	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3601	8740	13893		0.72	0.0E+00 AW684683.1	EST_HUMAN	h1B4g01.1 Socres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2318024 3'
3603	8742	13896		0.72	0.0E+00 AW684683.1	EST_HUMAN	h1B4g01.1 Socres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2318024 3'
3605	8744	13899		0.71	0.0E+00 48267683	NT	Homo sapiens heparan sulfate (glucosaminuria) 3-O-sulfotransf erase 1 (HSST1) mRNA
3610	8749	13905		1.08	0.0E+00 7682319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3610	8749	13908		1.19	0.0E+00 4557752	NT	Homo sapiens midline 1 (OptizBBB syndrome) (MID1) mRNA
3625	8764	13918		2.89	0.0E+00 D87327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3628	8767			38.83	0.0E+00 7689491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3644	8783	13857		4.72	0.0E+00 AB028542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3646	8785	13859		1.12	0.0E+00 AB007886.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3648	8787	13840		4.08	0.0E+00 AF124260.1	NT	Homo sapiens SH2-containing protein Nap2 mRNA, complete cds
3648	8787	13941		4.08	0.0E+00 AF124260.1	NT	Homo sapiens SH2-containing protein Nap2 mRNA, complete cds
3657	8788	13851		1.69	0.0E+00 AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3657	8786	13852		1.69	0.0E+00 AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3680	8799	13895		1.22	0.0E+00 AW851714.1	EST_HUMAN	MR2-O70222-281089-005-e05 C70222 Homo sapiens cDNA
3682	8801	13857		2.18	0.0E+00 5729228	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3684	8803	13959		1.06	0.0E+00 AB018339.1	NT	Homo sapiens mRNA for KIAA0786 protein, partial cds
3686	8805	13861		1.62	0.0E+00 O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HAC2303)
3688	8807	13863		1.16	0.0E+00 7682237	NT	Homo sapiens KIAA0370 protein (KIAA0370), mRNA
3688	8807	13984		1.15	0.0E+00 7682237	NT	Homo sapiens KIAA0370 protein (KIAA0370), mRNA
3682	8821	13976		4.6	0.0E+00 AW286134.1	EST_HUMAN	U1-H-BW0-48s-e-12-0-U1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:2733022 3'
3682	8821	13977		4.6	0.0E+00 AW286134.1	EST_HUMAN	U1-H-BW0-48s-e-12-0-U1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:2733022 3'
3710	8848	14002		1	0.0E+00 AB004630.1	NT	Human beta-fa Type XX collagen extr chain, exon 6
3711	8849	14003		0.9	0.0E+00 AA483859.1	EST_HUMAN	ectB4g01.1 Socres_Nhhu/Pu_S1 Homo sapiens cDNA clone IMAGE:812498 5' terminal to SWKB84 SHEEP PC2445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4, [1];
3718	8854	14008		1.3	0.0E+00 AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
3719	8857	14010		3.8	0.0E+00 7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121), mRNA
3728	8855	14019		0.92	0.0E+00 AB037885.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds

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**Table 4**  
**Single Exon Probes Expressed in BT474 Cells**

Probe Seq ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3740	8878	14029	6.49	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3748	8881	14032	35.82	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3751	8888	14038	1.22	0.0E+00	7657085	NT	Homo sapiens wnts avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3761	8889	14039	1.22	0.0E+00	7657085	NT	Homo sapiens wnts avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3788	8895		0.95	0.0E+00	AF188658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3789	8896	14082	2.6	0.0E+00	AF179133.1	NT	Pan troglodytes effector receptor (PTEN206) gene, partial cds
3802	8898	14088	2.11	0.0E+00	7687488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3802	8899	14087	2.11	0.0E+00	7687488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3803	8940	14088	1.31	0.0E+00	AF020691.1	NT	Homo sapiens smooth muscle myosin heavy chain SMM mRNA, alternatively spliced, partial cds
3807	8944	14083	1.23	0.0E+00	4759011	NT	Homo sapiens RAB9, member RAS oncogene family (RAB9) mRNA
3810	8947	14098	1.29	0.0E+00	AF152496.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3811	8948	14098	3.61	0.0E+00	4758198	NT	Homo sapiens desmoplakin (DPL) (DPL) mRNA
3814	8951	14099	20.71	0.0E+00	579685.1	NT	Homo sapiens ATP-sensitive inward rectifying K-channel subunit (KCNC1/BIR1) gene, complete cds
3816	8953	14101	2.23	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3817	8954	14102	0.85	0.0E+00	7662183	NT	Homo sapiens KCNA0569 gene product (KIAA0569), mRNA
3820	8957	14104	0.95	0.0E+00	AF069801.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3820	8957	14105	0.95	0.0E+00	AF069801.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3821	8961	14110	0.95	0.0E+00	AB001623.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3825	8961	14111	0.93	0.0E+00	AB001623.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3825	8964	14115	0.7	0.0E+00	6912135	NT	Homo sapiens transient receptor potential channel 5 (TRPC5) mRNA
3828	8964	14123	6.38	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3833	8969	14123	6.38	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3835	8971	14127	4.16	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3836	8972	14128	0.87	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITS) mRNA, complete cds
3839	8976	14130	1.24	0.0E+00	4826783	NT	Homo sapiens voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3842	8978	14133	0.91	0.0E+00	AF012815.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3842	8979	14134	2.52	0.0E+00	475971	NT	Homo sapiens SC35 interacting protein 1 (SPRP12), mRNA
3845	8981	14138	0.5	0.0E+00	AF098117.1	NT	WtQ101.X1 NC1 CGAP_Lyn12 Homo sapiens cDNA clone IMAGE2411065.3 similar to TR-033340
3853	8989	14145	2.76	0.0E+00	A1884727.1	EST_HUMAN	Hom sapiens SC35 interacting protein 1 (SPRP12), mRNA
3856	8992	14149	13.45	0.0E+00	4506742	NT	Hom sapiens ribosomal protein 58 (RPS5), mRNA
3860	8998	14153	1.84	0.0E+00	AL040388.1	EST_HUMAN	DKFZp434N0413_1 (434) Homo sapiens cDNA clone DKFZp434N0413_1

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 Table 4  
 Single Exon Probes Expressed In BT474 Cells

Probe Seq ID No.	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar BLAST E Value	(Top) Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3884	8000	14157	2.4	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3884	8000	14158	2.4	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3888	9002	14160	2.09	0.0E+00	4504138	NT	Homo sapiens glutamate receptor, metabotropic 3 (GFRN3) mRNA
3888	9004			1.7	0.0E+00	4505078	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3888	8006	14164	1.22	0.0E+00	AF148412.1	NT	Homo sapiens HBP77 heparin-binding protein gene, complete cds
3872	8006			1.65	0.0E+00	4508768	Homo sapiens lymphocyte receptor 3 (LYRF3) mRNA
3881	9017	14174	2.16	0.0E+00	4505862	NT	Homo sapiens zinc finger protein (KA0412) mRNA
3885	8021	14178	3.22	0.0E+00	BF55295.1	EST_HUMAN	RC3-HT0850-170800-011-a12 HT10860 Homo sapiens cDNA
3890	8026	14184					MXRAS Human mitch, tissue expression library Homo sapiens cDNA clone Incyte 1808726 similar to MXRAS
3891	9027	14185	2.82	0.0E+00	AW888221.1	EST_HUMAN	Matrix remodeling associated gene 5
3891	8027	14188	2.62	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1808726 similar to MXRAS
3899	8035	14194	1.69	0.0E+00	AF128533.1	NT	Matrix remodeling associated gene 5
3902	9038	14197	0.83	0.0E+00	U88281.1	NT	Homo sapiens F-box protein FBXb (FBXb) mRNA, partial cds
3902	9038	14198	0.83	0.0E+00	U88281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3905	8041	14201	3.91	0.0E+00	BE378602.1	EST_HUMAN	Homo sapiens MGE_44 Homo sapiens cDNA clone IMAGE:3608800 6
3913	9049	14208	1.33	0.0E+00	AW680740.1	EST_HUMAN	6012358657 Nil_MGE_44 Homo sapiens cDNA clone IMAGE:3608800 6
3948	9083	14235	4.18	0.0E+00	AF116186.1	NT	PMS-LT0031-100100-003-h09 LT0031 Homo sapiens cDNA
3948	9083	14236	4.18	0.0E+00	AF116186.1	NT	PMS-LT0031-100100-003-h09 LT0031 Homo sapiens cDNA
3969	8094			3.65	0.0E+00	M23910.1	PM3-LT0031-100100-003-h09 LT0031 Homo sapiens cDNA
3962	9097			5.73	0.0E+00	AL1633103.2	NT
3972	9103	14254	2.87	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21 CG088
3980	9114	14262	2.12	0.0E+00	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21 CG088
3983	9127			79.42	0.0E+00	4803470	NT
3997	9131			1.28	0.0E+00	AI857078.1	EST_HUMAN
4000	9133	14277	2.32	0.0E+00	U08366.1	NT	Human zinc finger protein ZNF-333
4020	9162	14286	8.2	0.0E+00	AB016610.1	NT	Chlorococculus acutifolius mRNA for ribosomal protein S4X, complete cds
4029	9160			3.39	0.0E+00	AJ238017.1	Homo sapiens mRNA for UQA suppressor (RNA-associated antigenic protein (RNAAs) gene)
4041	9172	14313	2.42	0.0E+00	AL163203.2	NT	Homo sapiens mRNA for repa-2 (repa gene)
4042	9173	14314	2.68	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for repa-2 (repa gene)
4042	9173	14315	2.68	0.0E+00	AJ277276.1	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4048	9180	14321	7.15	0.0E+00	5032028	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4049	9180	14322	7.15	0.0E+00	5032028	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar ("top") Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4081	8192	14333	0.87	0.0E+00	4503914	NT	Human sapiens phosphatidylinositol glycan anchor biosynthesis, phosphatidylinositol glycan anchor biosynthesis, phosphatidylinositol/glycanide synthetase, phosphatidylinositol-mannosidase synthetase (GART) mRNA
4083	8198	14335	4.93	0.0E+00	4885095	NT	Human sapiens G protein-coupled receptor 21 (GPR21), mRNA
4087	8197	14336	1.34	0.0E+00	AB005626.1	NT	Human sapiens mRNA for KIAA0287 gene, partial cds
4070	8200	14337	7.7	0.0E+00	11418287	NT	Human sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4071	8201	14338	4.23	0.0E+00	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BA/T2 genes
4078	8208	14346	3.09	0.0E+00	AF1866227.1	NT	Human sapiens DGCR8 (DGCR8) mRNA, complete cds
4087	8270	11433	1.6	0.0E+00	4826347	NT	Human sapiens protein kinase, X-linked (PRKX) mRNA
4087	8270	11434	1.8	0.0E+00	4826347	NT	Human sapiens protein kinase, X-linked (PRKX) mRNA
4091	8220	14353	1.34	0.0E+00	4803854	NT	Human sapiens GA-binding protein transcription factor, alpha subunit (GαD) (GABPA), mRNA
4091	8220	14357	1.34	0.0E+00	4803854	NT	Human sapiens GA-binding protein transcription factor, alpha subunit (GαD) (GABPA), mRNA
4094	8223	14359	1.34	0.0E+00	85222391	NT	Human sapiens hypothetical protein El_1103179 (El_1103179), mRNA
4094	8223	14360	1.34	0.0E+00	85222391	NT	Human sapiens hypothetical protein El_1103179 (El_1103179), mRNA
4098	8227	14363	0.9	0.0E+00	AB020702.1	NT	Human sapiens mRNA for KIAA0858 protein, partial cds
4104	8233	14370	4.5	0.0E+00	AI882587.1	EST_HUMAN	WU04404_X1_NCI_CGAP_GCG_Homo sapiens cDNA clone IMAGE:2515975_3'
4104	8233	14371	4.5	0.0E+00	AI882587.1	EST_HUMAN	WU04404_X1_NCI_CGAP_GCG_Homo sapiens cDNA clone IMAGE:2515975_3'
4107	8235	14373	1.23	0.0E+00	BE184856.1	EST_HUMAN	MRI-H107-100500-001-002 HT0707 Homo sapiens cDNA
4107	8235	14374	1.33	0.0E+00	BE184856.1	EST_HUMAN	MRI-H107-100500-001-002 HT0707 Homo sapiens cDNA
4112	8240		3.90	0.0E+00	BE274217.1	EST_HUMAN	601120778F_NIH_MGC_20_Homo sapiens cDNA clone IMAGE:2887680_5'
4117	8245	14381	4.44	0.0E+00	AB032851.1	NT	Human sapiens mRNA for KIAA1126 protein, partial cds
4117	8245	14382	4.44	0.0E+00	AB032851.1	NT	Human sapiens mRNA for KIAA1126 protein, partial cds
4118	8247	14384	0.92	0.0E+00	4507478	NT	Human sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-delta amide transferase) (TGMS) mRNA
4120	8248	14385	3.12	0.0E+00	5728725	NT	Human sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4128	8258		5.44	0.0E+00	AW876699.1	EST_HUMAN	Q85104_X1_NIH_MGC_10_Homo sapiens cDNA clone IMAGE:28000385 3' similar to SW:THI2_BOVIN
4133	8251	14389	1.02	0.0E+00	AW408788.1	EST_HUMAN	Q85108_NITROCHONDRIAL THIOREDOXIN PRECURSOR.
4134	8262	14400	1.84	0.0E+00	85222486	NT	Human sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
4134	8262	14401	1.84	0.0E+00	85222486	NT	Human sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
4143	8271		2.37	0.0E+00	6174832	NT	Human sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, ova utrin
4165	9281	14417	0.89	0.0E+00	AB037738.1	NT	Human sapiens mRNA for KIAA1318 protein, partial cds
4163	9289	14424	9.44	0.0E+00	AA401438.1	EST_HUMAN	ZU68107_51_Socres testis_NH1_Homo sapiens cDNA clone IMAGE:743197 3' similar to contains AU repetitive element contains element MER25 repetitive element;

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4163 9289	14425	Q44	0.0E+00	AA401438.1	EST_HUMAN	2168707_s1 Scores_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Ali repetitive element;contains element MER35 repetitive element;	
4167 9293	14431	1.16	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds	
4161 9307	14444	1.22	0.0E+00	7652125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA	
4183 5216	10328	1.12	0.0E+00	AA228128.1	EST_HUMAN	2758504_r1 Scores_NhMPU_S1 Homo sapiens cDNA clone IMAGE:887690 5' similar to TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;	
4163 5216	10329	1.12	0.0E+00	AA228128.1	EST_HUMAN	2758504_r1 Scores_NhMPU_S1 Homo sapiens cDNA clone IMAGE:887690 5' similar to TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XI COLLAGEN ;	
4168 8821	14463	1.21	0.0E+00	7681869	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA	
4169 8824	14454	13.69	0.0E+00	4768159	NT	Homo sapiens desmodakin (DP1, DPII) (DSP) mRNA	
4169 8824	14455	13.69	0.0E+00	4768159	NT	Homo sapiens desmodakin (DP1, DPII) (DSP) mRNA	
4208 8833		0.85	0.0E+00	AI163903.2	NT	Homo sapiens dihydrotestosterone 21' reductase HS2TC1Q3	
4233 8858	14490	1.07	0.0E+00	AJ010770.1	NT	Homo sapiens hyponine gene, exons 1-50	
4247 8872	14605	4.01	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds	
4262 8887	146524	1.06	0.0E+00	AW866689.1	EST_HUMAN	PM2DT0023-08350-004-008 D10223 Homo sapiens cDNA	
4267 8475	136338	0.6	0.0E+00	BE779039.1	EST_HUMAN	801464985F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3858246 5'	
4271 8385	146334	4.78	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein FB4 (FB4) mRNA, partial cds	
4279 9402	146441	0.84	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	
4279 9402	146442	0.84	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	
4280 9403		2.49	0.0E+00	AI168944.1	EST_HUMAN	q023108_r1 Scores_porcine_beta2microglobulin_Homo sapiens cDNA clone IMAGE:1724579 3' similar to contains MER20_b2 MER20 repetitive element;	
4284 9406		4.17	0.0E+00	U14520.1	NT	Human CBF43 (Cbfac) gene, partial cds	
4287 9409	146445	1.04	0.0E+00	5174674	NT	Homo sapiens myeloid lymphoid or mixed lineage leukaemia (Drosophila) homolog; translocated to 4q11.2	
4288 9418	146511	0.81	0.0E+00	4505848	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA	
4302 9424	146559	1.01	0.0E+00	6953384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA	
4303 9430	146559	1.01	0.0E+00	6953384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA	
4308 9430	146833	1.11	0.0E+00	U10891.1	NT	Human G2 protein mRNA, partial cds	
4318 9440	146888	1.11	0.0E+00	U10891.1	NT	Human G2 protein mRNA, partial cds	
4338 9460		8.58	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA	
4343 9465	14601	1.1	0.0E+00	AF165947.2	NT	Human Ig light chain V1 region germline (human) gene, partial cds	
4349 9471	14608	1.31	0.0E+00	U03801.1	NT	Human plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds	

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Table 4.

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Sources	Top Hit Descriptor
4353	9475	14813	4.82	0.0E+00	Z50780.1	NT	H_sapiens H2Bf1 gene
4353	9475	14814	4.82	0.0E+00	Z50780.1	NT	H_sapiens H2Bf1 gene
4354	9476	14815	1.17	0.0E+00	AW168933.1	EST_HUMAN	ZINC FINGER PROTEIN 64;
4360	9482	14821	1.65	0.0E+00	X60483.1	NT	H_sapiens H4a gene for H4 histone
4360	9482	14822	1.55	0.0E+00	X60483.1	NT	H_sapiens H4a genes for H4 histone
4368	9488	14823	8.91	0.0E+00	768291	NT	Homo sapiens KIAA0380 gene product (KIAA0380), mRNA
4368	9488	14829	8.91	0.0E+00	768291	NT	Homo sapiens KIAA0380 gene product (KIAA0380), mRNA
4373	9494	14838	1.28	0.0E+00	X62338.1	NT	Homo sapiens Marfan's disease gene, exon 4
4378	9497	14842	15.1	0.0E+00	4886128	NT	Homo sapiens caudal type homeobox transcription factor 4 (CDXA), mRNA
4377	9498	14843	1.48	0.0E+00	A1271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/22
4378	9499	14849	0.98	0.0E+00	A11632017.2	NT	Homo sapiens chromosome 21 segment HS21C007
4381	9502	14845	1.08	0.0E+00	AB037781.1	NT	Homo sapiens mRNA for KIAA1380 protein, partial cds
4410	9530	14870	1.24	0.0E+00	7019458	NT	Homo sapiens myelin regulatory/flight chain interacting protein (MIF), mRNA
4420	9540				AF188953.1	NT	Homo sapiens membrane-bound amineopeptidase P (XNPEP2) gene, complete cds
4429	9548	14884	2.27	0.0E+00	A1249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4428	9548	14885	2.27	0.0E+00	A1249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4430	9549	14891	0.75	0.0E+00	W28178.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4430	9549	14892	0.75	0.0E+00	W28179.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4447	9568				AF220628.1	NT	Homo sapiens HPS1 gene, intron 5
4467	9586				1	0.0E+00	M14123.1
4478	9598	14737	31.08	0.0E+00	AW084884.1	EST_HUMAN	X68603.x1 NC_0382 Homo sapiens cDNA clone IMAGE:2889448 3' similar to SWAHINK_HUMAN
4480	10310		1.72	0.0E+00	8051610	NT	Q108686 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK;
							Homo sapiens LIM domain kinase 2 (LMK2), transcript variant 2a, mRNA
4482	9601	14740	0.61	0.0E+00	AF016050.1	NT	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds
4484	9603				8.23	NT	Homo sapiens chromosome 21 segment HS21C007
4491	9810	14749	1.27	0.0E+00	A1278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4491	9810	14750	1.27	0.0E+00	A1278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4493	9812	14752	1.19	0.0E+00	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4494	9813	14753	2.85	0.0E+00	AF098830.1	NT	Homo sapiens serine-threonine protein kinase (MNKH) mRNA, complete cds
4499	9818	14769	1.01	0.0E+00	4506852	NT	(SIALT8) mRNA
4504	9823	14785	1.14	0.0E+00	S78694.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon

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Table 4  
Single Exon Probes Expressed In BT474 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4505 9824	14766	1.38	0.0E+00	AF111163.1	NT	Human	Human sapiens pyrin (MEFV) gene, complete cds
4606 9824	14767	1.38	0.0E+00	AF111163.1	NT	Human	Human sapiens pyrin (MEFV) gene, complete cds
4612 10311	14775	2.71	0.0E+00	60065673 NT	Human	Human sapiens zinc finger protein 185 (ZNF185) mRNA	
4517 9835	14780	5.83	0.0E+00	AF208181.1	NT	Human	Human sapiens synaptosomal precursor, mRNA, complete cds
4522 8840	14787	1.15	0.0E+00	AF152337.1	NT	Human	Human sapiens proto-oncogene C3 (PCDH-omega-C3) mRNA, complete cds
4625 8843	14791	1.88	0.0E+00	64541765 NT	Human	Human sapiens zinc finger protein 211 (ZNF211) mRNA	
4539 9854	14799	44.34	0.0E+00	4903470 NT	Human	Human sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1A1) mRNA	
4543 9861	14804	0.87	0.0E+00	45050168 NT	Human	Human sapiens low density lipoprotein receptor-related protein 8 (LRP8) mRNA, and translated products	
4547 9866	14807	1.03	0.0E+00	46030688 NT	Human	Human sapiens chondroitin sulfate proteoglycan 4 (matrigamma-associated) (CSPG4), mRNA	
4652 9870	14813	1.48	0.0E+00	45025568 NT	Human	Human sapiens calcineurin/calmodulin-dependent protein kinase IV (CAMK4) mRNA	
4555 9873		1.52	0.0E+00	385871908.1	EST HUMAN	6014473532F1 NIH 3T3	65 Human sapiens cDNA clone IMAGE:385871908.1
4658 9876		2.62	0.0E+00	135485.1	EST HUMAN	6014473532F1 NIH 3T3	65 Human sapiens diuronate sulphatase sulphatase (IDS) gene, complete cds
4560 9878	14816	10.88	0.0E+00	7662091 NT	Human	Human sapiens KIAA0380 gene product (KIAA0380) mRNA	
4560 9878	14817	10.69	0.0E+00	7662091 NT	Human	Human sapiens KIAA0390 gene product (KIAA0390) mRNA	
4575 6693	14830	2.49	0.0E+00	AF143314.1	NT	Human	Human sapiens PTEN (PTEN) gene, exons 3 through 5
4578 9885	14833	10.97	0.0E+00	AJ245418.1	NT	Human	Human sapiens mRNA for G76 protein (G76) gene located in the class III region of the major histocompatibility complex
4578 8698	14834	10.97	0.0E+00	AJ245418.1	NT	Human	Human sapiens mRNA for G76 protein (G76) gene located in the class III region of the major histocompatibility complex
4593 9711		2.31	0.0E+00	AA174072.1	EST HUMAN	2p18q8.51 Stratagene fetal retina 837202 Human sapiens cDNA clone IMAGE:909854 3'	
4595 9713		1.47	0.0E+00	7857410 NT	Human	Human sapiens odc (odd Oz/far-m, Oncopille) homolog 1 (ODZ1), mRNA	
4597 9715		2.4	0.0E+00	AL163284.2	NT	Human	Human sapiens chromosome 21 segment HS21 QDRA
4698 9716	14862	1.38	0.0E+00	AF184110.1	NT	Human	Human sapiens cycliphilin-related protein (NKTR) gene, complete cds
4598 9717	14853	4.87	0.0E+00	AL163300.2	NT	Human	Human sapiens chromosome 21 segment HS21C100
4600 9718		1.71	0.0E+00	AB037621.1	NT	Human	Human sapiens gene for retinoblast protein, partial cds
4602 9720	14854	0.74	0.0E+00	AF186658.1	NT	Human	Human sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4603 9724	14859	0.88	0.0E+00	AB007866.2	NT	Human	Human sapiens mRNA for KIAA0406 protein, partial cds
4609 9727	14863	1.09	0.0E+00	AL162231.1	NT	Neural human	Gene mapping to chromosome 1
4811 9729	14865	30.74	0.0E+00	4657887 NT	Human	Human sapiens keratin 18 (KRT18) mRNA	
4811 9729	14866	30.74	0.0E+00	4657887 NT	Human	Human sapiens keratin 18 (KRT18) mRNA	
4812 9730	14867	2.68	0.0E+00	AF187441.1	NT	Mus musculus	E-cadherin binding protein E1 mRNA, complete cds
4821 9739	14878	0.91	0.0E+00	L78810.1	NT	Human	Human sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4821 9739	14879	0.91	0.0E+00	L78810.1	NT	Human	Human sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds

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 Table 4  
 Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4621	9739	14880	0.81	0.0E+00	U7810.1	NT	Human sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4622	9740	14881	1.18	0.0E+00	AB028970.1	NT	Human sapiens mRNA for KIAA1047 protein, partial cds
4622	9740	14882	1.18	0.0E+00	AB028970.1	NT	Human sapiens mRNA for KIAA1047 protein, partial cds
4623	9747	14892	10.76	0.0E+00	YI8830.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pd and env genes
4636	9753	14890	1.28	0.0E+00	BE091827.1	EST_HUMAN	QV2-B-T0635-16040-142-h05 BT0635 Homo sapiens cDNA clone IMAGE-767605.3
4638	9754	14891	1.42	0.0E+00	AA118246.1	EST_HUMAN	ZG8507.31 Soares_NhHMPU_S1 Homo sapiens cDNA clone IMAGE-767605.3
4645	9761		2.12	0.0E+00	AF086841.1	NT	Human sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4650	9767	14912	2.23	0.0E+00	AB037820.1	NT	Human sapiens mRNA for KIAA1389 protein, partial cds
4650	9767	14913	2.23	0.0E+00	AB037820.1	NT	Human sapiens mRNA for KIAA1389 protein, partial cds
4651	9768	14914	2.34	0.0E+00	M74088.1	NT	Human displacement protein (CCAA1) mRNA
4654	9771	14917	1.02	0.0E+00	AV294801.1	EST_HUMAN	UH-B12-ah1-c-05-0-U1 st NCI CGAP_Sub4 Human sapiens cDNA clone IMAGE-2728702.3'
4654	9771	14918	1.02	0.0E+00	AV294801.1	EST_HUMAN	UH-B12-ah1-c-05-0-U1 st NCI CGAP_Sub4 Human sapiens cDNA clone IMAGE-2728702.3'
4658	9773	14919	2.18	0.0E+00	6453812	NT	Human sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4658	9773	14920	2.18	0.0E+00	6453812	NT	Human sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4658	5332	10477	4.19	0.0E+00	TG5945.1	EST_HUMAN	Y88301.22 Strategene fetal spleen (#837205) Human sapiens cDNA clone IMAGE-883010.5
4658	5332	10478	4.19	0.0E+00	TG5945.1	EST_HUMAN	Y88301.22 Strategene fetal spleen (#837205) Human sapiens cDNA clone IMAGE-883010.5
4681	979	14942	4.68	0.0E+00	MB0902.1	NT	Human AHNAK nucleoprotein mRNA, 6' end
4684	9800	14945	1.91	0.0E+00	MB09197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4684	9800	14946	1.91	0.0E+00	MB09197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4688	9804	14951	1.82	0.0E+00	AF184110.1	NT	Human sapiens cyclodiphilin-related protein (NKTR) gene, complete cds
4689	9805	14952	0.73	0.0E+00	7862479	NT	Human sapiens KIAA1084 protein (KIAA1084), mRNA
4697	9807	14953	2.63	0.0E+00	7862481	NT	Human sapiens KIAA0563 gene product (KIAA0563), mRNA
4697	9813	14961	1.68	0.0E+00	U97663.1	NT	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds
4702	9818	14963	1.18	0.0E+00	AL008857.1	NT	New human mRNA from chromosome 1, which has similarities to BAT2 genes
4709	9825		1.28	0.0E+00	X58467.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D6
4715	9831	14973	1.09	0.0E+00	7304922	NT	Human sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4715	9831	14974	1.09	0.0E+00	7304922	NT	Human sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4725	9838	14982	1.27	0.0E+00	AF025801.1	NT	Human sapiens sigma-3-type IX collagen (COL9A3) gene, promoter region, and exons 1-23
4727	9840	14984	1.04	0.0E+00	687770	NT	Human sapiens G-protein coupled receptor (RE2), mRNA
4727	9840	14985	1.04	0.0E+00	687770	NT	Human sapiens G-protein coupled receptor (RE2), mRNA
4729	9842	14987	0.83	0.0E+00	7018320	NT	Human sapiens protein#0008 (AD013), mRNA
4729	9842	14988	0.83	0.0E+00	7018320	NT	Human sapiens protein#0008 (AD013), mRNA

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Table 4

## Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4753	8888	15015	1.74	0.0E+00	AW44637.1	EST_HUMAN	UH-B13-ew-c-04-U1.st NCI CGAP Subs Homo sapiens cDNA clone [MAGE]2733284 3'
4769	8872	15023	1.41	0.0E+00	AF303134.1	NT	Homo sapiens adenylyl dehydrogenase 12 (ALDH12) mRNA, complete cds
4762	8875		1.63	0.0E+00	AF083242.1	NT	Homo sapiens HSPC0244 iso mRNA, complete cds
4807	8818	15060	1.09	0.0E+00	5901693	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
4810	8922		4.76	0.0E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4814	8928	15067	9.29	0.0E+00	XP87205.1	NT	Mus fasciculata mRNA for metalloproteinase-like, distal segment-like protein, IVa
4818	8928	16069	2.79	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Bauren syndrome deletion transcript 9 (WBSSCR9) mRNA, complete cds
4818	8830	16071	2.11	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4819	8931	16072	4.47	0.0E+00	4803788	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4821	8933	16074	27.4	0.0E+00	4885049	NT	Homo sapiens actin, alpha, cardiac muscle (ACTG), mRNA
4822	8934	15075	1.49	0.0E+00	PS2240	SWISSPROT	ZINC FINGER PROTEIN 12
4824	8928	15077	1.33	0.0E+00	8972180	NT	Human sapiens hypothetical protein DKFZp622e1312 (DKFZp762e1312) mRNA
4827	9939	16081	8.77	0.0E+00	8929080	NT	Human sapiens hypothetical protein FLJ20073 (FLJ20073) mRNA
4831	8943	16085	1.26	0.0E+00	7681979	NT	Human sapiens KIAA0187 gene product (KIAA0187), mRNA
4832	8944	15086	1.01	0.0E+00	MR4081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4832	9944	15087	1.61	0.0E+00	MR4081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4834	9948	16089	1.15	0.0E+00	X946238.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4834	9949	15090	1.15	0.0E+00	XR46238.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4838	9950	15094	2.24	0.0E+00	AL165280.2	NT	Human sapiens chromosome 21 segment H321C080
4840	8952	15097	1.06	0.0E+00	7706804	NT	Human sapiens MAGE-C2 (MAGEC2), mRNA
4848	8980	15104	1.28	0.0E+00	5032150	NT	Human sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28D (TAF2)
4854	8988	15111	0.9	0.0E+00	68008919	NT	Human sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4856	8968	15113	1.3	0.0E+00	XP28241.1	NT	Human sapiens MiCA gene
4858	8970	15116	2.22	0.0E+00	4585842	NT	Human sapiens zinc finger protein (KIAA0412) mRNA
4859	8971	15116	1.23	0.0E+00	AB037854.1	NT	Human sapiens mRNA for KIAA1443 protein, partial cds
4860	9972	15117	0.9	0.0E+00	Y09232.1	NT	Human sapiens ferrulin alpha pseudogene
4861	8973	16118	2.01	0.0E+00	AE014633.1	NT	Human sapiens mRNA for KIAA0833 protein, partial cds
4862	8974	16119	2.39	0.0E+00	8877848	NT	Mus musculus zinc finger protein interacting with K protein 1 (ZIKF1), mRNA
4863	9975	15120	1.5	0.0E+00	5174560	NT	Human sapiens membrane expressed antigen 8 (coiled-coil protein-rich) (MAGEA8), mRNA
4864	9978	15121	2.18	0.0E+00	QY0-EN0147-280400-213-011	EST_HUMAN	BT01147 Homo sapiens cDNA QY0-EN0147-280400-213-011

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**Table 4**  
**Single Exon Probes Expressed in BT474 Cells**

Probe SEQ ID NO:	Exon ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4884 9876	15122	2.16	0.0E+00	BE07836.1	EST_HUMAN	QVO-BN0147-280400-213-011 BN0147 Homo sapiens cDNA
4886 8978	15124	10.15	0.0E+00	4768189	NT	Homo sapiens desmoplakin (DPL, DP1) (DSP) mRNA
4887 8979	15125	1.35	0.0E+00	Y16723.1	NT	Homo sapiens gene encoding filensin, exon 8
4888 8980	15126	1.83	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MAGE4B) mRNA
4889 8980	15127	1.83	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MAGE4B) mRNA
4890 8981	15128	1.42	0.0E+00	7705548	NT	Homo sapiens zinc-finger DNA-binding protein (HUMMOX1) mRNA
4891 8982						Homo sapiens keratin 5/epithelial membrane protein chain, anti-RBD, therad 7
4892 8982						Homo sapiens mRNA for immunoglobulin kappa light chain, anti-RBD, therad 7
4893 8984	15131	6.4	0.0E+00	AF055068.1	NT	Homo sapiens MHC class I region
4894 8985						Homo sapiens gp130 receptor, delta 1 (OPRD1) mRNA
4895 8987	15134	2.08	0.0E+00	4566568	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
4896 8991	15138	2.43	0.0E+00	AF091711.1	NT	Homo sapiens partial TN gene for titin
4897 9001	15147	1.15	0.0E+00	AJ277692.1	NT	Homo sapiens COL4A6 genes for collagen, exon 44 and partial cds
4898 10005	15149	0.86	0.0E+00	D83562.1	NT	Homo sapiens farnesyldiphosphate synthase (farnesylyltransferase) (FDPS) mRNA
4899 10005	15149	1.58	0.0E+00	4503684	NT	Homo sapiens sialyltransferase 8 (alpha-N-acetylgalactosaminidase; alpha-2,8-sialyltransferase, GD3 synthase) (SIALT8) mRNA
4902 8918	14759	0.97	0.0E+00	4505652	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
4914 10024	16168	1.18	0.0E+00	AB026898.1	NT	Homo sapiens chitotriosidase 21 segment HS21_C084
4932 10042	15182	1.47	0.0E+00	AL163284.2	NT	Homo sapiens KIAA0806 gene product (KIAA0806) mRNA
4938 10048	15183	0.81	0.0E+00	7682219	NT	Homo sapiens #88723/1 Homo sapiens cDNA clone MAGE-B46547.3
4943 10055	15183	0.7	0.0E+00	AA205437.1	EST_HUMAN	#658506.5.1 Strategene neuroepithelial tumor (#88723/1) Homo sapiens cDNA clone MAGE-B46547.3
4950 10059	15187	1.45	0.0E+00	8922236	NT	Homo sapiens hypoxanthine-guanine phosphoribosyltransferase (HGPRT) mRNA
4951 8988	15144	0.83	0.0E+00	4507720	NT	Homo sapiens fibroblast structural protein 1, fibrillin (FBSP1) mRNA
4953 10061	15200	0.97	0.0E+00	4502388	NT	Homo sapiens nucleolar protein 21 mRNA, complete cds
4957 10068						Human endogenous retroviral DNA (-4), complete retroviral segment
4967 10076	15213	1.88	0.0E+00	AM10978.1	NT	Human endogenous retroviral DNA (-4), complete retroviral segment
4969 10077						601303728F1 NIH_3T3 cells cDNA clone IMAGE-3888118 6'
4973 10081	15218	6.21	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPL, DP1) (DSP) mRNA
4981 10089	15222	1.12	0.0E+00	AB028968.1	NT	Homo sapiens protein FLJ20477 (FLJ20477) mRNA
4985 10101	15231	2.04	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477) mRNA
4985 10101	15232	2.04	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477) mRNA
5007 10111	15240	0.78	0.0E+00	AA601248.1	EST_HUMAN	no14g99.91 NCI CGAP_Phen Homo sapiens cDNA clone IMAGE-1100704 3' similar to TR-E239140 E239140 SPALT PROTEIN;

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**Table 4**  
**Single Exon Probes Expressed in BT474 Cells**

Probe SEQ ID NO:	Exon ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5007	10111	15241	0.78	0.0E+00 AAB01248.1	EST_HUMAN	no1493_51 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5007	10111	15242	0.78	0.0E+00 AAB01246.1	EST_HUMAN	no1493_51 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5018	6403	10547	0.87	0.0E+00 AF198658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5018	10120	0.94	0.0E+00	4758226	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5023	10130	15259	1.39	0.0E+00 AF016705.1	NT	Homo sapiens EB-4P dimerization-protein ligase (UBE2A) gene, exon 3
5038	10138	1.18	0.0E+00 AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009	
5039	10141	44.4	0.0E+00 D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene	
6068	10171	15306	3.62	0.0E+00 X62898.1	NT	Bacillus amyloliquefaciens secB gene for levanasease (EC 2.4.1.10)
5070	10172	15307	0.72	0.0E+00 X72781.1	NT	Human endogenous retrovirus mRNA for gag protein
5102	10203	16342	1.17	0.0E+00	4667332	NT
5104	10205	15343	0.76	0.0E+00	5802055	NT
5108	10209	15346	1.06	0.0E+00 Y86032.1	NT	Human endogenous retrovirus-K_LTR U6 and gag gene
5120	10221	15355	0.62	0.0E+00	6502091	NT
5121	10222	15356	1.03	0.0E+00 AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
5138	10236	16372	1.31	0.0E+00	7682421	NT
5142	10242	16378	0.85	0.0E+00 AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBL1) mRNA, complete cds
5142	10242	16379	0.95	0.0E+00 AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBL1) mRNA, complete cds
5143	10243	15360	0.91	0.0E+00 JF71601.1	NT	Human zinc finger protein Zfp47 (Zfp47) mRNA, partial cds
5148	10246	15384	1.01	0.0E+00	4757889	NT
5147	10247	15386	0.88	0.0E+00 AF198668.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5151	10251	16380	0.85	0.0E+00	4829777	NT
5160	10260	0.94	0.0E+00 AB040846.1	NT	Homo sapiens mRNA for KIAA1613 protein, partial cds	
5179	10276	15414	1.32	0.0E+00 BE144726.1	EST_HUMAN	CMB-H10178-051089-084-805 HT0178 Homo sapiens cDNA

## CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human Breast comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 5,205 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
- 15 3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
- 20 4. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 5,206 - 10,317.
- 25 5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
- 30 6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
- 35 7. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid  
5 probes as claimed in any of claims 1 to 7, wherein at least  
50% of said single exon nucleic acid probes lack  
prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid  
10 probes as claimed in any of claims 1 to 8, wherein at least  
50% of said single exon nucleic acid probes lack  
homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid  
15 probes as claimed in any of claims 1 - 9 characterised in  
that said set of probes is addressably disposed upon a  
substrate.

11. A spatially-addressable set of single exon nucleic acid  
20 probes as claimed in claim 10 wherein said substrate is  
selected from glass, amorphous silicon, crystalline silicon  
and plastic.

12. A microarray comprising a spatially addressable set of  
25 single exon nucleic acid probes as claimed in any of claims  
1 - 11.

13. A single exon nucleic acid probe for measuring human  
gene expression in a sample derived from human Breast  
30 comprising a nucleotide sequence as set out in any of SEQ  
ID NOS.: 1 - 5,205 or a complementary sequence or a  
fragment thereof wherein said probe hybridizes at high  
stringency to a nucleic acid molecule expressed in the  
human Breast.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 5,206 - 10,317 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOS.: 10,318 - 15,438, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Breast.

16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

25

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human Breast, comprising:

5       contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human Breast; and then  
measuring the label detectably bound to each probe of  
10      said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

15      algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe, wherein said detectably labeled nucleic acids are derived from mRNA from the Breast of said eukaryote, said probe is  
20      a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

25

24. A method of assigning exons to a single gene, comprising:

30      identifying a plurality of exons from genomic sequence according to the method of claim 23; and then  
measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,  
35      wherein a common pattern of expression of said exons in

said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 10,317 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 10,317.

10 27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 10,318 - 15,438.

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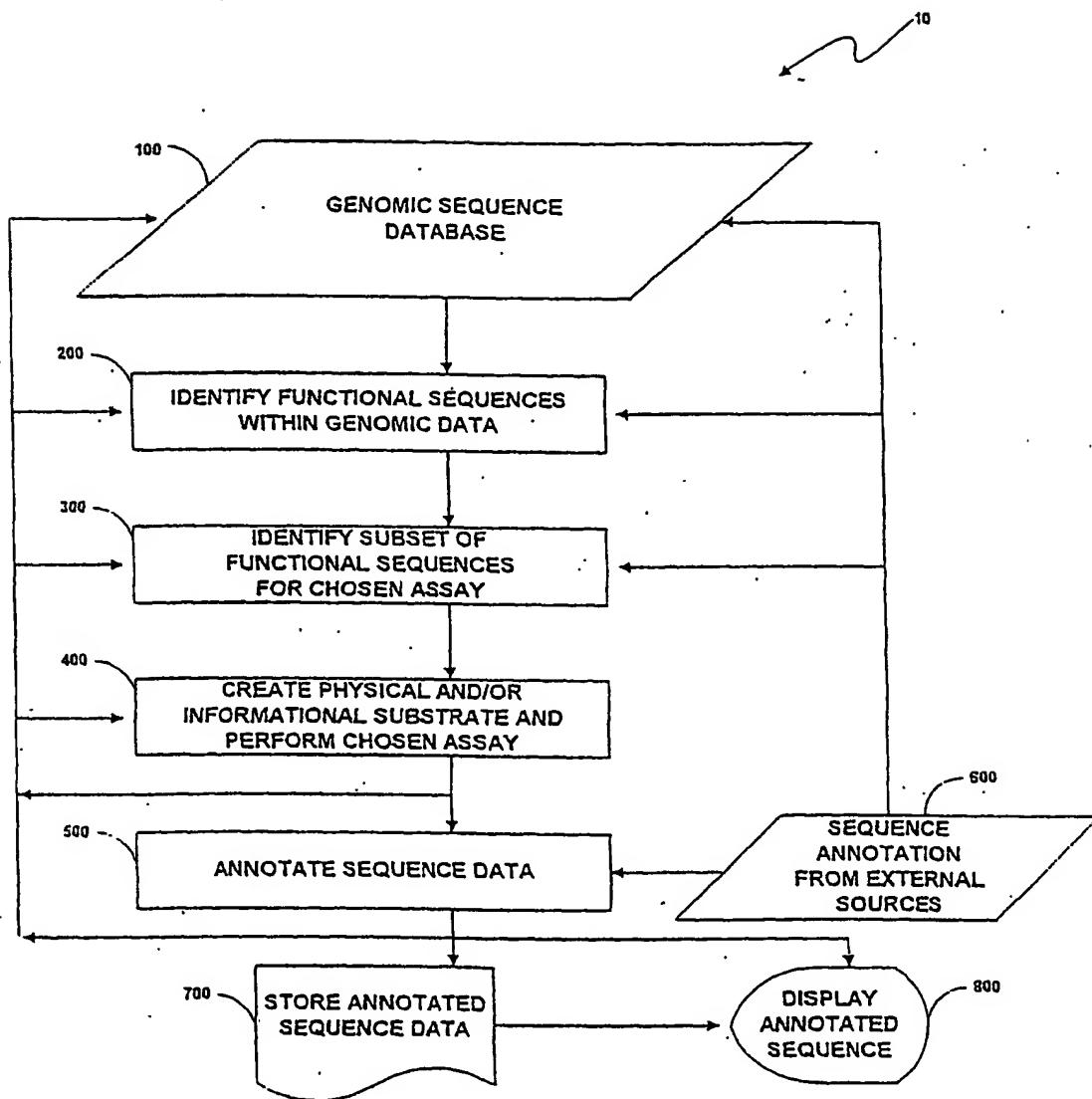


Fig. 1

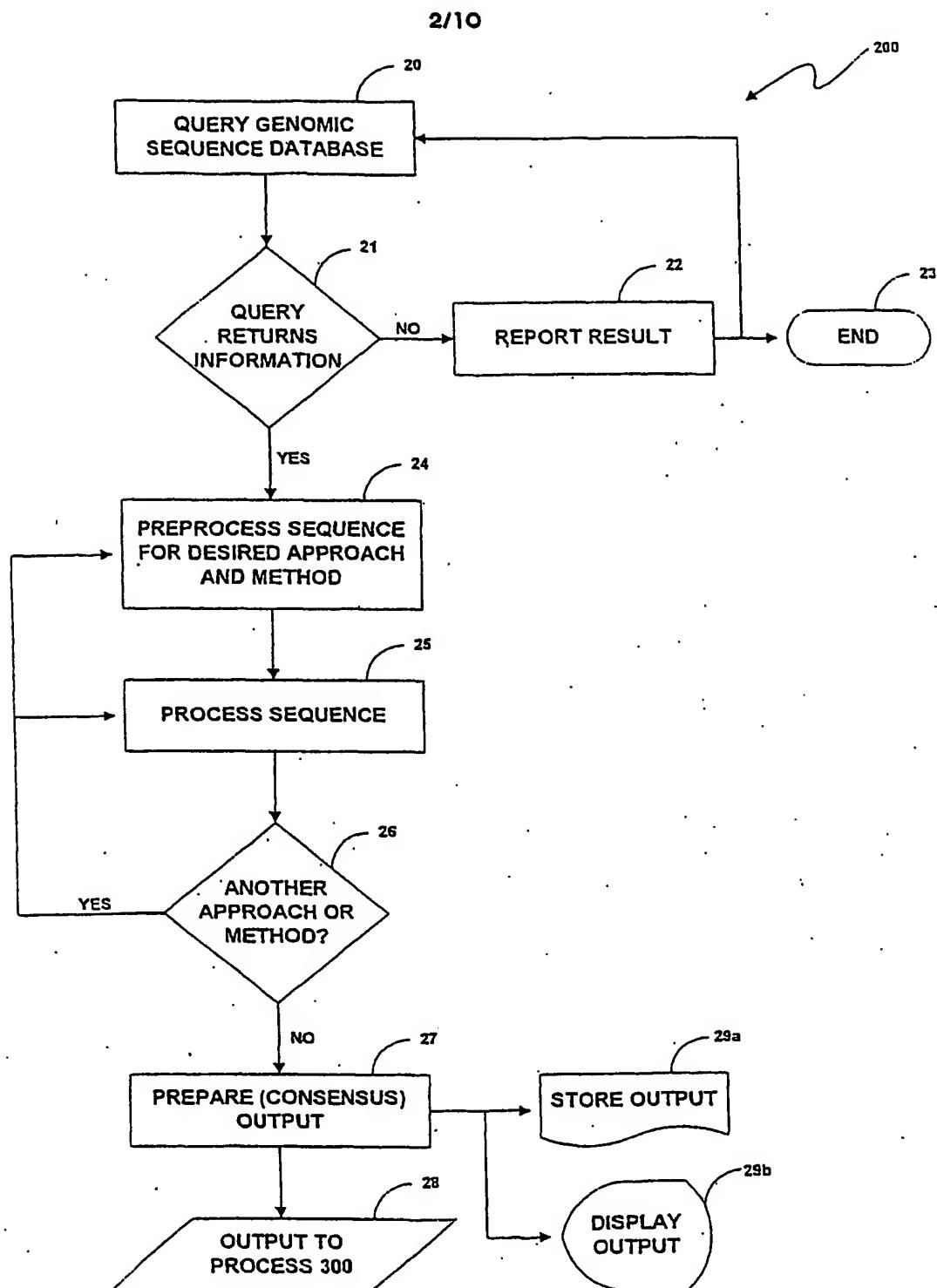


Fig. 2

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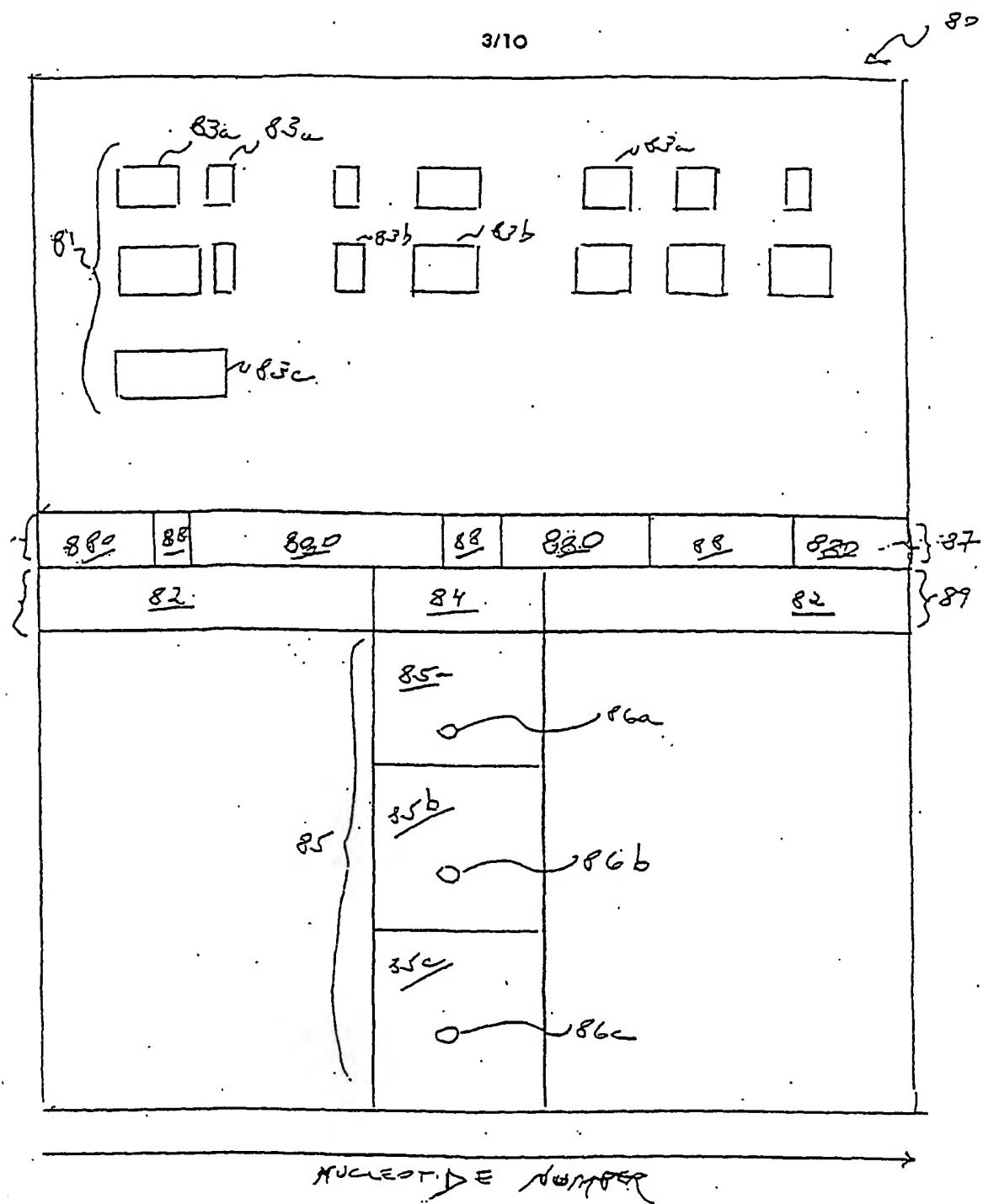


Fig. 3

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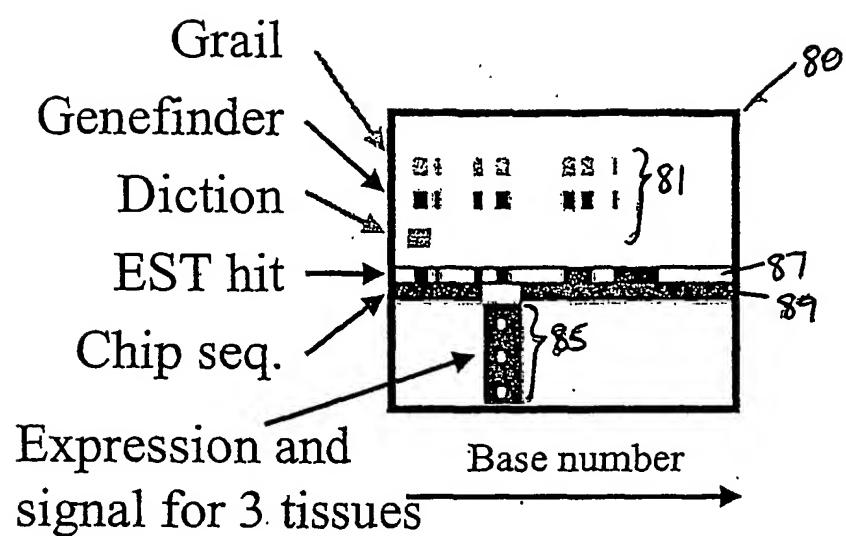


Fig. 4

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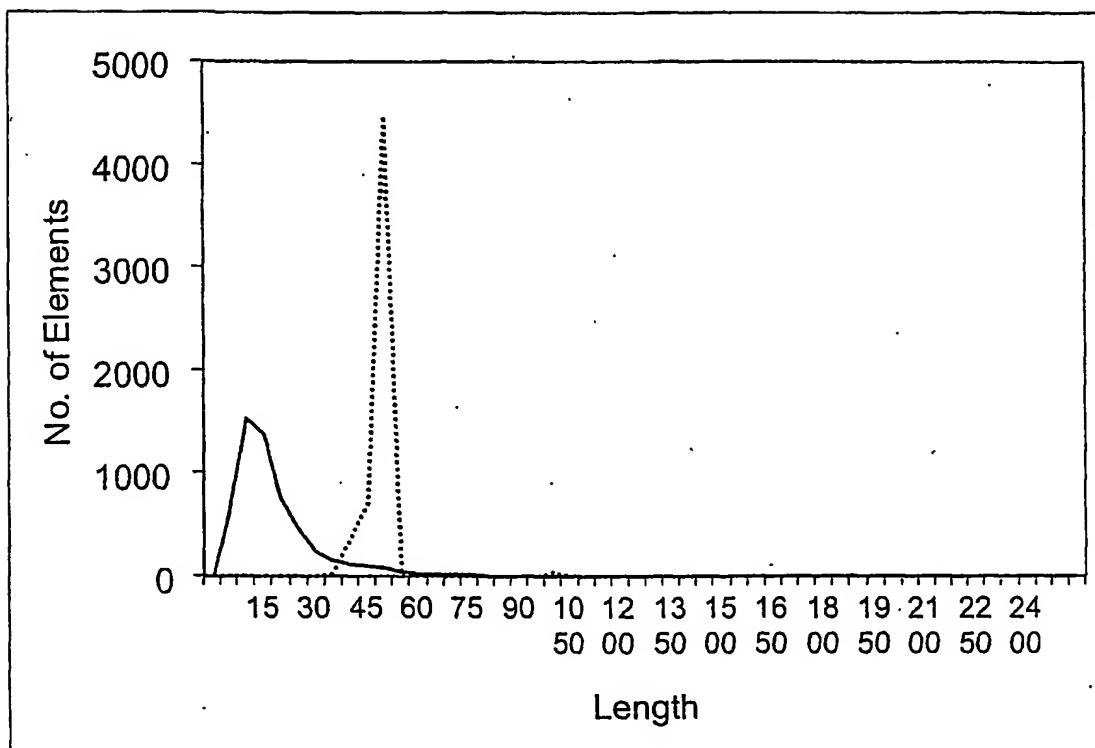


Fig. 5

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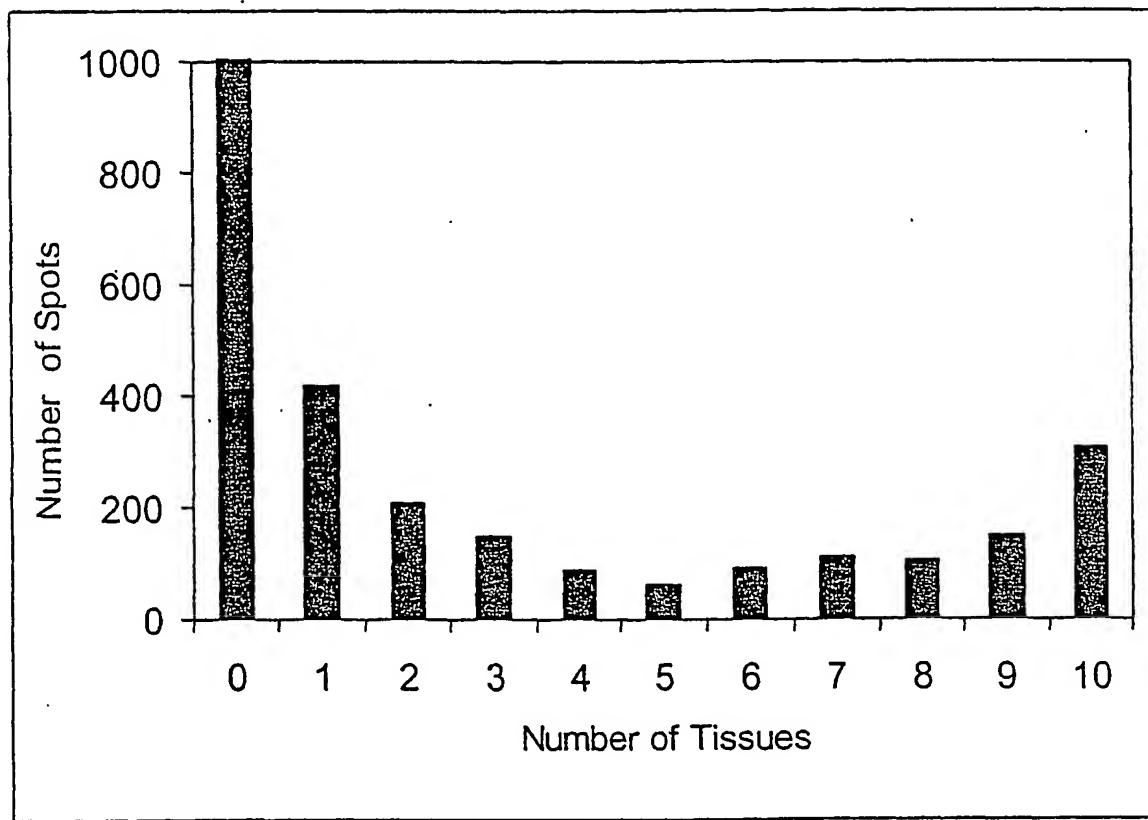
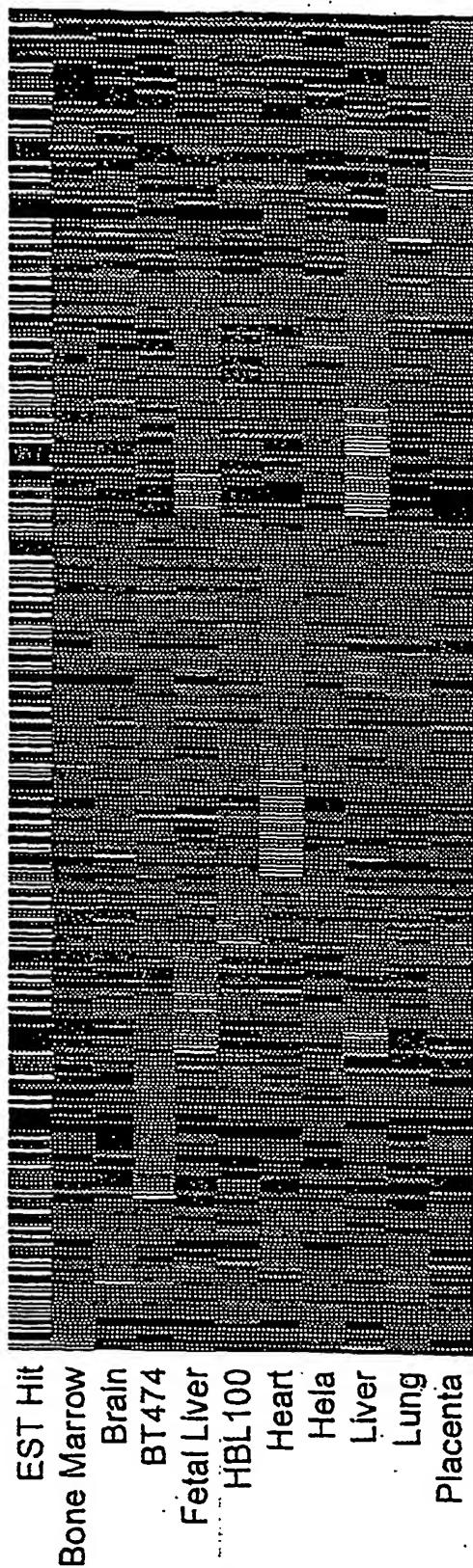
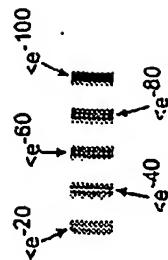
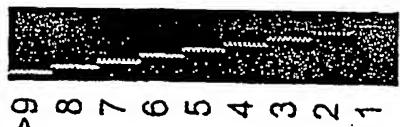


Fig. 6

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ratio legend

**Fig. 7b****Fig. 7c**

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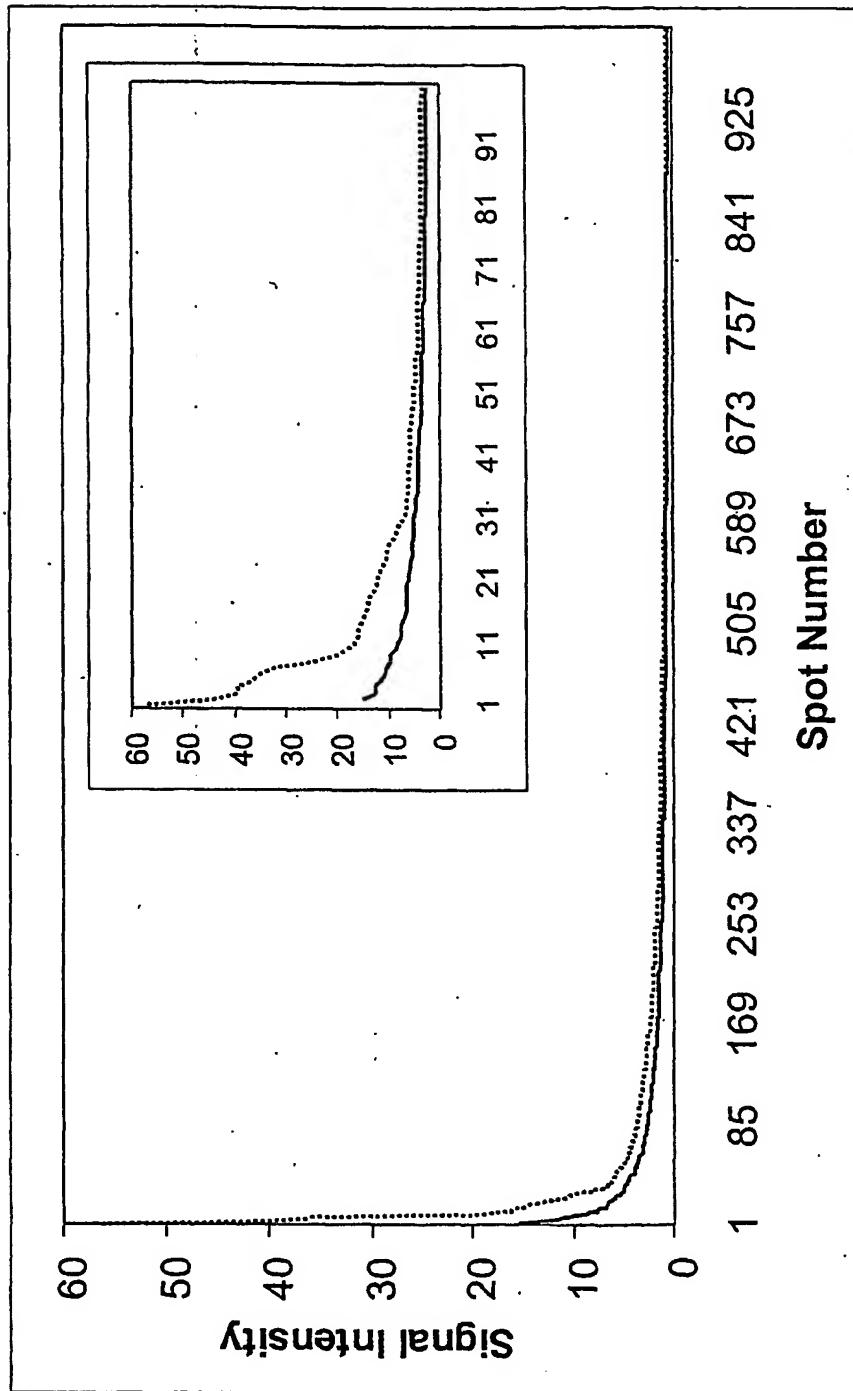


Fig. 8

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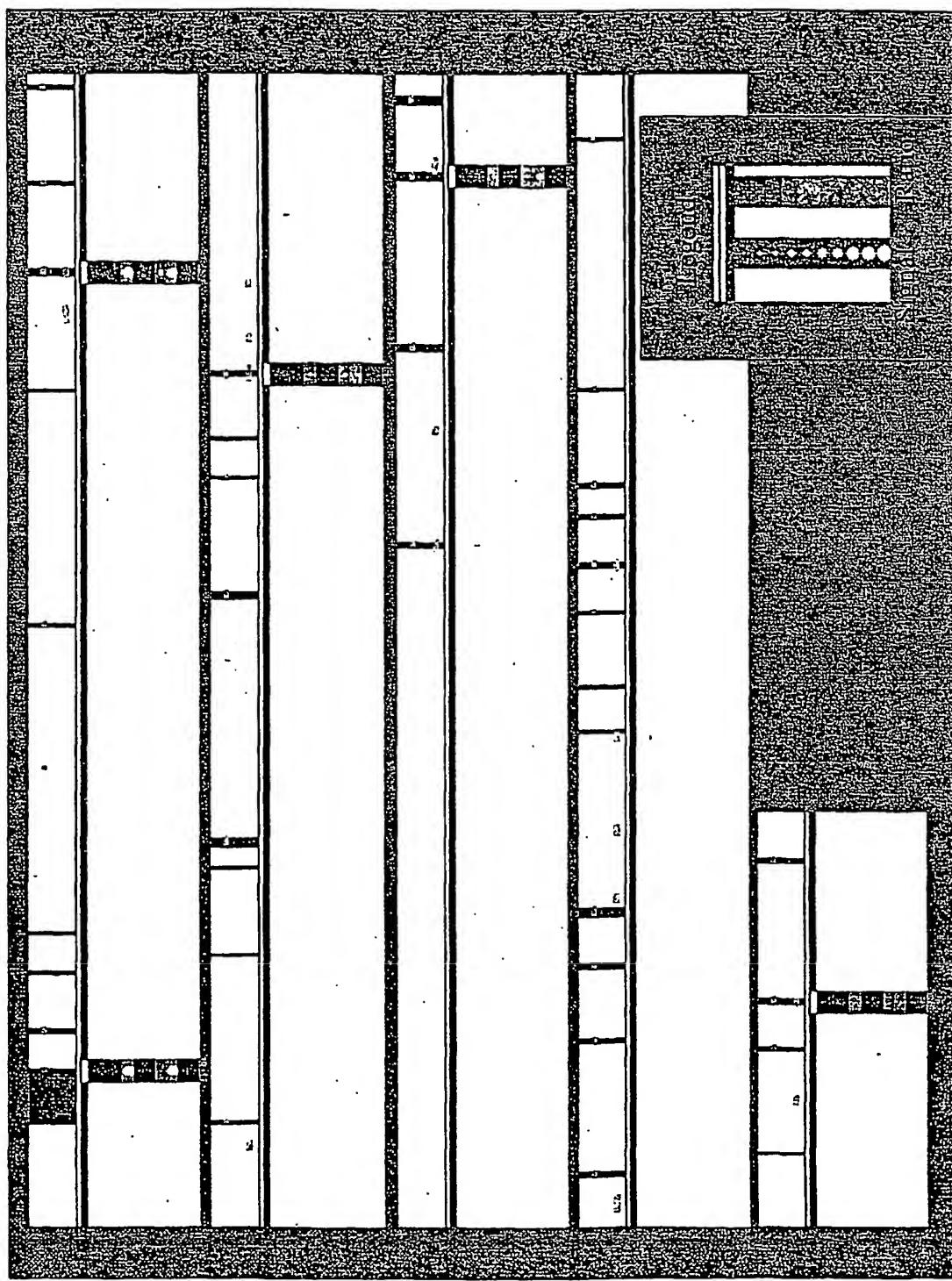
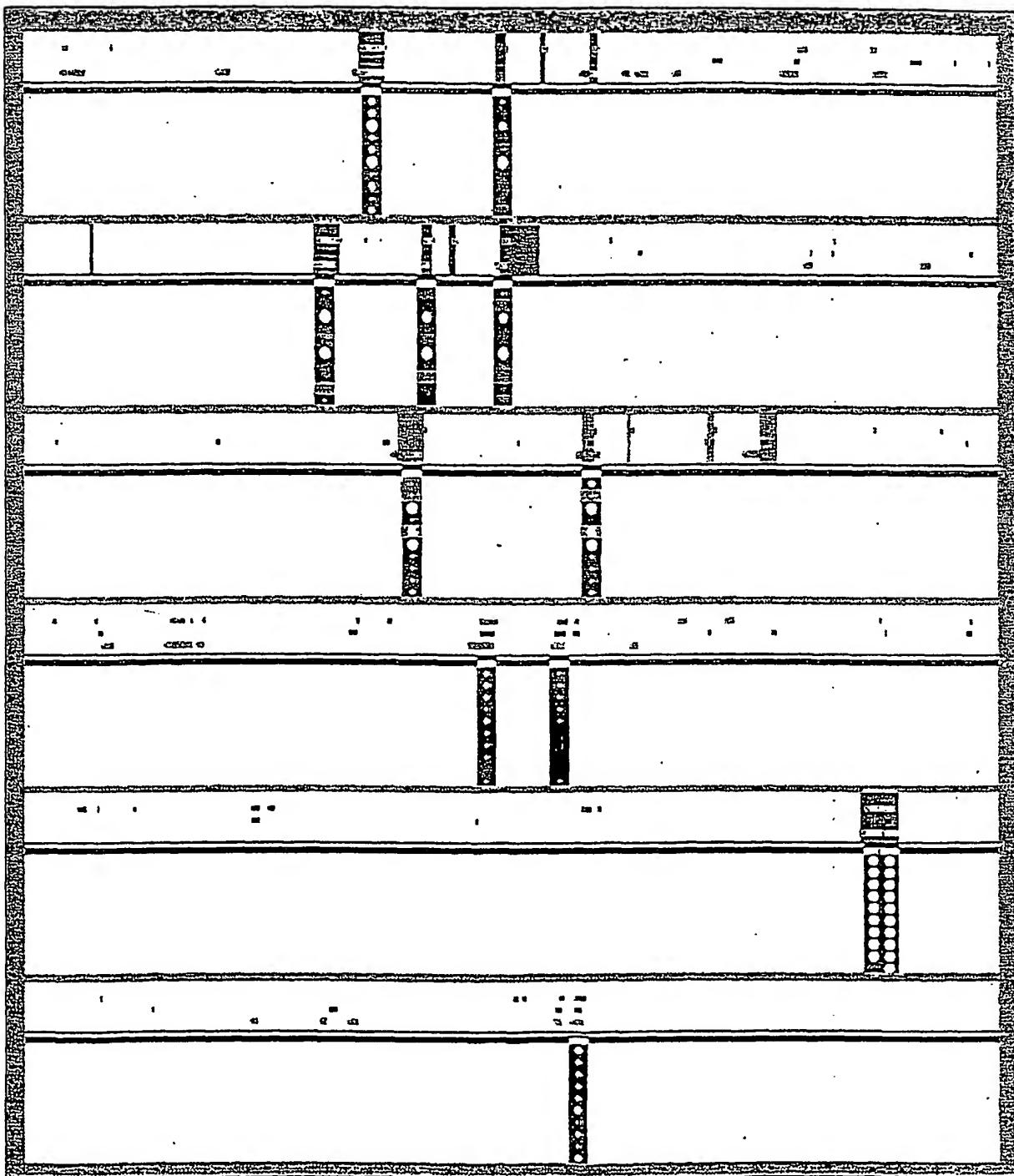


Fig. 9

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Fig. 10



(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
9 August 2001 (09.08.2001)

PCT

(10) International Publication Number  
**WO 01/057271 A3**

- (51) International Patent Classification<sup>7</sup>: C12Q 1/68    (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (21) International Application Number: PCT/US01/00662
- (22) International Filing Date: 30 January 2001 (30.01.2001)
- (25) Filing Language: English
- (26) Publication Language: English

- (30) Priority Data:
- |            |                                |    |
|------------|--------------------------------|----|
| 60/180,312 | 4 February 2000 (04.02.2000)   | US |
| 60/207,456 | 26 May 2000 (26.05.2000)       | US |
| 09/608,408 | 30 June 2000 (30.06.2000)      | US |
| 09/632,366 | 3 August 2000 (03.08.2000)     | US |
| 60/234,687 | 21 September 2000 (21.09.2000) | US |
| 60/236,359 | 27 September 2000 (27.09.2000) | US |
| 0024263.6  | 4 October 2000 (04.10.2000)    | GB |

- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(71) Applicant (*for all designated States except US*): AEROMICA, INC. [US/US]; 928 East Arques Avenue, Sunnyvale, CA 94085 (US).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): PENN, Sharron, G. [GB/US]; 617 South Delaware Street, San Mateo, CA 94402 (US). HANZEL, David, K. [US/US]; 988 Loma Verde Avenue, Palo Alto, CA 94303 (US). CHEN, Wensheng [CN/US]; 210 Easy Street, #25, Mountain View, CA 94043 (US). RANK, David, R. [US/US]; 117 El Dorado Commons, Fremont, CA 94539 (US).

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Published:

- with international search report
- with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

(88) Date of publication of the international search report:  
20 February 2003

(15) Information about Correction:

Previous Correction:

see PCT Gazette No. 49/2001 of 6 December 2001, Section II

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

WO 01/057271 A3

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND BT 474 CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human BT 474 cells is described. Also described are single exon nucleic acid probes expressed in the BT 474 cells and their use in methods for detecting gene expression.

## INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 01/00662

**A. CLASSIFICATION OF SUBJECT MATTER**  
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)  
IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, CHEM ABS Data, EMBASE, SCISEARCH, MEDLINE, EMBL

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL 'Online! 11 May 1999 (1999-05-11) HEILIG ET AL.: "Sequencing of the human chromosome 14" Database accession no. AL049837 XP002182997 abstract	13-21, 25
Y		1-12, 22-24, 26, 27
	—	—/—

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

\* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the International filing date
- "L" document which may throw doubts on priority, claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the International filing date but later than the priority date claimed

"T" later document published after the International filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"Z" document member of the same patent family

Date of the actual completion of the International search

Date of mailing of the International search report

07.08.2002

12 July 2002

Name and mailing address of the ISA  
European Patent Office, P.B. 5818 Patentlaan 2  
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Authorized officer

Bort, S

## INTERNATIONAL SEARCH REPORT

Int'l Application No  
PCT/US 01/00662

## C(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL 'Online! 14 November 1997 (1997-11-14) ADAMS ET AL.: "Use of a random BAC End sequence database for sequence-ready map building" Database accession no. B57793 XP002186124 abstract	13-21, 25
Y		1-12, 22-24, 26, 27
X	DATABASE EMBL 'Online! 9 May 1997 (1997-05-09) MARRA ET AL.: "The WashU-HHMI Mouse EST Project" Database accession no. AA414703 XP002205620 abstract	13-21, 25
Y		1-12, 22-24, 26, 27
X	DATABASE SWALL 'Online! 1 July 1997 (1997-07-01) "pro-pol-dutpase polyprotein (fragment)" Database accession no. 002711 XP002037954 abstract & BENIT ET AL.: "Cloning of a new murine endogenous retrovirus, MuERV-L, with strong similarity to the human HERV-L element with a gag coding sequence closely related to the Fv1 restriction gene" J. VIROL., vol. 71, 1997, page 5652	26, 27
Y	WO 98 30722 A (MACK DAVID H) 16 July 1998 (1998-07-16) the whole document	1-12, 22-24
Y	BURGE C ET AL: "Prediction of complete gene structure in human genomic DNA" JOURNAL OF MOLECULAR BIOLOGY, LONDON, GB, vol. 268, no. 1, 25 April 1997 (1997-04-25), pages 78-94, XP002109301 ISSN: 0022-2836 the whole document	1-12, 22-24, 26, 27
Y	CHURCH D M ET AL: "ISOLATION OF GENES FROM COMPLEX SOURCES OF MAMMALIAN GENOMIC DNA USING EXON AMPLIFICATION" NATURE GENETICS, NEW YORK, NY, US, vol. 6, 1994, pages 98-105, XP000608940 ISSN: 1061-4036 the whole document	1-12, 22-24, 26, 27

-/-

## INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 01/00662

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	LIPSHUTZ R J ET AL: "High density synthetic oligonucleotide arrays." NATURE GENETICS, (1999 JAN) 21 (1 SUPPL) 20-4. REF: 32 , XP002182912 the whole document _____	1-12

**INTERNATIONAL SEARCH REPORT**International application No.  
PCT/US 01/00662**Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)**

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2.  Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:  
see FURTHER INFORMATION sheet PCT/ISA/210
  
3.  Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)**

This International Searching Authority found multiple inventions in this International application, as follows:

see additional sheet

1.  As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
  
2.  As all searchable claims could be searched without effort justifying an additional fee; this Authority did not invite payment of any additional fee.
  
3.  As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:  
1-27 (all partially)
  
4.  No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

 The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

## Continuation of Box I.2

The following statements about the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject matter for which a search has been performed and identified as the first and second inventions in form 206 PCT.

Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising Seq. Id 1 or 2, as well as microarrays comprising said sets. In fact, the claims contain so many possible permutations, that a lack of conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole of the claimed scope impossible. Consequently, the search for the sets of probes comprising Seq. Id 1 or 2 has been limited to the Seq. Id as such.

Claims 1-3, 5, 6, 8-15 and 18-24 relate to portions or fragments of nucleic acids defined by Seq. Id. 1 or 2. The length or other similar characterizing features of the portions or fragments is not disclosed, bringing the total number of possible prior art sequences to exceptionally high numbers. The shorter the length, the higher the possibility that an overflow of, in principle unrelated, sequences are retrieved, making the establishment of a meaningful International Search Report impossible. For this reason the search has been limited to portions or fragments of Seq. Id. 1 or 2 having a significant minimum length and being supported by the description, namely at least 15 contiguous nucleotides (see claim 16).

Claims 15-21 relate to an extremely large number of nucleic acid probes. The probes are defined solely by their potential to code for peptide Seq. Id. 10326. However, due to the degeneracy of the genetic code, every peptide is potentially coded by an extremely high number of nucleic acid sequences. In fact, the claims contain so many potential nucleic acid sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole of the claimed scope impossible. The search has therefore been carried out for those parts of the claim which do appear to be clear and concise, namely the nucleic acid sequences disclosed in the application and identified as encoding the referred peptide in table 4 (Seq. Ids. 1 or 2 and 5214).

Likewise, claim 26, which refers to peptides encoded by Seq. Id. 1 or 2 and 5214, encompasses a high and undefined number of possible peptides. Besides three possible reading frames deriving from the encoding nucleic acid strand, as well as three additional reading frames deriving from the complementary nucleic acid strand, every possible fragment of these is being covered by the claim. This is due to the potential presence of stop codons within any of the six possible reading frames which can not be established a priori. Thus, claim 26 contains so many potential peptide sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole of the claimed scope impossible. Consequently, the search has been carried out for those parts of the claim which do appear to be

**FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210**

clear and concise, namely the peptide disclosed, identified by Seq. Id. 10326.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-27 (all partially)

A nucleic acid probe comprising SEQ ID 1, complementary sequences or fragments thereof (in particular comprising SEQ ID 5214). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by SEQ ID 1 (in particular the one defined by SEQ ID 10326).

Invention 2: claims 1-27 (all partially)

A nucleic acid probe comprising SEQ ID 2, complementary sequences or fragments thereof (in particular comprising SEQ ID 5214). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by SEQ ID 2 (in particular the one defined by SEQ ID 10326).

Inventions 3-5205: claims 1-27 (all partially)

A nucleic acid probe comprising SEQ ID n (where n ranges from 3-5205 according to the invention number above), complementary sequences or fragments thereof, in particular comprising the SEQ ID no. which is listed in the column "Exon SEQ ID no." in the same row that contains SEQ ID n in table 4. Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by SEQ ID n, in particular the one defined by the SEQ ID no in the column "ORF SEQ ID no" of the same row where SEQ ID n is listed.

## INTERNATIONAL SEARCH REPORT

Information on patent family members

b International Application No

PCT/US 01/00662

Patent document cited in search report	Publication date		Patent family member(s)		Publication date
WO 9830722	A 16-07-1998	AU	6035698 A		03-08-1998
		EP	0973939 A1		26-01-2000
		JP	2001508303 T		26-06-2001
		US	6303301 B1		16-10-2001
		WO	9830722 A1		16-07-1998
		US	2002028454 A1		07-03-2002
		US	2002039739 A1		04-04-2002